

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 11:48:47 ; Search time 72.4805 Seconds
(without alignments)
706.511 Million cell updates/sec

Title: us-10-733-563-12
Perfect score: 590
Sequence: 1 DVWMTQSLPLVTLGPAS.....CWQGTFFPYFGQTRLEIK 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A Geneseq 8:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*
 - 9: Geneseqp2005s:*
 - 10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	590	100.0	112	4	AAE06949 Humanised
2	590	100.0	112	4	AAU09921 Humanised
3	590	100.0	112	5	ABG75530 Humanised
4	590	100.0	112	5	AAO14973 Humanised
5	590	100.0	112	5	ADF98233 Humanised
6	590	100.0	112	8	ADQ99234 Humanised
7	590	100.0	112	9	AEBO9507 Humanised
8	590	100.0	112	9	AEC92165 Humanised
9	590	100.0	112	9	AED43684 Humanised
10	584	99.0	114	4	AAE07035 Humanised
11	584	99.0	114	8	ADQ99328 Humanised
12	584	99.0	114	9	AEBO9601 Humanised
13	577	97.8	112	4	AAE06950 Humanised
14	577	97.8	112	4	AAU09922 Humanised
15	577	97.8	112	5	ABG75531 Humanised
16	577	97.8	112	5	ADF98234 Humanised
17	577	97.8	112	8	ADQ99235 Humanised
18	577	97.8	112	9	AEBO9508 Humanised
19	577	97.8	112	9	AEC92166 Humanised
20	577	97.8	112	9	AED43685 Humanised
21	572	96.9	112	4	AAE07036 Humanised
22	572	96.9	112	4	AAU09925 Humanised
23	572	96.9	112	5	ABG75534 Humanised

24	572	96.9	112	5	ADF98237	Adf98237 Humanised
25	572	96.9	112	8	ADQ99329	Adq99329 Humanised
26	572	96.9	112	9	AEBO9602	Aeb09602 Humanized
27	572	96.9	112	9	AEC92169	Aec92169 Humanized
28	572	96.9	112	9	AED43688	Aed43688 Humanized
29	570	96.6	112	4	AAE06951	Aae06951 Humanised
30	570	96.6	112	4	AAU09923	Aau09923 Humanised
31	570	96.6	112	5	ABG75532	Abg75532 Humanised
32	570	96.6	112	5	ADF98235	Adf98235 Humanised
33	570	96.6	112	8	ADQ99236	Adq99236 Humanised
34	570	96.6	112	9	AEBO9509	Aeb09509 Humanized
35	570	96.6	112	9	AEC92167	Aec92167 Humanized
36	570	96.6	112	9	AED43686	Aed43686 Humanized
37	569	96.4	112	8	ADQ31290	Adq31290 Humanised
38	566	95.9	112	8	ADQ31289	Adq31289 Humanised
39	565	95.8	112	4	AAE06952	Aae06952 Humanised
40	565	95.8	112	4	AAU09924	Aau09924 Humanised
41	565	95.8	112	5	ABG75533	Abg75533 Humanised
42	565	95.8	112	5	AAO14976	Aao14976 Humanised
43	565	95.8	112	5	ADF98236	Adf98236 Humanised
44	565	95.8	112	8	ADQ99237	Adq99237 Humanised
45	565	95.8	112	9	AEBO9510	Aeb09510 Humanized

ALIGNMENTS

RESULT 1	
AAE06949	
ID	AAE06949 standard; protein; 112 AA.
XX	
AC	AAE06949;
XX	
DT	11-SEP-2003 (revised)
DT	16-OCT-2001 (first entry)
XX	
DE	Humanised murine 1D9 antibody kappa light chain variable region, 1D9RKA.
XX	
KW	Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus;
KW	HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
KW	inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
KW	multiple sclerosis; atherosclerosis; arteriosclerosis; stenosis; atheroma;
KW	anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
KW	fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;
KW	inflammatory glomerulopathy; vascular intervention; 1D9 antibody;
KW	neointimal hyperplasia; VK; kappa light chain variable region; 1D9RKA.
XX	
Mus sp.	
OS	Homo sapiens.
OS	Chimeric.
XX	
Key	Location/Qualifiers
Region	23..39
FT	/label= CDR1
FT	/note= "Complementarity determining region 1"
FT	
Region	55..61
FT	/label= CDR2
FT	/note= "Complementarity determining region 2"
FT	
Region	94..102
FT	/label= CDR3
FT	/note= "Complementarity determining region 3"
XX	
PN	WO200157226-A1.
XX	
PD	09-AUG-2001.
XX	
PF	02-FEB-2001; 2001WO-US003537.
XX	
PR	03-FEB-2000; 2000US-00497625.
XX	
PA	(MILL-) MILLENNIUM PHARM INC.
XX	

PI	Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;	
XX	WPI; 2001-488888/53.	
XX	Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated	
PT	disorder in a patient, comprises a binding specificity for CCR2, and a	
PT	non-human antigen binding region and human immunoglobulin.	
XX	Claim 61; Fig 11; 183pp; English.	
XX	The patent discloses a humanised antibody or its antigen-binding	
CC	fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),	
CC	comprising an antigen binding region of non-human origin and at least a	
CC	portion of an immunoglobulin of human origin. The humanised antibodies	
CC	are useful for inhibiting the interaction of a cell expressing CCR2. They	
CC	are useful for inhibiting or treating HIV infection. The proteins of the	
CC	invention are useful for inhibiting leukocyte trafficking, for treating	
CC	CCR2-mediated disorders such as inflammatory disorder, autoimmune	
CC	disorders such as rheumatoid arthritis and multiple sclerosis,	
CC	atherogenesis and atherosclerosis, and for inhibiting restenosis. They	
CC	are useful in therapy or diagnosis, and in the manufacture of a	
CC	medicament for treating CCR2 mediated disease. They are also useful for	
CC	treating allergy, anaphylaxis, malignancy, chronic and acute	
CC	inflammation, histamine and IgE- mediated allergic reaction, shock,	
CC	stenosis, allograft rejection, fibrotic disease, asthma, inflammatory	
CC	glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis	
CC	associated with vascular intervention, including angioplasty and/or stent	
CC	placement in a mammal. Humanised antibodies are also useful for	
CC	inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting	
CC	neointimal hyperplasia of a vessel in a mammal, preferably associated	
CC	with vascular intervention. The present sequence is humanised murine 1D9	
CC	antibody kappa light chain variable (VK) region, 1D9KA. (Updated on 11-	
CC	SEP-2003 to standardise OS field)	
XX	Sequence 112 AA;	
SQ	Sequence 112 AA;	
Query Match 100.0%; Score 590; DB 4; Length 112;		
Best Local Similarity 100.0%; Pred. No. 2.5e-46;		
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 DVVMTQSLPLVTLGQPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLYLVSKLD 60	
Db	1 DVVMTQSLPLVTLGQPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLYLVSKLD 60	
Qy	61 SGVPDRFSGSGGTDFTLKISRVEADVGYYVCWQGTTHFPYTFGQGTTRLEIK 112	
Db	61 SGVPDRFSGSGGTDFTLKISRVEADVGYYVCWQGTTHFPYTFGQGTTRLEIK 112	
RESULT 2		
AAU09921	AAU09921 standard; protein; 112 AA.	
ID	AAU09921;	
AC	AAU09921;	
DT	18-JUN-2002 (first entry)	
XX	Humanised 1D9 light chain variable region, 1D9RKA protein sequence.	
XX	Human; mouse; 1D9 light chain variable region; vasotropic;	
KW	antiinflammatory; collagen disease; immunosuppressive; antiasthmatic;	
KW	insulin-dependent diabetes mellitus; inflammatory bowel disease;	
KW	ulcerative colitis; HF-21/28; Graft rejection; allergic disease;	
KW	antipsoriatic; 1D9RKA; antiarthritis; nephrotropic; antithyroid;	
KW	restenosis; dermatological; anaphylaxis; cell adhesion inhibitor;	
KW	vascular injury; autoimmune disease; immunoglobulin;	
KW	complementarity determining region; CDR; CD18; CCR2; atherosclerosis;	
KW	mutant; mutein.	
XX	Homo sapiens.	
OS	Mus sp.	
OS	Synthetic.	
OS	Chimeric.	
XX	Key Region	Location/Qualifiers
XX	24..39	/note= "Complementarity determining region 1 (CDR1),
FT		grafted from mouse mAb 1D9 light chain sequence
FT		(AAU09918)"
FT	Region	55..61
FT		/note= "Complementarity determining region 2 (CDR2),
FT		grafted from mouse mAb 1D9 light chain sequence
FT		(AAU09918)"
FT	Region	94..102
FT		/note= "Complementarity determining region 3 (CDR3),
FT		grafted from mouse mAb 1D9 light chain sequence
FT		(AAU09918)"
FT	Misc-difference 112	/note= "Addition of Lys residue normally present in mouse
FT		mAb 1D9 sequence and absent in human antibody HF-21/28
FT		sequence (AAU09920)"
XX	WO200170266-A2.	
PN	27-SEP-2001.	
XX	15-MAR-2001; 2001WO-US008266.	
XX	17-MAR-2000; 2000US-00528267.	
XX	(MILL-) MILLENNIUM PHARM INC.	
XX	Horvath CJ, Rao PE;	
XX	WPI; 2001-607511/69.	
XX	Inhibiting stenosis or restenosis of a blood vessel following vascular	
PT	injury or angioplasty in a subject by administering agent which inhibits	
PT	recruitment or adhesion of neutrophils, mononuclear cells to injury site.	
XX	Claim 32; Fig 17; 108pp; English.	
PS	The present invention relates to a new method of inhibiting stenosis or	
CC	restenosis of a blood vessel following vascular injury in a subject. The	
CC	new method comprises administering to the subject agents which inhibit	
CC	the adhesion and/or recruitment of neutrophils and mononuclear cells to a	
CC	site of vascular injury by binding CD18 or CCR2. The method of the	
CC	invention inhibits stenosis or restenosis of a blood vessel following	
CC	vascular injury arising from a vascular intervention procedure such as	
CC	vascular by-pass or transplantation surgery. The method is also useful	
CC	for treating a subject having an inflammatory disease or condition	
CC	mediated by neutrophil and mononuclear cell activity e.g. asthma and	
CC	graft versus host disease. Chronic inflammatory diseases of the lung,	
CC	collagen diseases, and insulin-dependent diabetes mellitus can also be	
CC	treated. The method is further useful for treating inflammatory bowel	
CC	diseases, such as ulcerative colitis. Additional diseases or conditions	
CC	include inflammatory or allergic diseases and conditions, including	
CC	systemic anaphylaxis of hypersensitivity responses, drug allergies,	
CC	psoriasis and inflammatory dermatoses, autoimmune diseases such as	
CC	arthritis, graft rejection and other diseases including atherosclerosis.	
CC	The present sequence represents the variable region of one of several	
CC	humanised 1D9 light chains (AAU0921-AAU0925). These light chains were	
CC	used in the invention for the production of anti-CCR2 antibody or antigen	
CC	-binding fragment	
XX	Sequence 112 AA;	
SQ	Sequence 112 AA;	
Query Match 100.0%; Score 590; DB 4; Length 112;		
Best Local Similarity 100.0%; Pred. No. 2.5e-46;		
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 DVVMTQSLPLVTLGQPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLYLVSKLD 60	
Db	1 DVVMTQSLPLVTLGQPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLYLVSKLD 60	
Qy	61 SGVPDRFSGSGGTDFTLKISRVEADVGYYVCWQGTTHFPYTFGQGTTRLEIK 112	
Db	61 SGVPDRFSGSGGTDFTLKISRVEADVGYYVCWQGTTHFPYTFGQGTTRLEIK 112	

XX Hancock WW;
 XX WPI; 2002-351265/38.
 XX Inhibiting graft rejection, graft versus host disease or chronic
 XX rejection of a transplanted graft, involves administering a CCR2
 XX antagonist.
 XX Claim 26; Fig 1; 16pp; English.
 XX The invention comprises a method of inhibiting graft rejection, graft
 XX versus host disease or chronic rejection of a transplanted graft. The
 XX method involves administering an antagonist of CC chemokine receptor 2
 XX (CCR2) and optionally an immunosuppressive agent. The CCR2 antagonist may
 XX be an anti-CCR2 antibody (i.e. containing light and heavy chain
 XX complementarity determining regions from various non-human origins). CCR2
 XX is known to be involved in the rejection of transplanted grafts. The
 XX method of the invention is useful for inhibiting graft rejection -
 XX particularly allografts such as kidney, liver, lung, heart-lung,
 XX pancreas, bowel and heart. The method of the invention is also useful for
 XX inhibiting graft versus host disease and for inhibiting chronic rejection
 XX of a transplanted graft. The present amino acid sequence represents a
 XX humanised murine antibody light chain variable region (1D9Rka V_k)
 XX Sequence 112 AA;
 SQ Query Match 100.0%; Score 590; DB 5; Length 112;
 Best Local Similarity 100.0%; Pred. No. 2.5e-46;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVVMTQSPVLSPLPTLGQPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLIYLVSKLD 60
 DB 1 DVVMTQSPVLSPLPTLGQPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLIYLVSKLD 60
 QY 61 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCWQGTFFPYTFGGQTRLEIK 112
 DB 61 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCWQGTFFPYTFGGQTRLEIK 112
 RESULT 5
 ADF98233
 ID ADF98233 standard; protein; 112 AA.
 XX ADF98233;
 AC ADF98233;
 DT 26-FEB-2004 (first entry)
 XX Humanised 1D9 light chain variable region, 1D9RKA V kappa, SEQ ID 3.
 XX Immunosuppressive; CCR2 function inhibitor; graft rejection;
 KW graft versus host disease; CC chemokine receptor 2; CCR2;
 KW anti-CCR2 antibody.
 XX Synthetic.
 OS Mus musculus.
 OS Homo sapiens.
 XX WO200178653-A2.
 PN 25-OCT-2001.
 PD 13-APR-2001; 2001WO-US012139.
 XX 14-APR-2000; 2000US-00549448.
 PR (WILL-) MILLENNIUM PHARM INC.
 PA Hancock WW;
 PI WPI; 2002-017543/02.
 XX Inhibition of rejection of graft e.g. heart or graft versus host disease

PT involves use of CC chemokine receptor 2 inhibitor.
 XX Claim 26; Fig 1; 44pp; English.
 XX The present invention relates to a method for inhibiting graft rejection
 XX or graft versus host diseases. The method comprises administration of a
 XX CC chemokine receptor 2 (CCR2) function antagonist to a subject or
 XX recipient of a transplanted graft. The CCR2 function antagonist is an
 XX anti-CCR2 antibody or its antigen-binding fragment (ADF98233-ADF98237,
 XX ADF98240-ADF98249). The method is useful for inhibiting rejection,
 XX particularly chronic rejection of a graft, particularly an allograft of
 XX kidney, liver, lung, heart-lung, pancreas, bowel and heart, and for
 XX inhibiting graft versus host disease for a bone marrow graft.
 XX Sequence 112 AA;
 SQ Query Match 100.0%; Score 590; DB 5; Length 112;
 Best Local Similarity 100.0%; Pred. No. 2.5e-46;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVVMTQSPVLSPLPTLGQPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLIYLVSKLD 60
 DB 1 DVVMTQSPVLSPLPTLGQPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLIYLVSKLD 60
 QY 61 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCWQGTFFPYTFGGQTRLEIK 112
 DB 61 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCWQGTFFPYTFGGQTRLEIK 112
 RESULT 6
 ADQ89234
 ID ADQ89234 standard; protein; 112 AA.
 XX ADQ89234;
 AC ADQ89234;
 DT 21-OCT-2004 (first entry)
 XX Humanised immunoglobulin protein #1.
 XX Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;
 KW inflammatory disease; autoimmune disorder; graft rejection;
 KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;
 KW anti-HIV; virucide; antiarteriosclerotic.
 XX Synthetic.
 OS US2004151721-A1.
 PN 05-AUG-2004.
 PD 10-DEC-2003; 2003US-00733563.
 XX 19-OCT-2001; 2001US-0350166P.
 PR 26-JUN-2002; 2002US-0392364P.
 PR 17-OCT-2002; 2002US-00272899.
 XX (OKEE/) O'KEEFE T.
 PA (PONA/) PONATH P.
 XX O'keefe T, Ponath P;
 PI WPI; 2004-580175/56.
 DR New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,
 XX useful for diagnosing and/or treating inflammatory or autoimmune
 XX diseases, and HIV infection.
 XX Claim 5; SEQ ID NO 12; 128pp; English.
 XX The invention relates to humanised immunoglobulin heavy and light chains
 XX which have specificity for the CC-chemokine receptor 2 (CCR2) and an
 XX immunoglobulin or its antigen binding fragment comprising the chains. The
 XX humanised immunoglobulin or its antigen binding fragment preferably

CC comprises two heavy chains and two light chains. The humanised
 CC immunoglobulin and its heavy and light chains are useful for the
 CC diagnosis, prevention and/or treatment of diseases or conditions
 CC associated with aberrant expression or activity of the CCR2 polypeptide,
 CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV
 CC infection and atherosclerosis. This sequence represents a humanised
 CC immunoglobulin protein of the invention.

XX Sequence 112 AA;

Query Match 100.0%; Score 590; DB 8; Length 112;
 Best Local Similarity 100.0%; Pred. No. 2.5e-46;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVVMTQSPVLSPLPTLGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSKLD 60
 DB 1 DVVMTQSPVLSPLPTLGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSKLD 60
 QY 61 SGVDFRFGSGSGTDFTLKISRVEADVGVVYCWQGTTHFPYTFQGQTRLEIK 112
 DB 61 SGVDFRFGSGSGTDFTLKISRVEADVGVVYCWQGTTHFPYTFQGQTRLEIK 112

RESULT 7
 AEB09507
 ID AEB09507 standard; protein; 112 AA.

XX AEB09507;
 AC AEB09507;
 DT 08-SEP-2005 (first entry)
 XX Humanized ID9 kappa light chain variable region SEQ ID NO 12.
 DE antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;
 KW antibody engineering; therapeutic; diagnosis; inflammation;
 KW autoimmune disease; immune disorder; graft rejection; HIV infection;
 KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;
 KW light chain variable region.

OS Homo sapiens.
 OS Mus musculus.
 OS Synthetic.
 XX WO2005060368-A2.
 XX 07-JUL-2005.
 XX 10-DEC-2003; 2003WO-US039599.
 XX 10-DEC-2003; 2003WO-US039599.
 XX (MILL-) MILLENNIUM PHARM INC.

XX Okeefe T, Ponath P;
 XX WPI; 2005-488561/49.
 XX New humanized immunoglobulin or its antigen binding portion having
 PT binding specificity for CC-chemokine receptor 2 and having a heavy chain
 PT and light chain, for treating inflammatory diseases, HIV, and autoimmune
 PT diseases.

PS Claim 1; SEQ ID NO 12; 192pp; English.

XX The invention describes a humanized immunoglobulin (I) or its antigen
 CC binding portion having binding specificity for CC-chemokine receptor 2
 CC (CCR2) and having a heavy chain and a light chain, where the heavy chain
 CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)
 CC sequence, given in specification or its portion, and the light chain
 CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given
 CC in specification. Also described are: a humanized immunoglobulin heavy
 CC chain, or its antigen binding fragment, having binding specificity for
 CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the

CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized
 CC immunoglobulin light chain, or its antigen binding fragment, having
 CC binding specificity for CCR2 and comprising the amino acid sequence of
 CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)
 CC sequence, given in specification. The following are disclosed: isolated
 CC nucleic acid molecules comprising nucleic acid sequence encoding (i); a
 CC construct comprising nucleic acid molecule encoding (i); and host cell
 CC comprising the nucleic acid molecule. (i) Is useful as a therapeutic
 CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus
 CC reducing inflammatory response, for use in the treatment of diseases
 CC associated with leukocyte infiltration of tissue, e.g. in the treatment
 CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV
 CC infection and monocyte-mediated disorders such as atherosclerosis. (i) Is
 CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.
 CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel
 CC fluid), and for modulating binding function and/or leukocyte trafficking
 CC modulated by CCR2. This is the amino acid sequence of a humanized ID9
 CC kappa light chain variable region used in the creation of a humanized
 CC anti-CCR2-antibody.

XX Sequence 112 AA;

Query Match 100.0%; Score 590; DB 9; Length 112;
 Best Local Similarity 100.0%; Pred. No. 2.5e-46;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVVMTQSPVLSPLPTLGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSKLD 60
 DB 1 DVVMTQSPVLSPLPTLGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSKLD 60
 QY 61 SGVDFRFGSGSGTDFTLKISRVEADVGVVYCWQGTTHFPYTFQGQTRLEIK 112
 DB 61 SGVDFRFGSGSGTDFTLKISRVEADVGVVYCWQGTTHFPYTFQGQTRLEIK 112

RESULT 8
 AEC92165
 ID AEC92165 standard; protein; 112 AA.

XX AEC92165;
 AC AEC92165;
 DT 01-DEC-2005 (first entry)
 XX Humanized ID9 mAb light chain variable kappa region protein, 1D9RKA Vκ.
 DE Therapeutic; restenosis; vasotropic; cardiovascular disease; stenosis;
 KW pulmonary disease; respiratory-gen.; respiratory disease;
 KW inflammatory bowel disease; antiinflammatory; gastrointestinal-gen.;
 KW gastrointestinal disease; inflammation; allergy; antiallergic;
 KW immune disorder; autoimmune disease; immunosuppressive; graft rejection;
 KW inflammation; antiinflammatory; ID9; monoclonal antibody;
 KW humanized antibody; light chain variable region.

XX Mus sp.
 OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FT Region 24..39
 FT Region /note= "Complementarity determining region (CDR) 1"
 FT Region 55..61
 FT Region /note= "Complementarity determining region (CDR) 2"
 FT Region 94..102
 FT Region /note= "Complementarity determining region (CDR) 3"

XX US2005214299-A1.

XX 29-SEP-2005.
 XX 12-SEP-2003; 2003US-00662061.
 XX 17-MAR-2000; 2000US-00528267.
 PR 15-MAR-2001; 2001US-00809739.

XX (WILL-) MILLENNIUM PHARM INC.
 XX Horvath CJ, Rao PE;
 XX WPI; 2005-648726/66.
 XX
 XX Inhibiting stenosis in a human blood vessel, by administering an anti-
 PT CD18 antibody, which binds specifically with the CD18 portion of a
 PT mammalian protein which comprises CD18, where stenosis is inhibited in
 PT the vessel.
 XX
 XX Disclosure; SEQ ID NO 14; 56pp; English.
 XX
 XX The invention relates to a method of inhibiting stenosis or restenosis of
 CC a blood vessel following vascular injury, wherein the recruitment and/or
 CC adhesion of neutrophils and the adhesion and/or recruitment of
 CC mononuclear cells to a site of vascular injury is inhibited. The methods
 CC of the invention are useful for inhibiting stenosis or restenosis in a
 CC human blood vessel, inhibiting interaction of a leukocyte having a CD18-
 CC containing cell-surface protein with vascular endothelium in a human,
 CC assessing the presence of leukocytes associated with vascular stenosis in
 CC blood obtained from a human and alleviating a disorder associated with
 CC stenosis in a blood vessel of a human. The invention is useful for
 CC treating mastitis, cholangitis and cholecystitis, chronic inflammatory
 CC diseases of the lungs such as interstitial lung disease and idiopathic
 CC pulmonary disease, hypersensitivity pneumonitis, pancreatitis, insulin-
 CC dependent diabetes mellitus, inflammatory bowel disease such as Crohn's
 CC disease, ulcerative colitis and sprue, inflammatory or allergic diseases
 CC including anaphylaxis, psoriasis, dermatitis, eczema, atopic dermatitis
 CC and allergic rhinitis, autoimmune diseases including arthritis, multiple
 CC sclerosis, myasthenia gravis, juvenile onset diabetes and autoimmune
 CC thyroiditis, graft rejection and other diseases or conditions in which
 CC undesirable inflammatory responses are to be inhibited including
 CC atherosclerosis or myositis. The present sequence is humanized murine 1D9
 CC monoclonal antibody (mAb; also termed as LS132.1D9, ID9-2-121-3-6) light
 CC chain variable kappa region (Vk) protein.
 XX
 XX Sequence 112 AA;
 SQ
 Query Match 100.0%; Score 590; DB 9; Length 112;
 Best Local Similarity 100.0%; Pred. No. 2.5e-46;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVVMTQSLPLPVTLGQPASISCKSSQSLSDSGKTFLNWFQRPQGSPPRLIYLVSKLD 60
 DB 1 DVVMTQSLPLPVTLGQPASISCKSSQSLSDSGKTFLNWFQRPQGSPPRLIYLVSKLD 60
 QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYYVCWQGHFFPYTFGQGRLEIK 112
 DB 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYYVCWQGHFFPYTFGQGRLEIK 112
 RESULT 9
 AED43684
 ID AED43684 standard; protein; 112 AA.
 XX
 XX AED43684;
 XX
 XX 15-DEC-2005 (first entry)
 DT
 XX Humanized murine 1D9 antibody kappa light chain variable region 1D9RKA.
 XX
 XX pharmaceutical; anticholinergic; CCR2 receptor; monoclonal antibody;
 KW respiratory.Gen.; antinflammatory; inflammation; respiratory disease;
 KW antibody 1D9; humanized antibody.
 XX
 XX Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 XX WO2005094798-A2.
 PN
 XX

PD 13-OCT-2005.
 XX
 PF 22-MAR-2005; 2005WO-EP003005.
 XX
 XX 30-MAR-2004; 2004EP-00007635.
 PR
 XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 PA (BOEH) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.
 PA
 XX Paired M;
 PI
 XX WPI; 2005-714339/73.
 DR
 XX New pharmaceutical composition containing one or more anticholinergics
 PT and a CCR2 receptor antagonist, and optionally together with an
 PT excipient, useful for treating inflammatory or obstructive diseases of
 PT the respiratory tract.
 XX
 PS Claim 22; SEQ ID NO 3; 39pp; English.
 XX
 CC The invention relates to a pharmaceutical composition containing one or
 CC more anticholinergics and a CCR2 receptor antagonist optionally in the
 CC form of individual optical isomers, their mixtures or racemates, addition
 CC salts, solvates or hydrates, and optionally together with an excipient.
 CC The pharmaceutical composition comprises the anticholinergic that is
 CC selected from tiotropium salts, oxitropium salts or ipratropium salts,
 CC preferably tiotropium salts. The anticholinergic is present in the form
 CC of the chloride, bromide, iodide, methanesulfonate or para-
 CC toluenesulfonate, preferably in the form of the bromide. The CCR2
 CC antagonist is an antibody, which can compete with the CCR2 binding of the
 CC monoclonal antibody 1D9 (ATCC HB-12549). The pharmaceutical composition
 CC is useful for preparing a medicament for treating inflammatory or
 CC obstructive diseases of the respiratory tract. The anticholinergic and
 CC CCR2 antagonist are useful for preparing the pharmaceutical composition.
 CC The present sequence represents the kappa light chain variable (VK)
 CC region of a humanized murine 1D9 antibody.
 XX
 SQ Sequence 112 AA;
 Query Match 100.0%; Score 590; DB 9; Length 112;
 Best Local Similarity 100.0%; Pred. No. 2.5e-46;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVVMTQSLPLPVTLGQPASISCKSSQSLSDSGKTFLNWFQRPQGSPPRLIYLVSKLD 60
 DB 1 DVVMTQSLPLPVTLGQPASISCKSSQSLSDSGKTFLNWFQRPQGSPPRLIYLVSKLD 60
 QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYYVCWQGHFFPYTFGQGRLEIK 112
 DB 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYYVCWQGHFFPYTFGQGRLEIK 112
 RESULT 10
 AAEO7035
 ID AAEO7035 standard; protein; 114 AA.
 XX
 XX AAEO7035;
 XX
 XX 11-SEP-2003 (revised)
 DT
 XX 16-OCT-2001 (first entry)
 DT
 XX Humanised murine antibody light chain 1D9RKA protein.
 DE
 XX Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angiodysplasia; acquired immune deficiency syndrome; AIDS;
 KW inflammatory glomerulopathy; vascular intervention;
 XX neointimal hyperplasia; antibody 1D9 light chain; 1D9RKA.
 XX

OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX WO200157226-A1.
XX 09-AUG-2001.
XX 02-FEB-2001; 2001WO-US003537.
XX 03-FEB-2000; 2000US-00497625.
XX (MILL-) MILLENNIUM PHARM INC.
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;
XX WPI; 2001-488888/53.
XX N-PSDB; AAD13180.
XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated
PT disorder in a patient, comprises a binding specificity for CCR2, and a
PT non-human antigen binding region and human immunoglobulin.
XX Disclosure; Fig 24; 183pp; English.
XX The patent discloses a humanised antibody or its antigen-binding
CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),
CC comprising an antigen binding region of non-human origin and at least a
CC portion of an immunoglobulin of human origin. The humanised antibodies
CC are useful for inhibiting the interaction of a cell expressing CCR2. They
CC are useful for inhibiting or treating HIV infection. The proteins of the
CC invention are useful for inhibiting leukocyte trafficking, for treating
CC CCR2-mediated disorders such as inflammatory disorder, autoimmune
CC disorders such as rheumatoid arthritis and multiple sclerosis,
CC atherogenesis and atherosclerosis, and for inhibiting restenosis. They
CC are useful in therapy or diagnosis, and in the manufacture of a
CC medicament for treating CCR2 mediated disease. They are also useful for
CC treating allergy, anaphylaxis, malignancy, chronic and acute
CC inflammation, histamine and IgE-mediated allergic reaction, shock,
CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory
CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis
CC associated with vascular intervention, including angioplasty and/or stent
CC placement in a mammal. Humanised antibodies are also useful for
CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting
CC neointimal hyperplasia of a vessel in a mammal, preferably associated
CC with vascular intervention. The present sequence is humanised murine
CC antibody light chain region, 1D9RKA. (Updated on 11-SEP-2003 to
CC standardise OS field)
XX Sequence 114 AA;
Query Match 99.0%; Score 584; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 9e-46;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VVMTQSLSLPVTLGQPASISCKSSQSLSDGKTFNLNWFQORPGQSPRRLIYLVSKLDS 61
DB 2 VVMTQSLSLPVTLGQPASISCKSSQSLSDGKTFNLNWFQORPGQSPRRLIYLVSKLDS 61
QY 62 GVDPFRSGSGGTDFTLKISRVEAEDVGVYYCWQGTFFPYTFQGTRLEIK 112
DB 62 GVDPFRSGSGGTDFTLKISRVEAEDVGVYYCWQGTFFPYTFQGTRLEIK 112
RESULT 11
ADQ89328
ID ADQ89328 standard; protein; 114 AA.
XX AC ADQ89328;
XX 21-OCT-2004 (first entry)
XX Humanised immunoglobulin protein #10.

XX Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;
KW inflammatory disease; autoimmune disorder; graft rejection;
KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;
KW anti-HIV; virucide; antiarteriosclerotic.
XX Synthetic.
XX US2004151721-A1.
XX 05-AUG-2004.
XX 10-DEC-2003; 2003US-00733563.
XX 19-OCT-2001; 2001US-0350166P.
XX 26-JUN-2002; 2002US-0392364P.
XX 17-OCT-2002; 2002US-00272899.
XX (OKEE/) O'KEEFE T.
PA (PONA/) PONATH P.
XX O'keefe T, Ponath P;
XX WPI; 2004-580175/56.
XX N-PSDB; ADQ89320.
XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,
PT useful for diagnosing and/or treating inflammatory or autoimmune
PT diseases, and HIV infection.
XX Disclosure; SEQ ID NO 106; 128pp; English.
XX The invention relates to humanised immunoglobulin heavy and light chains
CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an
CC immunoglobulin or its antigen binding fragment comprising the chains. The
CC humanised immunoglobulin or its antigen binding fragment preferably
CC comprises two heavy chains and two light chains. The humanised
CC immunoglobulin and its heavy and light chains are useful for the
CC diagnosis, prevention and/or treatment of diseases or conditions
CC associated with aberrant expression or activity of the CCR2 polypeptide,
CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV
CC infection and atherosclerosis. This sequence represents a humanised
CC immunoglobulin protein of the invention.
XX Sequence 114 AA;
Query Match 99.0%; Score 584; DB 8; Length 114;
Best Local Similarity 100.0%; Pred. No. 9e-46;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VVMTQSLSLPVTLGQPASISCKSSQSLSDGKTFNLNWFQORPGQSPRRLIYLVSKLDS 61
DB 2 VVMTQSLSLPVTLGQPASISCKSSQSLSDGKTFNLNWFQORPGQSPRRLIYLVSKLDS 61
QY 62 GVDPFRSGSGGTDFTLKISRVEAEDVGVYYCWQGTFFPYTFQGTRLEIK 112
DB 62 GVDPFRSGSGGTDFTLKISRVEAEDVGVYYCWQGTFFPYTFQGTRLEIK 112
RESULT 12
AEB09601
ID AEB09601 standard; protein; 114 AA.
XX AC AEB09601;
XX 08-SEP-2005 (first entry)
XX Humanized light chain 1D9RKA.
XX antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;
KW antibody engineering; therapeutic; diagnosis; inflammation;
KW autoimmune disease; immune disorder; graft rejection; HIV infection;
KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;

KW light chain variable region.
 OS Synthetic.
 XX WO2005060368-A2.
 PN 07-JUL-2005.
 PD
 XX
 XX 10-DEC-2003; 2003WO-US039599.
 PF
 XX 10-DEC-2003; 2003WO-US039599.
 PR
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX O'Keefe T, Ponath P;
 PI WPI; 2005-488561/49.
 XX N-PSDB; AEB09593.
 DR
 XX New humanized immunoglobulin or its antigen binding portion having
 PT binding specificity for CC-chemokine receptor 2 and having a heavy chain
 PT and light chain, for treating inflammatory diseases, HIV, and autoimmune
 PT diseases.
 PT
 XX Disclosure; SEQ ID NO 106; 192pp; English.
 PS
 XX The invention describes a humanized immunoglobulin (I) or its antigen
 CC binding portion having binding specificity for CC-chemokine receptor 2
 CC (CCR2) and having a heavy chain and a light chain, where the heavy chain
 CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)
 CC sequence, given in specification or its portion, and the light chain
 CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given
 CC in specification. Also described are: a humanized immunoglobulin heavy
 CC chain, or its antigen binding fragment, having binding specificity for
 CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the
 CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized
 CC immunoglobulin light chain, or its antigen binding fragment, having
 CC binding specificity for CCR2 and comprising the amino acid sequence of
 CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)
 CC sequence, given in specification. The following are disclosed: isolated
 CC nucleic acid molecules comprising nucleic acid sequence encoding (I); a
 CC construct comprising nucleic acid molecule encoding (I); and host cell
 CC comprising the nucleic acid molecule. (I) Is useful as a therapeutic
 CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus
 CC reducing inflammatory response, for use in the treatment of diseases
 CC associated with leukocyte infiltration of tissue, e.g. in the treatment
 CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV
 CC infection and monocyte-mediated disorders such as atherosclerosis. (I) Is
 CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.
 CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel
 CC fluid), and for modulating binding function and/or leukocyte trafficking
 CC modulated by CCR2. This is the amino acid sequence of humanized light
 CC chain 1D9RKB.
 XX
 SQ Sequence 114 AA;
 Query Match 99.0%; Score 584; DB 9; Length 114;
 Best Local Similarity 100.0%; Pred. No. 9e-46;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VVMTQSPVLTIGQPASISCKSSQSLDSDGKTFLNWFQQRPGSGPRRLIYLVSKLDS 61
 DB 2 VVMTQSPVLTIGQPASISCKSSQSLDSDGKTFLNWFQQRPGSGPRRLIYLVSKLDS 61
 QY 62 GVPDFRFGSGSGDTFTLKISRVEAEDVGVYCYWGTHFPYTFQGGTRLEIK 112
 DB 62 GVPDFRFGSGSGDTFTLKISRVEAEDVGVYCYWGTHFPYTFQGGTRLEIK 112
 RESULT 13
 AAE06950
 ID AAE06950 standard; protein; 112 AA.
 XX

AC AAE06950;
 XX
 DT 11-SEP-2003 (revised)
 DT 16-OCT-2001 (first entry)
 XX
 DE Humanised murine 1D9 antibody kappa light chain variable region, 1D9RKB.
 XX
 KW Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherosclerosis; restenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;
 KW inflammatory glomerulopathy; vascular intervention; 1D9 antibody.
 KW neointimal hyperplasia; VK; kappa light chain variable region; 1D9RKB.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 OS
 XX Key Location/Qualifiers
 FH Region 23..39
 FT /label= CDR1
 FT /note= "Complementarity determining region 1"
 FT Region 55..61
 FT /label= CDR2
 FT /note= "Complementarity determining region 2"
 FT Region 94..102
 FT /label= CDR3
 FT /note= "Complementarity determining region 3"
 XX
 PN WO200157226-A1.
 XX
 XX 09-AUG-2001.
 PD
 XX 02-FEB-2001; 2001WO-US003537.
 PF
 XX 03-FEB-2000; 2000US-00497625.
 PR
 XX (MILL-) MILLENNIUM PHARM INC.
 XX
 XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'Keefe T;
 XX WPI; 2001-488888/53.
 DR
 XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated
 PT disorder in a patient, comprises a binding specificity for CCR2, and a
 PT non-human antigen binding region and human immunoglobulin.
 XX
 PS Claim 61; Fig 11; 183pp; English.
 XX
 CC The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),
 CC comprising an antigen binding region of non-human origin and at least a
 CC portion of an immunoglobulin of human origin. The humanised antibodies
 CC are useful for inhibiting the interaction of a cell expressing CCR2. They
 CC are useful for inhibiting or treating HIV infection. The proteins of the
 CC invention are useful for inhibiting leukocyte trafficking, for treating
 CC CCR2-mediated disorders such as inflammatory disorder, autoimmune
 CC disorders such as rheumatoid arthritis and multiple sclerosis,
 CC atherogenesis and atherosclerosis, and for inhibiting restenosis. They
 CC are useful in therapy or diagnosis, and in the manufacture of a
 CC medicament for treating CCR-2 mediated disease. They are also useful for
 CC treating allergy, anaphylaxis, malignancy, chronic and acute
 CC inflammation, histamine and IgE-mediated allergic reaction, shock,
 CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory
 CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis
 CC associated with vascular intervention, including angioplasty and/or stent
 CC placement in a mammal. Humanised antibodies are also useful for
 CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting
 CC neointimal hyperplasia of a vessel in a mammal, preferably associated
 CC with vascular intervention. The present sequence is humanised murine 1D9

CC antibody kappa light chain variable (VK) region, 1D9RKB. (Updated on 11-SEP-2003 to standardise OS field)

XX SEP-2003 to standardise OS field

SQ Sequence 112 AA;

Query Match 97.8%; Score 577; DB 4; Length 112;
 Best Local Similarity 98.2%; Pred. No. 3.9e-45;
 Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DVVMTQSPVLTGLQPASISCKSSQSLDSDGKTFNLNWFQRPQSPRLIYLVSKLD 60
 |||||
 Db 1 DVVMTQSPVLTGLQPASISCKSSQSLDSDGKTFNLNWFQRPQSPRLIYLVSKLD 60
 |||||

Qy 61 SGVPDRFSGSGGTFTLKISRVEAEDVGVYVCWQGTFFPYTFGGQTRLEIK 112
 |||||
 Db 61 SGVPDRFSGSGGTFTLKISRVEAEDVGVYVCWQGTFFPYTFGGQTRLEIK 112
 |||||

RESULT 14
 AAU09922
 ID AAU09922 standard; protein; 112 AA.
 AC AAU09922;
 XX

DT 18-JUN-2002 (first entry)
 XX

DE Humanised 1D9 light chain variable region, 1D9RKB protein sequence.
 XX

KW Human; mouse; 1D9 light chain variable region; vasotropic;
 KW antiinflammatory; collagen disease; immunosuppressive; antiasthmatic;
 KW insulin-dependent diabetes mellitus; inflammatory bowel disease;
 KW ulcerative colitis; HF-21/28; graft rejection; allergic disease;
 KW antiporiatic; 1D9RKB; antiarthritic; nephrotropic; antithyroid;
 KW restenosis; dermatological; anaphylaxis; cell adhesion inhibitor;
 KW vascular injury; autoimmune disease; immunoglobulin; atherosclerosis;
 KW complementarity determining region; CDR; CD18; CCR2; atherosclerosis;
 KW mutant; mutein.
 XX

OS Homo sapiens.
 OS Mus sp.
 OS Synthetic.
 OS Chimeric.
 XX

Key Location/Qualifiers
 FH 24. .39
 FT /note= "Complementarity determining region 1 (CDR1),
 FT grafted from mouse mAb 1D9 light chain sequence
 FT (AAU09918)"
 FT Misc-difference 41
 FT /note= "Substitution of Phe residue normally present in
 FT human HF-21/28 sequence (AAU09920) by Leu residue
 FT normally present in mouse mAb 1D9 light chain sequence
 FT (AAU09918)"
 FT Misc-difference 42
 FT /note= "Substitution of Gln residue normally present in
 FT human HF-21/28 sequence (AAU09920) by Leu residue
 FT normally present in mouse mAb 1D9 light chain sequence
 FT (AAU09918)"
 FT Region 55. .61
 FT /note= "Complementarity determining region 2 (CDR2),
 FT grafted from mouse mAb 1D9 light chain sequence
 FT (AAU09918)"
 FT Region 94. .102
 FT /note= "Complementarity determining region 3 (CDR3),
 FT grafted from mouse mAb 1D9 light chain sequence
 FT (AAU09918)"
 FT Misc-difference 112
 FT /note= "Addition of Lys residue normally present in mouse
 FT mAb 1D9 sequence and absent in human antibody HF-21/28
 FT sequence (AAU09920)"
 XX
 PN WO200170266-A2.
 XX

PD 27-SEP-2001.
 XX
 PF 15-MAR-2001; 2001WO-US008266.
 XX
 PR 17-MAR-2000; 2000US-00528267.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 XX Horvath CJ, Rao PE;
 PI WPI; 2001-607511/69.
 XX
 DR Inhibiting stenosis or restenosis of a blood vessel following vascular
 PT injury or angioplasty in a subject by administering agent which inhibits
 PT recruitment or adhesion of neutrophils, mononuclear cells to injury site.
 XX
 XX Claim 32; Fig 17; 108pp; English.
 XX

CC The present invention relates to a new method of inhibiting stenosis or
 CC restenosis of a blood vessel following vascular injury in a subject. The
 CC new method comprises administering to the subject agents which inhibit
 CC the adhesion and/or recruitment of neutrophils and mononuclear cells to a
 CC site of vascular injury by binding CD18 or CCR2. The method of the
 CC invention inhibits stenosis or restenosis of a blood vessel following
 CC vascular injury arising from a vascular intervention procedure such as
 CC for treating a subject having an inflammatory disease or condition
 CC mediated by neutrophil and mononuclear cell activity e.g. asthma and
 CC graft versus host disease. Chronic inflammatory diseases of the lung,
 CC collagen diseases, and insulin-dependent diabetes mellitus can also be
 CC treated. The method is further useful for treating inflammatory bowel
 CC diseases, such as ulcerative colitis. Additional diseases or conditions
 CC include inflammatory or allergic diseases and conditions, including
 CC systemic anaphylaxis of hypersensitivity responses, drug allergies,
 CC psoriasis and inflammatory dermatoses, autoimmune diseases such as
 CC arthritis, graft rejection and other diseases including atherosclerosis.
 CC The present sequence represents the variable region of one of several
 CC humanised 1D9 light chains (AAU09921-AAU09925). These light chains were
 CC used in the invention for the production of anti-CCR2 antibody or antigen
 CC -binding fragment
 XX

SQ Sequence 112 AA;
 Query Match 97.8%; Score 577; DB 4; Length 112;
 Best Local Similarity 98.2%; Pred. No. 3.9e-45;
 Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DVVMTQSPVLTGLQPASISCKSSQSLDSDGKTFNLNWFQRPQSPRLIYLVSKLD 60
 |||||
 Db 1 DVVMTQSPVLTGLQPASISCKSSQSLDSDGKTFNLNWFQRPQSPRLIYLVSKLD 60
 |||||

Qy 61 SGVPDRFSGSGGTFTLKISRVEAEDVGVYVCWQGTFFPYTFGGQTRLEIK 112
 |||||
 Db 61 SGVPDRFSGSGGTFTLKISRVEAEDVGVYVCWQGTFFPYTFGGQTRLEIK 112
 |||||

RESULT 15
 ABG75531
 ID ABG75531 standard; protein; 112 AA.
 XX
 AC ABG75531;
 XX
 DT 16-APR-2003 (first entry)
 XX

DE Humanised mouse mAb 1D9 light chain variable region, 1D9RKBVK.
 XX

KW Mouse; stenosis; restenosis; blood vessel; vascular injury; antibody;
 KW antigen binding fragment; cellular adhesion molecule; adhesion;
 KW recruitment; neutrophil; antagonist; CCR2; mononuclear cell; angioplasty;
 KW percutaneous transluminal coronary angioplasty; PTCA; stent;
 KW vascular by-pass surgery; vascular grafting; endarterectomy; atherectomy;
 KW endovascular stenting; prosthetic valve; transplantation;
 KW inflammatory disease; mastitis; vaginitis; cholecystitis;

KW chronic bronchitis; asthma; graft-versus-host disease;
 KW chronic inflammatory disease; hypersensitivity pneumonitis;
 KW collagen disease; sarcoidosis; idiopathic; pancreatitis; HF-21/28;
 KW insulin dependent; diabetes mellitus; inflammatory bowel disease;
 KW Crohn's disease; allergic disease; psoriasis; atopic dermatitis; human;
 KW allergic rhinitis; autoimmune disease; arthritis; multiple sclerosis;
 KW graft rejection; atherosclerosis; myositis; therapy; ID9; ID9RKBVK;
 KW light chain variable region; VK; complementarity determining region; CDR;
 KW mutant; mutein.

XX Mus sp.
 OS Homo sapiens.
 OS Synthetic.

PH Key Location/Qualifiers
 FT Region 24. .39
 FT /note= "Mouse complementarity determining region 1
 FT (CDR1)"
 FT Misc-difference 41. .42
 FT /note= "Leu's derived from the mouse ID9 mAb sequence"
 FT Region 55. .61
 FT /note= "Mouse complementarity determining region 2
 FT (CDR2)"
 FT Region 94. .102
 FT /note= "Mouse complementarity determining region 3
 FT (CDR3)"
 FT Misc-difference 112
 FT /note= "Lys derived from the mouse ID9 mAb sequence"

FT US2002106369-A1.

PN 08-AUG-2002.

XX 15-MAR-2001; 2001US-00809739.

XX 17-MAR-2000; 2000US-00528267.

XX (MILL-) MILLENNIUM PHARM INC.

XX Horvath CJ, Rao PE;

PI WPI; 2002-697861/75.

XX Inhibiting (re)stenosis of blood vessel following vascular injury, by
 PT administering first and second agents that inhibit adhesion and/or
 PT recruitment of neutrophils and mononuclear cells, respectively to site of
 PT vascular injury.

XX Claim 32; Fig 17; 59pp; English.

XX The invention discloses a method for inhibiting stenosis or restenosis of
 CC a blood vessel following vascular injury in a subject. The method
 CC involves administering to the subject a first therapeutic agent, which
 CC comprises an antibody or its antigen binding fragment which binds a
 CC cellular adhesion molecule, that inhibits the adhesion and/or recruitment
 CC of neutrophils to a site of vascular injury and a second therapeutic
 CC agent, which comprises an antagonist of CCR2 function, that inhibits
 CC adhesion and/or recruitment of mononuclear cells to a site of vascular
 CC injury. The vascular injury arises from a vascular intervention procedure
 CC such as angioplasty (e.g. percutaneous transluminal coronary angioplasty
 CC (PTCA) or angioplasty including placement of a stent), vascular by-pass
 CC surgery, vascular grafting, endarterectomy, atherectomy, endovascular
 CC stenting, insertion of a prosthetic valve and transplantation of organs,
 CC tissues or cells. The method is also useful for treating inflammatory
 CC diseases or conditions mediated by early neutrophil activity and later
 CC mononuclear cell activity. Preferably, the method is useful for treating
 CC a subject having mastitis, vaginitis, cholecystitis, chronic bronchitis,
 CC asthma and graft-versus-host disease, chronic inflammatory disease of
 CC lung, hypersensitivity pneumonitis, collagen diseases, sarcoidosis and
 CC other idiopathic conditions, pancreatitis and insulin dependant diabetes
 CC mellitus. The method is also useful for treating inflammatory bowel
 CC disease, Crohn's disease, inflammatory or allergic diseases (such as
 CC psoriasis, atopic dermatitis and allergic rhinitis), autoimmune diseases

CC (such as arthritis and multiple sclerosis), graft rejection,
 CC atherosclerosis and myositis. The method enables simultaneous inhibition
 CC of neutrophil and mononuclear cell participation in response to vascular
 CC injury or inhibition of neutrophil participation followed by inhibition
 CC of mononuclear cell participation, and thus provides superior therapy for
 CC inhibiting stenosis or restenosis following vascular injury. The sequence
 CC presented is the humanised mouse monoclonal antibody (mAb), ID9, light
 CC chain variable region (VK), ID9RKBVK, which is comprised of the mouse ID9
 CC mAb complementarity determining regions (CDR's) linked by human HF-21/28
 CC positions 41 and 42
 XX
 XX SQ Sequence 112 AA;

Query Match 97.8%; Score 577; DB 5; Length 112;
 Best Local Similarity 98.2%; Pred. No. 3.9e-45;
 Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DVVMTQSPVLSPLPTLQGPASISCKSQSLDSDGKTFLNWFQRPQSPRRLLIYLVSKLD 60
 DB 1 DVVMTQSPVLSPLPTLQGPASISCKSQSLDSDGKTFLNWLLQRPQSPRRLLIYLVSKLD 60
 QY 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTTHPPYTFGQTRLEIK 112
 DB 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTTHPPYTFGQTRLEIK 112

Search completed: June 10, 2006, 11:56:14
 Job time : 73.4805 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 12:05:52 ; Search time 19.3393 Seconds
(without alignments)
506.917 Million cell updates/sec

Title: US-10-733-563-12
Perfect score: 590
Sequence: 1 DVVMTOSPLPVTLGQPAS.....CWQGTFFPYTGGQTRLEIK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /EMC Cellerai_SIDS3/ptodata/2/iaa/5 COMB.pep.*
2: /EMC Cellerai_SIDS3/ptodata/2/iaa/6 COMB.pep.*
3: /EMC Cellerai_SIDS3/ptodata/2/iaa/7 COMB.pep.*
4: /EMC Cellerai_SIDS3/ptodata/2/iaa/H COMB.pep.*
5: /EMC Cellerai_SIDS3/ptodata/2/iaa/ECTUS COMB.pep.*
6: /EMC Cellerai_SIDS3/ptodata/2/iaa/RE COMB.pep.*
7: /EMC Cellerai_SIDS3/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	590	100.0	112	2	US-09-809-739-14
2	590	100.0	112	2	US-09-840-459-12
3	590	100.0	112	2	US-09-497-625A-12
4	584	99.0	114	2	US-09-840-459-106
5	584	99.0	114	2	US-09-497-625A-106
6	577	97.8	112	2	US-09-809-739-15
7	577	97.8	112	2	US-09-840-459-13
8	577	97.8	112	2	US-09-497-625A-13
9	572	96.9	112	2	US-09-809-739-18
10	572	96.9	112	2	US-09-840-459-107
11	570	96.6	112	2	US-09-809-739-16
12	570	96.6	112	2	US-09-840-459-14
13	570	96.6	112	2	US-09-497-625A-14
14	565	95.8	112	2	US-09-809-739-17
15	565	95.8	112	2	US-09-840-459-15
16	565	95.8	112	2	US-09-497-625A-15
17	536	90.8	112	2	US-09-809-739-11
18	536	90.8	112	2	US-09-840-459-9
19	536	90.8	112	2	US-09-497-625A-9
20	536	90.8	142	2	US-09-840-459-102
21	536	90.8	142	2	US-09-497-625A-102
22	527	89.3	257	2	US-09-419-788-113
23	526	89.2	111	2	US-09-809-739-13
24	526	89.2	111	2	US-09-840-459-59
25	526	89.2	111	2	US-09-497-625A-11
26	526	89.2	111	2	US-09-497-625A-59

Sequence 89, Appl
Sequence 89, Appl
Sequence 89, Appl
Sequence 97, Appl
Sequence 7, Appl
Sequence 12, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 8, Appl
Sequence 4, Appl
Sequence 11, Appl
Sequence 58, Appl
Sequence 58, Appl
Sequence 149, App
Sequence 150, App
Sequence 163, App
Sequence 164, App
Sequence 2, Appl
Sequence 38, Appl

27 526 89.2 112 1 US-08-477-877B-89
28 526 89.2 112 1 US-08-472-281A-89
29 526 89.2 112 1 US-08-477-989B-89
30 526 89.2 112 2 US-09-462-140D-97
31 524 88.8 113 2 US-09-698-705-7
32 524 88.8 218 2 US-09-698-705-12
33 521 88.3 112 2 US-09-840-459-54
34 521 88.3 112 2 US-09-497-625A-54
35 521 88.3 112 2 US-09-254-180C-8
36 521 88.3 353 2 US-09-203-958A-4
37 520 88.1 111 2 US-09-840-459-11
38 520 88.1 112 2 US-09-840-459-58
39 520 88.1 112 2 US-09-497-625A-58
40 518 87.8 112 2 US-09-647-468-149
41 518 87.8 112 2 US-09-647-468-150
42 518 87.8 131 2 US-09-647-468-163
43 518 87.8 131 2 US-09-647-468-164
44 518 87.8 243 2 US-09-297-181-2
45 516 87.5 535 2 US-08-983-035A-38

ALIGNMENTS

RESULT 1
US-09-809-739-14
; Sequence 14, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809, 739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-14

Query Match 100.0%; Score 590; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.4e-51;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DVVMTOSPLPVTLGQPASISCKSSQSLSDSGKTFLNWFQORPGQSPRLIYLSKLD 60
Db 1 DVVMTOSPLPVTLGQPASISCKSSQSLSDSGKTFLNWFQORPGQSPRLIYLSKLD 60
Qy 61 SGVPDRFSGSGGTDTLTKISRVEADGVVYCWQGTTHFFPYTGGQTRLEIK 112
Db 61 SGVPDRFSGSGGTDTLTKISRVEADGVVYCWQGTTHFFPYTGGQTRLEIK 112

RESULT 2
US-09-840-459-12
; Sequence 12, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

```
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR FILING DATE: 2001-02-02
; PRIOR FILING DATE: 2001-02-02
; PRIOR FILING DATE: 2000-02-03
; PRIOR FILING DATE: 1999-07-22
; PRIOR FILING DATE: 1999-07-22
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-12

Query Match 100.0%; Score 590; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.4e-51;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVMTQSPVLSPLPVTLGPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLIYLVSKLD 60
Db 1 DVVMTQSPVLSPLPVTLGPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLIYLVSKLD 60

QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTTHFFYTFGQGTRLLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTTHFFYTFGQGTRLLEIK 112

RESULT 3
US-09-497-625A-12
; Sequence 12, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-12

Query Match 100.0%; Score 590; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.4e-51;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVMTQSPVLSPLPVTLGPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLIYLVSKLD 60
Db 1 DVVMTQSPVLSPLPVTLGPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLIYLVSKLD 60

QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTTHFFYTFGQGTRLLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTTHFFYTFGQGTRLLEIK 112
```

```
QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTTHFFYTFGQGTRLLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTTHFFYTFGQGTRLLEIK 112

RESULT 4
US-09-840-459-106
; Sequence 106, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain
US-09-840-459-106

Query Match 99.0%; Score 584; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.4e-50;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVMTQSPVLSPLPVTLGPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLIYLVSKLDS 61
Db 2 VVMTQSPVLSPLPVTLGPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLIYLVSKLDS 61

QY 62 GVPDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTTHFFYTFGQGTRLLEIK 112
Db 62 GVPDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTTHFFYTFGQGTRLLEIK 112

RESULT 5
US-09-497-625A-106
; Sequence 106, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
```



```
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain
US-09-497-625A-106

Query Match          99.0%; Score 584; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.4e-50;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 VVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRLIYLVSKLDS 61
Db  2 VVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRLIYLVSKLDS 61

Qy  62 GVPDRFSGSGGTDFTLKISRVEADVGVYVCWQGHFFPYTFQGQTRLEIK 112
Db  62 GVPDRFSGSGGTDFTLKISRVEADVGVYVCWQGHFFPYTFQGQTRLEIK 112

RESULT 6
US-09-809-739-15
; Sequence 15, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-15

Query Match          97.8%; Score 577; DB 2; Length 112;
Best Local Similarity 98.2%; Pred. No. 6.6e-50;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRLIYLVSKLD 60
Db  1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWLLQRPQSPRRLIYLVSKLD 60

Qy  61 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCWQGHFFPYTFQGQTRLEIK 112
Db  61 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCWQGHFFPYTFQGQTRLEIK 112

RESULT 7
US-09-840-459-13
; Sequence 13, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012

Query Match          99.0%; Score 584; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.4e-50;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 VVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRLIYLVSKLDS 61
Db  2 VVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRLIYLVSKLDS 61

Qy  62 GVPDRFSGSGGTDFTLKISRVEADVGVYVCWQGHFFPYTFQGQTRLEIK 112
Db  62 GVPDRFSGSGGTDFTLKISRVEADVGVYVCWQGHFFPYTFQGQTRLEIK 112

RESULT 6
US-09-809-739-15
; Sequence 15, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-15

Query Match          97.8%; Score 577; DB 2; Length 112;
Best Local Similarity 98.2%; Pred. No. 6.6e-50;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRLIYLVSKLD 60
Db  1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWLLQRPQSPRRLIYLVSKLD 60

Qy  61 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCWQGHFFPYTFQGQTRLEIK 112
Db  61 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCWQGHFFPYTFQGQTRLEIK 112

RESULT 7
US-09-840-459-13
; Sequence 13, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012

Query Match          97.8%; Score 577; DB 2; Length 112;
Best Local Similarity 98.2%; Pred. No. 6.6e-50;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRLIYLVSKLD 60
Db  1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWLLQRPQSPRRLIYLVSKLD 60

Qy  61 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCWQGHFFPYTFQGQTRLEIK 112
Db  61 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCWQGHFFPYTFQGQTRLEIK 112
```

```
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-13

Query Match          97.8%; Score 577; DB 2; Length 112;
Best Local Similarity 98.2%; Pred. No. 6.6e-50;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRLIYLVSKLD 60
Db  1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWLLQRPQSPRRLIYLVSKLD 60

Qy  61 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCWQGHFFPYTFQGQTRLEIK 112
Db  61 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCWQGHFFPYTFQGQTRLEIK 112

RESULT 8
US-09-497-625A-13
; Sequence 13, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-13

Query Match          97.8%; Score 577; DB 2; Length 112;
Best Local Similarity 98.2%; Pred. No. 6.6e-50;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRLIYLVSKLD 60
Db  1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWLLQRPQSPRRLIYLVSKLD 60

Qy  61 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCWQGHFFPYTFQGQTRLEIK 112
Db  61 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCWQGHFFPYTFQGQTRLEIK 112
```

Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCWOQTHFFPYTFGQGRLEIK 112

```

RESULT 9
US-09-809-739-18
; Sequence 18, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855-1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-18

```

Query Match	96.9%	Score 572;	DB 2;	Length 112;
Best Local Similarity	97.3%	Pred. NO. 2.1e-49;		
Matches 109;	Conservative	0;	Mismatches 3;	Indels 0;
Gaps	0;			

Qy	1	DVNTQSP	LSL	PVT	LQ	PAS	IS	CK	SS	Q	S	L	D	S	G	K	T	F	N	W	F	Q	P	Q	S	P	R	R	L	I	V	I	V	S	K	L	D	60	
Db	1	DVNTQSP	LSL	PVT	L	CH	PAS	IS	CK <td>SS</td> <td>Q <td>S</td> <td>L</td> <td>D <td>S</td> <td>G <td>K <td>T <td>F <td>N</td> <td>L</td> <td>L</td> <td>O</td> <td>R</td> <td>P</td> <td>G</td> <td>O</td> <td>S</td> <td>P</td> <td>R</td> <td>R</td> <td>L</td> <td>I</td> <td>V <td>S</td> <td>K</td> <td>L</td> <td>D</td> <td>60</td> </td></td></td></td></td></td></td>	SS	Q <td>S</td> <td>L</td> <td>D <td>S</td> <td>G <td>K <td>T <td>F <td>N</td> <td>L</td> <td>L</td> <td>O</td> <td>R</td> <td>P</td> <td>G</td> <td>O</td> <td>S</td> <td>P</td> <td>R</td> <td>R</td> <td>L</td> <td>I</td> <td>V <td>S</td> <td>K</td> <td>L</td> <td>D</td> <td>60</td> </td></td></td></td></td></td>	S	L	D <td>S</td> <td>G <td>K <td>T <td>F <td>N</td> <td>L</td> <td>L</td> <td>O</td> <td>R</td> <td>P</td> <td>G</td> <td>O</td> <td>S</td> <td>P</td> <td>R</td> <td>R</td> <td>L</td> <td>I</td> <td>V <td>S</td> <td>K</td> <td>L</td> <td>D</td> <td>60</td> </td></td></td></td></td>	S	G <td>K <td>T <td>F <td>N</td> <td>L</td> <td>L</td> <td>O</td> <td>R</td> <td>P</td> <td>G</td> <td>O</td> <td>S</td> <td>P</td> <td>R</td> <td>R</td> <td>L</td> <td>I</td> <td>V <td>S</td> <td>K</td> <td>L</td> <td>D</td> <td>60</td> </td></td></td></td>	K <td>T <td>F <td>N</td> <td>L</td> <td>L</td> <td>O</td> <td>R</td> <td>P</td> <td>G</td> <td>O</td> <td>S</td> <td>P</td> <td>R</td> <td>R</td> <td>L</td> <td>I</td> <td>V <td>S</td> <td>K</td> <td>L</td> <td>D</td> <td>60</td> </td></td></td>	T <td>F <td>N</td> <td>L</td> <td>L</td> <td>O</td> <td>R</td> <td>P</td> <td>G</td> <td>O</td> <td>S</td> <td>P</td> <td>R</td> <td>R</td> <td>L</td> <td>I</td> <td>V <td>S</td> <td>K</td> <td>L</td> <td>D</td> <td>60</td> </td></td>	F <td>N</td> <td>L</td> <td>L</td> <td>O</td> <td>R</td> <td>P</td> <td>G</td> <td>O</td> <td>S</td> <td>P</td> <td>R</td> <td>R</td> <td>L</td> <td>I</td> <td>V <td>S</td> <td>K</td> <td>L</td> <td>D</td> <td>60</td> </td>	N	L	L	O	R	P	G	O	S	P	R	R	L	I	V <td>S</td> <td>K</td> <td>L</td> <td>D</td> <td>60</td>	S	K	L	D	60

Qy	61	SGVPRFSGSGSDFTLKLRSVEADVGVYVCWGTHPPYTFGGTRLEIK	112
D _b	61	SGVPRFSGSGSDFTLKLRSVEADVGVYVCWGTHPPYTFGGTRLEIK	112

```

RESULT 10
US-09-840-459-107
; Sequence 107, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-107

```

	Query Match	96.9%	Score 572;	DB 2;	Length 112;
	Best Local Similarity	97.3%;	Pred. No. 2.le-49;		
	Matches 109;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	1	DVWMTQSLPVLVTLPQSPASISCKSSQSLDSDGKTEFLNWFQORPGQSPRRLIYLVSKLD	60		
Db	1	DVWMTQSLPVLVTLPQSPASISCKSSQSLDSDGKTEFLNLLQORPGQSPRRLIYLVSKLD	60		
Qy	61	SGVPDRFSGSGGTDFTLTKISRVEAEADVGVVYCWGTHFFPYTFGGTRLIK	112		
Db	61	SGVPDRFSGSGGTDFTLTKISRVEAEADVGVVYCWGTHFFPYTFGGTRLIK	112		

```

RESULT 11
US-09-809-739-16
; Sequence 16, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-16

```

Query Match	96.6%	Score 570;	DB 2;
Best Local Similarity	97.3%;	Pred. No. 3.3e-49;	Length 112;
Matches 109;	Conservative	0;	Mismatches 3;
			Indels 0;
			Gaps 0;

Qy	1	DVMTQPSLSLPTVLIGQPASISCKSSQLSDSGKTFINWFQQPGQSPRRLLIYLVSKLD	60
Db	1	DVMTQPSLSLPTVLIGQPASISCKSSQLSDSGKTFINWLLORPGQSPRRLLIYLVSKLD	60

Q7 61 SGVDRFSGSGSTDTFTLKISRVEAEDGYYCQGTHFPYTFGGTRLEIK 112
|||
p6 61 SGVDRFSGSGSTDTFTLKISRVEAEDGYYCQGTHFPYTFGGTRLEIK 112

RESULT 12
US-09-840-459-14
Sequence 14, Application US/09840459
Patent No. 6696550
GENERAL INFORMATION:
APPLICANT: Larosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22

```
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-14

Query Match          96.6%; Score 570; DB 2; Length 112;
Best Local Similarity 97.3%; Pred. No. 3.3e-49;
Matches 109; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DVVMTQSPVLSPLPVTLGGPASPISCKSSQSLDSDGKTFLNWFFQRPQGPSPRLIYLVSKLD 60
Db 1 DVVMTQSPVLSPLPVTLGGPASPISCKSSQSLDSDGKTFLNWLLQRPQGPSPRLIYLVSKLD 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYWCQGTHFPYTFGGGTRLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYWCQGTHFPYTFGGGTRLEIK 112

RESULT 13
US-09-497-625A-14
; Sequence 14, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-14

Query Match          96.6%; Score 570; DB 2; Length 112;
Best Local Similarity 97.3%; Pred. No. 3.3e-49;
Matches 109; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DVVMTQSPVLSPLPVTLGGPASPISCKSSQSLDSDGKTFLNWFFQRPQGPSPRLIYLVSKLD 60
Db 1 DVVMTQSPVLSPLPVTLGGPASPISCKSSQSLDSDGKTFLNWLLQRPQGPSPRLIYLVSKLD 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYWCQGTHFPYTFGGGTRLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYWCQGTHFPYTFGGGTRLEIK 112

RESULT 14
US-09-809-739-17
; Sequence 17, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-17

Query Match          95.8%; Score 565; DB 2; Length 112;
Best Local Similarity 96.4%; Pred. No. 1e-48;
Matches 108; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DVVMTQSPVLSPLPVTLGGPASPISCKSSQSLDSDGKTFLNWFFQRPQGPSPRLIYLVSKLD 60
Db 1 DVVMTQSPVLSPLPVTLGGPASPISCKSSQSLDSDGKTFLNWLLQRPQGPSPRLIYLVSKLD 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYWCQGTHFPYTFGGGTRLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYWCQGTHFPYTFGGGTRLEIK 112

RESULT 15
US-09-840-459-15
; Sequence 15, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-15

Query Match          95.8%; Score 565; DB 2; Length 112;
Best Local Similarity 96.4%; Pred. No. 1e-48;
Matches 108; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DVVMTQSPVLSPLPVTLGGPASPISCKSSQSLDSDGKTFLNWFFQRPQGPSPRLIYLVSKLD 60
Db 1 DVVMTQSPVLSPLPVTLGGPASPISCKSSQSLDSDGKTFLNWLLQRPQGPSPRLIYLVSKLD 60
```

Qy 61 SGVDFRFGSGGTDFTLKISRVEAEDVGVYCWQGTHTFPYTFGGTRLEIK 112
Db 61 SGVDFRFGSGGTDFTLKISRVEAEDVGVYCWQGTHTFPYTFGGTRLEIK 112

Search completed: June 10, 2006, 12:08:44
Job time : 20.3393 secs

Query Match 89.8%; Score 530; DB 2; Length 132;

Best Local Similarity 88.4%; Pred. No. 1e-42;
Matches 99; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

[illegible]

Qy	61	SGVPRFSGSGSTDFTLKISRVEAEDGVYVCWGTHFPYTFGGTRLEIK	112
		:	
Db	81	SGVPRFTGSGSTDFTLKISRVEADLGYYVCWGTHFPRTFGGTGLEIK	132

RESULT 3
 23230
 g kappa chain precursor V-J region - human (fragment)
 Species: Homo sapiens (man)
 Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
 Accession: S23230
 Kennedy, M.A.

J. Exp. Med. 173, 1033-1036, 1991

A; Title: Novel chromosome translocation caused by fusion of immunoglobulin heavy and light chain genes

A; Reference number: S23230; MUID:91178438; PMID:1840606

A; Accession: S23230

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-133 <KEN>

A; Cross-references: UNIPARC:UP10000115EA9; EMBL:X55400; NID:g33999; PIDN:CAA39072.1; PID:1840606

C; Genetics:

A; Introns: 17/1

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotetramer; immunoglobulin

F; 36-115/Domain: immunoglobulin homology <IMM>

```
Query Match      89.2%; Score 526; DB 2; Length 133;
Best Local Similarity 90.2%; Pred. No. 2.5e-42;
Matches 101; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
```

	61	SGVPDRFSGSSGTDFTLKSIRVEADGVVYCWQGHFPFGQTRLEI	111
Qy		:	
	92	SGVPDRFSGSSGTDFTLKSIRVEADGVVYCMQGHWPFFFGQTRLEI	142
Dd		:	

```

RESULT 5
A36259
19 kappa chain V region (TE34) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 21-Jan-2000
C/Accession: A36259
R/Zilber, B.; Scherf, T.; Levitt, M.; Anglistser, J.
Biochemistry 29, 10032-10041, 1990
A>Title: NMR-derived model for a peptide-antibody complex.
A/Reference number: A36259; PMID:2271636
A/Accession: A36259
A>Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-112 <ZIL>
A/Cross-references: UNIPARC:UPI0000176AFD; GB:M30459; GB:M30480;
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

```

```

Query Match      87.6%; Score 517; DB 2; Length 112;
Best Local Similarity 86.6%; Pred. No. 1.4e-41;
Matches 97; Conservative 8; Mismatches 7; Indels 0; Gaps 0

Qy      1 DVVMTQSPISLPTVLTGQPASISCKSSQSLSDSGKTEFLNFWQQRQSPRRLLIYLVSKLD 60
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      1 DVVMIQTPLTLLSVTTGQPASISCKSSQSLSDSGKTYLNLWRQPGQSPKRLIYLVSKLD 60
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy      61 SGVPRFSGSGSGTFTLKISRVAEDGVYVYCWQGHPTFTGQGRLEIK 112
      ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      61 SGVPRFTGSGSGTFTLKISRVAEDGVYVYCWQGHPTFTGQGRLEIK 112
      ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 6
K2HURP
Ig kappa chain precursor V-II region (RPMI) - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C/Accession: A01890
R/Kloebbeck, H.G.; Meindl, A.; Combrinato, G.; Solomon, A.; Zachau, H.G.
Nucleic Acids Res. 13, 6499-6513, 1985
A/Title: Human immunoglobulin kappa 1 light chain genes of subgroups II and III.
A/Reference number: A93588; MUID:86041882; PMID:2937711

```

A/Accession: rot01
A/Molecule type: DNA
A/Residues: 1-133 <KLO>
A/Cross-references: UNIPROT:P06310; UNIPARC:UPI000012E159
A/Note: the sequence was determined from the differentiated gene
C/Genetics:
A/Gene: GDB:ICKV2
A/Cross-references: GDB:136265
A/Map position: 2p12-2p12
A/Introns: 17/1
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate to form a hexamer.
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-20/Domain: signal sequence #status predicted <SIG>
F/21-133/Product: Ig kappa chain V-II region (RPMI) #status predicted <MAT>
F/21-43/Region: framework 1
F/36-115/Domain: immunoglobulin homology <IMM>
F/44-59/Region: complementarity-determining 1
F/60-74/Region: framework 2
F/75-81/Region: complementarity-determining 2
F/82-113/Region: framework 3
F/114-122/Region: complementarity-determining 3
F/123-133/Region: framework 4
F/43-113/Disulfide bonds: #status predicted

```
Query Match      87.1%; Score 514; DB 1; Length 133;
Best Local Similarity 87.5%; Pred. No. 3.3e-41;
Matches 98; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DVVMTQSPVLTIGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSKLD 60
Db 21 DVVMTQSPVLTIGQPASISCKSSQSLVSDGNTYLNWFQQRPGQSPRLIYKVSNRD 80

Qy 61 SGVDPDRFSGSGGTDFTLKISRVEAEDGIVYVYCWQGHWSYTFGGGTGLEIK 112
Db 81 SGVDPDRFSGSGGTDFTLKISRVEAEDGIVYVYCWQGHWSYTFGGGTGLEIK 132

RESULT 7
S49572
Ig kappa chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1995 #sequence_revision 14-Jul-1995 #text_change 21-Jan-2000
C:Accession: S49572
R:Glachino, C.; Padovan, E.; Lanzavecchia, A.
A:Submitted to the EMBL Data Library, November 1994
A:Description: k+1+ dual receptor B cells are present in the human peripheral repertoire
A:Reference number: S49571
A:Accession: S49572
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-114 <GIA>
A:CROSS-references: UNIPARC:UPI0000116709; EMBL:Z46626; NID:G575261; PIDN:CAA86596.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match      87.0%; Score 513.5; DB 2; Length 114;
Best Local Similarity 87.6%; Pred. No. 3.1e-41;
Matches 99; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

Qy 1 DVVMTQSPVLTIGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSKLD 60
Db 1 DVVMTQSPVLTIGQPASISCKSSQSLVYTDGNTYLNWFQQRPGQSPRLIYKVSNRD 60

Qy 61 SGVDPDRFSGSGGTDFTLKISRVEAEDGIVYVYCWQGHFP-YTGGQTRLEIK 112
Db 61 SGVDPDRFSGSGGTDFTLKISRVEAEDGIVYVYCWQGHFPYTFGGGTGLEIK 113

RESULT 8
S20709
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S20709
R:Brennan, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Osb
A:Submitted to the EMBL Data Library, April 1992
A:Description: Binding specificity and variable region sequences of two monoclonal anti
A:Reference number: S20706
A:Accession: S20709
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-111 <BRE>
A:CROSS-references: UNIPARC:UPI00001163E1; EMBL:Z11917; NID:G52655; PIDN:CAA77975.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match      86.8%; Score 512; DB 2; Length 111;
Best Local Similarity 85.6%; Pred. No. 4.2e-41;
Matches 95; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DVVMTQSPVLTIGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSKLD 60
Db 1 DIQLTQSPVLTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPRLIYLVSKLD 60

Qy 61 SGVDPDRFSGSGGTDFTLKISRVEAEDGIVYVYCWQGHFPYTFGGGTGLEIK 111
Db 61 SGVDPDRFSGSGGTDFTLKISRVEAEDGIVYVYCWQGHFPYTFGGGTGLEIK 111
```

```
Db 61 SGVDPDRFSGSGGTDFTLKISRVEAEDGIVYVYCWQGHFPYTFGGGTGLEIK 111

RESULT 9
A55491
Proteolytic antibody light chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
C:Accession: A55491
R:Guo, Q.S.; Sun, M.; Tyutyulkova, S.; Webster, D.; Rees, A.; Tramontano, A.; Massey, R.
J. Biol. Chem. 269, 32389-32393, 1994
A:Title: Molecular cloning of a proteolytic antibody light chain.
A:Reference number: A55491; MUID:95096089; PMID:7798238
A:Accession: A55491
A:Molecule type: mRNA
A:Residues: 1-112 <GAO>
A:CROSS-references: UNIPROT:Q8K0F8; UNIPARC:UPI0000176CCE; GB:L34775
A:Note: authors translated the codon TAT for residue 37 as Thr
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match      86.8%; Score 512; DB 2; Length 112;
Best Local Similarity 85.7%; Pred. No. 4.2e-41;
Matches 96; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DVVMTQSPVLTIGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSKLD 60
Db 1 DVVMTQSPVLTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPRLIYLVSKLD 60

Qy 61 SGVDPDRFSGSGGTDFTLKISRVEAEDGIVYVYCWQGHFPYTFGGGTGLEIK 112
Db 61 SGVDPDRFSGSGGTDFTLKISRVEAEDGIVYVYCWQGHFPYTFGGGTGLEIK 112

RESULT 10
A24452
Ig kappa chain precursor V-II region (RPMI 6410) - human
C:Species: Homo sapiens (man)
C:Date: 24-Jan-1988 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
C:Accession: A24452
R:Weir, L.; Leder, P.
Nucleic Acids Res. 14, 3957-3970, 1986
A:Title: Structure and expression of a human subgroup II immunoglobulin kappa gene.
A:Reference number: A24452; MUID:86232631; PMID:3086847
A:Accession: A24452
A:Molecule type: DNA
A:Residues: 1-133 <WEI>
A:CROSS-references: UNIPARC:UPI0000113B46; GB:M36859; NID:G185932; PIDN:AAA58920.1; PID:
C:Note: this sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV2
A:CROSS-references: GDB:136265
A:Map position: 2p12-2p12
A:Introns: 17/1
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-133/Product: Ig kappa chain V-II region (RPMI 6410) #status predicted <MAT>
F;36-115/Domain: immunoglobulin homology <IMM>
F;43-113/Disulfide bonds: #status predicted

Query Match      85.8%; Score 506; DB 1; Length 133;
Best Local Similarity 86.8%; Pred. No. 1.8e-40;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DVVMTQSPVLTIGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSKLD 60
Db 21 DVVMTQSPVLTIGQPASISCKSSQSLVSDNTYLNWLLQRPQSPRLIYKVSNRD 80

Qy 61 SGVDPDRFSGSGGTDFTLKISRVEAEDGIVYVYCWQGHFPYTFGGGTGLEIK 112
```


J. Neuroimmunol. 36, 29-39, 1992
A;Title: DNA sequence analysis and comparison of the variable heavy and light chain regi
A;Reference number: S42610; MUID:92138794; PMID:1370957
A;Accession: S42611
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-133 <SPA>
A;Cross-references: UNIPARC:UPI000011378B; EMBL:X54137; NID:9433989; PIDN:CAA38072.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;36-115/Domain: immunoglobulin homology <IMM>

Query Match	84.9%	Score 501;	DB 2;	Length 133;
Best Local Similarity	85.6%	Fred. No. 5.4e-40;		
Matches	95;	Conservative 7;	Mismatches 9;	Indels 0; Gaps 0;

Qy	1	DVVMTQSPLSLPVTLGQPASISCKSSOSLSDSDGKTFLNWFQQRPGQSPRRLIYLVSKLD	60
Db	21	DVVMTQSPLSLPVTLGQPASISCKSSQSLVFSDDGNTYLNWFQQRPGQSPRRLIYKVSNRD	80

Qy	61	SGVPDRFSGSGGTDTFTLKISRVEAEDVGVVYCWQGTHTFPYTFGGTRLEI	111
Db	81	SGVPDRFSGSGGTDTFTLKISRVEAEDVGIYCMQGAHWPPLTFGGTKVEI	131

Search completed: June 10, 2006, 12:06:44
Job time : 12.9399 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 11:49:06 ; Search time 92.1562 Seconds
(without alignments)
1124.198 Million cell updates/sec

Title: US-10-733-563-12
Perfect score: 590
Sequence: 1 DVNMQSPLSLVTLGPAS.....CWOQTHPPYFGQGRLEIK 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	514	87.1	133	1 KV2F_HUMAN	P06310 homo sapien
2	511	86.6	239	2 Q8TCD0_HUMAN	Q8tcd0 homo sapien
3	496.5	84.2	114	2 Q9UL80_HUMAN	Q9ul80 homo sapien
4	491	83.2	239	2 Q58EU8_MOUSE	Q58eu8 mus musculus
5	459	77.8	239	2 Q6P491_HUMAN	Q6p491 homo sapien
6	450	76.3	113	1 KV2D_HUMAN	P01617 homo sapien
7	449	76.1	113	1 KV2B_HUMAN	P01615 homo sapien
8	447	75.8	239	2 Q8NEK0_HUMAN	Q8nek0 homo sapien
9	445	75.4	248	2 Q65Z07_MOUSE	Q65zq7 mus sp. b3(
10	444.5	75.3	115	1 KV2A_HUMAN	P01614 homo sapien
11	438	74.2	117	1 KV2E_HUMAN	P06309 homo sapien
12	430.5	73.0	115	2 Q5F210_MOUSE	Q5f210 mus musculus
13	430	72.9	113	1 KV2G_MOUSE	P01631 mus musculus
14	428	72.5	112	2 Q53VP8_MOUSE	Q53vp8 mus musculus
15	418	70.8	219	2 Q65ZC0_MOUSE	Q65zco mus musculus
16	417.5	70.8	240	2 Q6PIH6_HUMAN	Q6pih6 homo sapien
17	411	69.7	234	2 Q5XK24_MOUSE	Q5xkg4 mus musculus
18	405.5	68.7	112	1 KV2C_HUMAN	P01616 homo sapien
19	402	68.1	113	1 KV2E_MOUSE	P03976 mus musculus
20	397	67.3	113	1 KV2C_MOUSE	P01628 mus musculus
21	396	67.1	112	1 KV2D_MOUSE	P01629 mus musculus
22	396	67.1	113	1 KV2A_MOUSE	P01630 mus musculus
23	390	66.1	112	1 KV2F_MOUSE	P01626 mus musculus
24	390	66.1	112	2 Q6LEH8_MOUSE	Q6leh8 mus musculus
25	386.5	65.5	134	1 KV4C_HUMAN	P06314 homo sapien
26	385.5	65.3	108	1 KV1_CANFA	P01618 canis famil
27	380.5	64.5	114	1 KV4A_HUMAN	P01625 homo sapien
28	378.5	64.2	111	1 KV3L_MOUSE	P01664 mus musculus
29	378.5	64.2	111	1 KV3M_MOUSE	P01665 mus musculus
30	377.5	64.0	111	1 KV3O_MOUSE	P01667 mus musculus
31	372.5	63.1	111	1 KV3Q_MOUSE	P01669 mus musculus

32	371.5	63.0	111	1 KV3N_MOUSE	P01666 mus musculus
33	371	62.9	110	1 KV3P_MOUSE	P01668 mus musculus
34	370	62.7	86	2 Q7Z3Y5_HUMAN	Q7z3y5 homo sapien
35	369.5	62.6	111	2 Q811U6_MOUSE	Q811u6 mus musculus
36	368.5	62.5	111	1 KV3H_MOUSE	P01660 mus musculus
37	365.5	61.9	111	1 KV3J_MOUSE	P01662 mus musculus
38	363	61.5	120	1 KV2B_MOUSE	P01627 mus musculus
39	361.5	61.3	111	2 Q920E9_MOUSE	Q920e9 mus musculus
40	360.5	61.1	131	1 KV3I_MOUSE	P01661 mus musculus
41	360.5	61.1	255	2 Q6KB05_MOUSE	Q6kb05 mus musculus
42	359	60.8	133	1 KV4B_HUMAN	P06313 homo sapien
43	356.5	60.4	111	1 KV3K_MOUSE	P01663 mus musculus
44	356.5	60.4	111	1 KV3U_MOUSE	P01673 mus musculus
45	355.5	60.3	240	2 Q52L64_MOUSE	Q52l64 mus musculus

ALIGNMENTS

RESULT 1

KV2F_HUMAN					
ID_KV2F_HUMAN	STANDARD;	PRT;	133 AA.		
AC_P06310;					
DT_01-JAN-1988,	sequence integrated into UniProtKB/Swiss-Prot.				
DT_01-JAN-1988,	sequence version 1.				
DT_07-MAR-2006,	entry version 41.				
DE_Ig kappa chain V-II region RPMI 6410 precursor.					
OS_Homo sapiens (Human).					
OC_Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC_Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;					
OC_Homo.					
OX_NCBI_TaxID=9606;					
RN_1					
RP_NUCLEOTIDE SEQUENCE [GENOMIC DNA].					
RX_MEDLINE=86041852; PubMed=2997711;					
RA_Klobeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;					
RT_''Human immunoglobulin kappa light chain genes of subgroups II and III.''					
RL_Nucleic Acids Res. 13:6499-6513(1985).					
CC_	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms				
CC_	Distributed under the Creative Commons Attribution-NoDerivs License				
CC_	EMBL; Z00020; CAA77315.1; -; Genomic_DNA.				
DR_PIR; A01890; K2HURP.					
DR_HSSP; Q99M37; I191.					
DR_SMR; P06310; 21-133.					
DR_Ensembl; ENSG00000173758; Homo sapiens.					
DR_LinkHub; P06310; -.					
DR_GO; GO:0005576; C:extracellular region; NAS.					
DR_GO; GO:0003823; F:antigen binding; NAS.					
DR_GO; GO:0006955; P:immune response; NAS.					
DR_InterPro; IPR003599; Ig.					
DR_InterPro; IPR007110; Ig-like.					
DR_InterPro; IPR003596; Ig_v.					
DR_InterPro; IPR013106; V-set.					
DR_Pfam; PF07686; V-set; 1.					
DR_SMART; SM00409; IG; 1.					
DR_SMART; SM00406; IGV; 1.					
DR_PROSITE; PS00835; IG_LIKE; 1.					
KW_Immunoglobulin domain; Immunoglobulin V region; Signal.					
FT_SIGNAL	1	20			
FT_CHAIN	21	133			
FT_REGION	21	43			
FT_REGION	44	59			
FT_REGION	60	74			
FT_REGION	75	81			
FT_REGION	82	113			
FT_REGION	114	122			
FT_REGION	123	132			
FT_REGION	133	133			
FT_DISULFID	43	133			
FT_NON_TER	133				

Ig kappa chain V-II region RPMI 6410.
/FTid=PRO_0000015173.
Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
Framework-3.
Complementarity-determining-3.
Framework-4.
By similarity.

```
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;
Query Match 87.1%; Score 514; DB 1; Length 133;
Best Local Similarity 87.5%; Pred. No. 1.6e-45;
Matches 98; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 DVVMTQSPVLTLPVLTQGPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLIYVSKLD 60
DQ 21 DVVMTQSPVLTLPVLTQGPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLIYVSKLD 80
QY 61 SGVDFRFGSGSGTDFTLKISRVEADVGVYVCWQGHFPPYTFQGGTRLEIK 112
DQ 81 SGVDFRFGSGSGTDFTLKISRVEADVGVYVCWQGHFPPYTFQGGTRLEIK 132

RESULT 2
Q8TCD0_HUMAN
ID Q8TCD0_HUMAN PRELIMINARY; PRT; 239 AA.
AC Q8TCD0;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 24.
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX Strauberg R.;
RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92285150; PubMed=1598223;
RA Hirabayashi Y., Munakata Y., Sasaki T., Sano H.;
RT "Variable regions of a human anti-DNA antibody O-81 possessing lupus
nephritis-associated idiotype.";
RL Nucleic Acids Res. 20:2601-0(1992).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92201291; PubMed=1551402;
RA Lautner-Rieseke A., Huber C., Meindl A., Pargent W., Schable K.F.,
RA Thiebe R., Zocher I., Zachau H.G.;
RT "The human immunoglobulin kappa locus. Characterization of the
duplicated A regions.";
RL Eur. J. Immunol. 22:1023-1029(1992).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94080891; PubMed=8258341;
RA Klein R., Jaenichen R., Zachau H.G.;
RT "Expressed human immunoglobulin kappa genes and their hypermutation.";
RL Eur. J. Immunol. 23:3248-3262(1993).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93170387; PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
distributed over a large portion of the V kappa locus and do not show
somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; BC022362; AAH22362.1; -; mRNA.
DR PIR; S22658; S22658.
DR PIR; S34095; S34095.
DR PIR; S40324; S40324.
DR PIR; S40374; S40374.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR HSP; P01834; I17Z.
DR SNR; Q8TCD0; 21-237.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG1; 1.
DR SMART; SM00407; IG1; 1.
DR SMART; SM00406; IG1; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26235 MW; FACEDC3A3B03871D CRC64;
Query Match 86.6%; Score 511; DB 2; Length 239;
Best Local Similarity 86.6%; Pred. No. 6.3e-45;
Matches 97; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 DVVMTQSPVLTLPVLTQGPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLIYVSKLD 60
DQ 21 DVVMTQSPVLTLPVLTQGPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLIYVSKLD 80
QY 61 SGVDFRFGSGSGTDFTLKISRVEADVGVYVCWQGHFPPYTFQGGTRLEIK 112
DQ 81 SGVDFRFGSGSGTDFTLKISRVEADVGVYVCWQGHFPPYTFQGGTRLEIK 132

RESULT 3
Q9UL80_HUMAN
ID Q9UL80_HUMAN PRELIMINARY; PRT; 114 AA.
AC Q9UL80;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
```

```
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92352481; PubMed=1322670;
RA Stuber F., Lee S.K., Bridges S.L. Jr, Koopman W.J., Schroeder H.W. Jr,
RA Gaskin F., Fu S.M.;
RT "A rheumatoid factor from a normal individual encoded by VH2 and V
RT kappa II gene segments.";
RL Arthritis Rheum. 35:900-904(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93170387; PubMed=8436174;
RA Wagner S.D., Luzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92289816; PubMed=1601042;
RA Huber C., Klobeck H.G., Zachau H.G.;
RT "Ongoing V kappa-J kappa recombination after formation of a productive
RT V kappa-J kappa coding joint.";
RL Eur. J. Immunol. 22:1561-1565(1992).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF035034; AAD56270.1; -; mRNA.
DR PIR; B49002; B49002.
DR PIR; S23638; S23638.
DR PIR; S34094; S34094.
DR PIR; S34095; S34095.
DR HSP; P01625; 1LVE.
DR SMR; Q9UL80; 1-114.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig v.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
DR Immunoglobulin domain.
FT NON_TER 1
FT TER 114
FT NON_TER 114
FT TER 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 84.2%; Score 496.5; DB 2; Length 114;
Best Local Similarity 85.8%; Pred. No. 9e-44;
Matches 97; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

Qy 1 DVVMTQSPVLSPLPVTLGQPASISCKSSQSLDSDGKFTLNWFOQRPGQSPRLIYLVSKLD 60
Dy 1 DVVMTQSPVLSPLPVTLGQPASISCKSSQSPVSDGNTYLNWFOQRPGQSPRLIYKVSNRD 60
Qy 61 SGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYVYCWQGHF-PYTFGGQTRLRIK 112
Dy 61 SGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYVYCWQGHFWPTFGQTKVEIK 113

RESULT 4
Q58EU8_MOUSE PRELIMINARY; PRT; 239 AA.
ID Q58EU8_MOUSE
AC Q58EU8;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Igk-C protein.
GN Name=Igk-C;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
```

```
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=C2ECH II; TISSUE=Mammary tumor metastasized to lung.
MMTV-LTR/Wnt1 model. Expression driven by an MMTV-LTR enhancer.;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=C2ECH II; TISSUE=Mammary tumor metastasized to lung.
MMTV-LTR/Wnt1 model. Expression driven by an MMTV-LTR enhancer.;
NIH MGC Project;
Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BC091750; AAH91750.1; -; mRNA.
DR SMR; Q58E08; 21-239.
DR MGI; MGI:96495; Igk-C.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 239 AA; 26302 MW; 98FC4BA8EB404215 CRC64;

Query Match 83.2%; Score 491; DB 2; Length 239;
Best Local Similarity 83.9%; Pred. No. 7.8e-43;
Matches 94; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DVVMTQSPVLSPLPVTLGQPASISCKSSQSLDSDGKFTLNWFOQRPGQSPRLIYLVSKLD 60
Dy 21 DVVMTQSPVLSPLPVTLGQPASISCKSSQSLHSNGKFTLNWFOQRPGQSPKLLIYLVSKLE 80
Qy 61 SGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYVYCWQGHF-PYTFGGQTRLRIK 112
Dy 81 SGVDPDRFSGSGSGTDFTLKISRVEAEDLVGYVYVYCWQGHF-PYTFGGQTRLRIK 132

RESULT 5
Q6P491_HUMAN PRELIMINARY; PRT; 239 AA.
ID Q6P491_HUMAN
AC Q6P491;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
```



```
DR PIR; S40357; S40357.
DR HSSP; P01834; 117Z.
DR SMR; Q8NEK0; 21-237.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig V.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IG1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match
Best Local Similarity 75.8%; Score 447; DB 2; Length 239;
Matches 85; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 DVVMTQSPVLSPLVTLGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRLLIYLVSKLD 60
Db 21 DIVMTQSPVLSPLVTPGEPASISCKSSQSLDSDGNYLDWYLOKPGQSPQLLIYLVGSNRA 80
QY 61 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCWQTHFPYTFGQGRLEIK 112
Db 81 SGVPDRFSGSGGTDFTLKISRVEADVGVYVCWQTHFPYTFGQGRLEIK 132

RESULT 9
Q65ZQ7_9MURI
ID Q65ZQ7_9MURI PRELIMINARY; PRT; 248 AA.
AC Q65ZQ7;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE B3(Fv)-PE40 (Fragment).
GN Name=B3(Fv)-PE40;
OS Mus sp.
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92020904; PubMed=1924323;
RA Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.;
RT "B3(Fv)-PE38KDEL, a single-chain immunotoxin that causes complete
regression of a human carcinoma in mice."
RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; S57990; AAB19971.2; -; mRNA.
DR SMR; Q65ZQ7; 4-247.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig V.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG LIKE; 2.
KW Immunoglobulin domain.
FT NON TER 248
SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;

Query Match
Best Local Similarity 75.4%; Score 445; DB 2; Length 248;
Matches 83; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

QY 1 DVVMTQSPVLSPLVTLGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRLLIYLVSKLD 60

us-10-733-563-12.rup Page 6
```



```

QSF210_MOUSE
ID QSF210_MOUSE PRELIMINARY; PRT; 115 AA.
AC QSF210;
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 15-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Kappa light chain variable region (Fragment).
DE Name=IgG1 anti-TS1 VL;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22716456; PubMed=12833571; DOI=10.1002/jmr.617;
RX Erlandsson A., Holm P., Ullen A., Stigbrand T., Sundstrom B.E.;
RT "Studies of the interactions between the anticytokeratin 8 monoclonal
PT antibody TS1, its antigen and its anti-idiotypic antibody alphaTS1."
RL J. Mol. Recognit. 16:157-163(2003).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP Erlandsson A.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AJ884575; CAI56337.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig V.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin domain.
FT NON TER 1
FT NON TER 115
SQ SEQUENCE 115 AA; 12560 MW; E4D3BF1D63E88007 CRC64;

Query Match 73.0%; Score 430.5; DB 2; Length 115;
Best Local Similarity 74.3%; Pred. No. 7.3e-37;
Matches 84; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

Qy 1 DVVMTQPSLPLVTLGPASISCKSSQSLSDSGKTFLNWQFORPGQSPRLIYLVSKLD 60
Db 1 DVVMTQPSLPLVSLGDQASISCRSSQSLVHSGNTYLVHWYLOKPGQSPKLLIYKSNRF 60

Qy 61 SGVPRDFSGSGSGCTDFTLKISRVEADGVYYCWCQGTHF-PYTFGQSTRLEIK 112
Db 61 SGVPRDFSGSGSGCTDFTLKISRVEADGLGVYFCSQTHVPPYTFGGGTKLEMK 113

RESULT 13
KV2G MOUSE STANDARD; PRT; 113 AA.
ID KV2G_MOUSE AC P01631;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 07-MAR-2006, entry version 39.
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN PROTEIN SEQUENCE.
RP STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse

```

```
RT anti-digoxin hybridoma antibody." ;
RL Biochemistry 22:1153-1158(1993).
CC -I- MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma
CC protein that binds digoxin.
-----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
-----
CC PIR; A01914; KWS26.
DR HSP; Q99M37; I191.
DR Ensembl; ENSMUSG0000055315; Mus musculus.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Direct protein sequencing; Hybridoma; Immunoglobulin domain;
KW Immunoglobulin V region; Monoclonal antibody.
FT CHAIN 1 >113
FT /FtId=PRO 0000059776.
FT REGION 1 23 Framework-1.
FT REGION 24 39 Complementarity-determining-1.
FT REGION 40 54 Framework-2.
FT REGION 55 61 Complementarity-determining-2.
FT REGION 62 93 Framework-3.
FT REGION 94 102 Complementarity-determining-3.
FT REGION 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON_TER 113 113
FT SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 72.9%; Score 430; DB 1; Length 113;
Best Local Similarity 74.1%; Pred. No. 8.1e-37;
Matches 83; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 DVVMTQSPVLSPLVTLQGPASISCKSSQLSDSGKTFLNWFQQRPGQSPRLIYLVSKLD 60
DB 1 DVVMTQTPLSPLVSLGDAQSISCRSSQSLVHSNGNTYLNWYLOKAGQSPKLLIYKVSNR 60
QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYVYCWQGTTPFTFGQGTLEIK 112
DB 61 SGVPDRFSGSGGTDFTLKISRVEAEDGLGYFCSQTHVPTFTGGGTLEIK 112

RESULT 14
Q53VP8_MOUSE PRELIMINARY; PRT; 112 AA.
AC Q53VP8_MOUSE
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Kappa chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=96319505; PubMed=8768802;
RA Kipp B., Schlaak M., Becker W.M.;
RT "Cloning and expression of a recombinant mouse Fab-fragment
RT recognizing a defined linear epitope of Chironomus thummi major
RT allergen Chit 1." ;
RL Int. Arch. Allergy Immunol. 110:348-353(1996).
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
-----
CC EMBL; Z37499; CAA85724.1; -; mRNA.
DR MGI; MGI:96495; IGK-C.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS0290; IG_MHC; 1.
KW Immunoglobulin domain; Repeat.
FT NON_TER 1 1
FT NON_TER 219 219
```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 12:31:52 ; Search time 63.5676 Seconds
(without alignments)
816.140 Million cell updates/sec

Title: US-10-733-563-12

Perfect score: 590

Sequence: 1 DVVMTQSPSLPVTLCQPAS.....CWQGTFFPYTFGGQTRLEIK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC_Celerra_SID33/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SID33/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SID33/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SID33/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	590	100.0	112	3	US-09-835-087-3 ; Sequence 3, Appli
2	590	100.0	112	3	US-09-809-739-14 ; Sequence 14, Appl
3	590	100.0	112	3	US-09-840-459-14 ; Sequence 12, Appl
4	590	100.0	112	4	US-10-766-773-12 ; Sequence 12, Appl
5	590	100.0	112	4	US-10-766-610-12 ; Sequence 12, Appl
6	590	100.0	112	4	US-10-733-563-12 ; Sequence 12, Appl
7	590	100.0	112	5	US-10-662-061-14 ; Sequence 14, Appl
8	590	100.0	112	6	US-11-075-184A-3 ; Sequence 3, Appli
9	584	99.0	114	4	US-09-840-459-106 ; Sequence 106, App
10	584	99.0	114	4	US-10-766-773-106 ; Sequence 106, App
11	584	99.0	114	4	US-10-766-610-106 ; Sequence 106, App
12	584	99.0	114	4	US-10-733-563-106 ; Sequence 106, App
13	577	97.8	112	3	US-09-835-087-4 ; Sequence 4, Appli
14	577	97.8	112	3	US-09-809-739-15 ; Sequence 15, Appl
15	577	97.8	112	3	US-09-840-459-13 ; Sequence 13, Appl
16	577	97.8	112	4	US-10-766-773-13 ; Sequence 13, Appl
17	577	97.8	112	4	US-10-766-610-13 ; Sequence 13, Appl
18	577	97.8	112	4	US-10-733-563-13 ; Sequence 13, Appl
19	577	97.8	112	5	US-10-662-061-15 ; Sequence 15, Appl
20	577	97.8	112	6	US-11-075-184A-4 ; Sequence 4, Appli
21	572	96.9	112	3	US-09-835-087-7 ; Sequence 7, Appli
22	572	96.9	112	3	US-09-809-739-18 ; Sequence 18, Appl
23	572	96.9	112	3	US-09-840-459-107 ; Sequence 107, App
24	572	96.9	112	4	US-10-766-610-107 ; Sequence 107, App
25	572	96.9	112	4	US-10-733-563-107 ; Sequence 107, App
26	572	96.9	112	5	US-10-662-061-18 ; Sequence 18, Appl
27	572	96.9	112	6	US-11-075-184A-7 ; Sequence 7, Appli

28	570	96.6	112	3	US-09-835-087-5	Sequence 5, Appli
29	570	96.6	112	3	US-09-809-739-16	Sequence 16, Appl
30	570	96.6	112	3	US-09-840-459-14	Sequence 14, Appl
31	570	96.6	112	4	US-10-766-773-14	Sequence 14, Appl
32	570	96.6	112	4	US-10-766-610-14	Sequence 14, Appl
33	570	96.6	112	4	US-10-733-563-14	Sequence 14, Appl
34	570	96.6	112	5	US-10-662-061-16	Sequence 16, Appl
35	570	96.6	112	6	US-11-075-184A-5	Sequence 5, Appli
36	565	95.8	112	3	US-09-835-087-6	Sequence 6, Appli
37	565	95.8	112	3	US-09-809-739-17	Sequence 17, Appl
38	565	95.8	112	3	US-09-840-459-15	Sequence 15, Appl
39	565	95.8	112	4	US-10-766-773-15	Sequence 15, Appl
40	565	95.8	112	4	US-10-766-610-15	Sequence 15, Appl
41	565	95.8	112	4	US-10-733-563-15	Sequence 15, Appl
42	565	95.8	112	5	US-10-662-061-17	Sequence 17, Appl
43	565	95.8	112	6	US-11-075-184A-6	Sequence 6, Appli
44	559	94.7	113	5	US-10-476-265-9	Sequence 9, Appli
45	559	94.7	219	5	US-10-476-265-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-835-087-3
; Sequence 3, Application US/09835087
; Patent No. US20020042370A1
; GENERAL INFORMATION:
; APPLICANT: Wayne W. Hancock
; TITLE OF INVENTION: Method of Treating Graft Rejection Using
; TITLE OF INVENTION: Inhibitors of CCR2 Function
; FILE REFERENCE: 1855.2008-003
; CURRENT APPLICATION NUMBER: US/09/835,087
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/549,448
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-835-087-3

Query Match	100.0%	Score 590;	DB 3;	Length 112;
Best Local Similarity	100.0%;	Pred. No. 3.1e-47;		
Matches 112;	Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	DVVMTQSPSLPVTLCQPASISCKSSQSLDSDGKTFLNWFQORPGQSPRLIYLVSKLD	60	
Db	1	DVVMTQSPSLPVTLCQPASISCKSSQSLDSDGKTFLNWFQORPGQSPRLIYLVSKLD	60	
Qy	61	SGVPDFRFGSGSGTDFTLKISRVEAEDVGYYCQGTTHFPYTFGGQTRLEIK	112	
Db	61	SGVPDFRFGSGSGTDFTLKISRVEAEDVGYYCQGTTHFPYTFGGQTRLEIK	112	

RESULT 2
US-09-809-739-14
; Sequence 14, Application US/09809739
; Patent No. US20020106369A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17

```
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-14

Query Match      100.0%; Score 590; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.le-47;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVMTQSPVLSPLVTGQPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLIYLVSKLD 60
Db 1 DVVMTQSPVLSPLVTGQPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLIYLVSKLD 60

QY 61 SGVPDRFSGSGGTDFTLTKISRVEAEDVGYYVCWQGTFFPYTFGGQTRLEIK 112
Db 61 SGVPDRFSGSGGTDFTLTKISRVEAEDVGYYVCWQGTFFPYTFGGQTRLEIK 112

RESULT 3
US-09-840-459-12
; Sequence 12, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-12

Query Match      100.0%; Score 590; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.le-47;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVMTQSPVLSPLVTGQPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLIYLVSKLD 60
Db 1 DVVMTQSPVLSPLVTGQPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLIYLVSKLD 60

QY 61 SGVPDRFSGSGGTDFTLTKISRVEAEDVGYYVCWQGTFFPYTFGGQTRLEIK 112
Db 61 SGVPDRFSGSGGTDFTLTKISRVEAEDVGYYVCWQGTFFPYTFGGQTRLEIK 112

RESULT 4
US-10-766-773-12
; Sequence 12, Application US/10766773
```

```
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-10-766-773-12

Query Match      100.0%; Score 590; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.le-47;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVMTQSPVLSPLVTGQPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLIYLVSKLD 60
Db 1 DVVMTQSPVLSPLVTGQPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLIYLVSKLD 60

QY 61 SGVPDRFSGSGGTDFTLTKISRVEAEDVGYYVCWQGTFFPYTFGGQTRLEIK 112
Db 61 SGVPDRFSGSGGTDFTLTKISRVEAEDVGYYVCWQGTFFPYTFGGQTRLEIK 112

RESULT 5
US-10-766-610-12
; Sequence 12, Application US/10766610
; Publication No. US20040132980A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-029
; CURRENT APPLICATION NUMBER: US/10/766,610
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/840,459
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 112
; TYPE: PRT
```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-10-766-610-12

```

Query Match	100.0%	Score 590;	DB 4;	Length 112;
Best Local Similarity	100.0%;	Pred. No. 3.1e-47;		
Matches 112;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps	0;			

	Qy	Qy	Db	Qy	Db
1	DVVMTOSPLSLPWTLCQPASISCKSSQSILDSGKTFLNWFOORQGSPPRLIYLVSKLD	60	1	DVVMTOSPLSLPWTLCQPASISCKSSQSILDSGKTFLNWFOORQGSPPRLIYLVSKLD	60
61	SGVPDRFSGSGGSDTFLKISRVEAEDVGYYVCWQGTFFPYTFGGGTLEIK	112	61	SGVPDRFSGSGGSDTFLKISRVEAEDVGYYVCWQGTFFPYTFGGGTLEIK	112

Query Match	100.0%	Score 590;	DB 4;	Length 112;
Best Local Similarity	100.0%;	Pred. No. 3.1e-47;		
Matches 112:	Conservative	0;	Mismatches 0;	Indels 0;
	Gaps	0;		

Qy 61 SGVPDRFSGSGTDFTLKISRVEADYGVVYCWQTHFPYTFQGTRLEIK 112
 |||||
 Db 61 SGVPDRFSGSGTDFTLKISRVEADYGVVYCWQTHFPYTFQGTRLEIK 112
 |||||

```

; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 112
; TYPE: prt
; ORGANISM: Artificial Sequence
; FEATURE:
;   OTHER INFORMATION: Humanized sequence
US-10-662-061-14

```

Qy	1	DVMTQSP	LSL	PVTI	GPQ	PAS	IS	CK	SS	Q	S	L	D	S	D	G	K	T	F	L	N	F	Q	R	P	G	S	P	R	L	I	Y	L	V	S	K	L	D	60			
Db	1	DVMTQSP	LSL	PVTI	GPQ	PAS	IS	CK	SS	Q	S	L	D	S	D	G	K	T	F	L	N	F	Q	R	P	G	S	P	R	L	I	Y	L	V	S	K	L	D	60			
Qy	61	SGVPR	F	SG	S	G	S	G	T	F	L	K	I	S	R	V	E	A	E	D	V	G	V	Y	C	M	O	G	T	H	P	P	T	F	G	G	T	R	L	E	K	112
Db	61	SGVPR	F	SG	S	G	S	G	T	F	L	K	I	S	R	V	E	A	E	D	V	G	V	Y	C	M	O	G	T	H	P	P	T	F	G	G	T	R	L	E	K	112

Query Match	100.0%;	Score 590;	DB 6;	Length 112;
Best Local Similarity	100.0%;	Pred. No. 3.1e-47;		
Matches 112;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 61 SGVPDRFSGSGTDFLLKISRVEADGVVYCWQTHFPYTFGQTRLEIK 112
 |||||
 Db 61 SGVPDRFSGSGTDFLLKISRVEADGVVYCWQTHFPYTFGQTRLEIK 112
 |||||

; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized light chain
US-10-733-563-106

Query Match 99.0%; Score 584; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.le-46;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFNLNWFQORPGQSPRLIYLVSKLDS 61
Db 2 VVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFNLNWFQORPGQSPRLIYLVSKLDS 61

Qy 62 GVPDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTFFPYTFGGQTRLEIK 112
Db 62 GVPDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTFFPYTFGGQTRLEIK 112

RESULT 13
US-09-835-087-4
; Sequence 4, Application US/09835087
; Patent No. US2002042370A1
; GENERAL INFORMATION:
; APPLICANT: Wayne W. Hancock
; TITLE OF INVENTION: Method of Treating Graft Rejection Using
; TITLE OF INVENTION: Inhibitors of CCR2 Function
; FILE REFERENCE: 1855-2008-003
; CURRENT APPLICATION NUMBER: US/09/835,087
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/549,448
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-835-087-4

Query Match 97.8%; Score 577; DB 3; Length 112;
Best Local Similarity 98.2%; Pred. No. 5e-46;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFNLNWFQORPGQSPRLIYLVSKLD 60
Db 1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFNLNWFQORPGQSPRLIYLVSKLD 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTFFPYTFGGQTRLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTFFPYTFGGQTRLEIK 112

RESULT 14
US-09-809-739-15
; Sequence 15, Application US/09809739
; Patent No. US20020106369A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739

; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-15

Query Match 97.8%; Score 577; DB 3; Length 112;
Best Local Similarity 98.2%; Pred. No. 5e-46;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFNLNWFQORPGQSPRLIYLVSKLD 60
Db 1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFNLNWFQORPGQSPRLIYLVSKLD 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTFFPYTFGGQTRLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTFFPYTFGGQTRLEIK 112

RESULT 15
US-09-840-459-13
; Sequence 13, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Sibhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-13

Query Match 97.8%; Score 577; DB 3; Length 112;
Best Local Similarity 98.2%; Pred. No. 5e-46;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFNLNWFQORPGQSPRLIYLVSKLD 60
Db 1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFNLNWFQORPGQSPRLIYLVSKLD 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTFFPYTFGGQTRLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTFFPYTFGGQTRLEIK 112

Search completed: June 10, 2006, 12:38:40
Job time : 64.5676 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 12:32:32 ; Search time 3.86787 Seconds
(without alignments)
366.103 Million cell updates/sec

Title: US-10-733-563-12
Perfect score: 590
Sequence: 1 DVWMTQSPSLPVTILGPAS.....CQWGHFFPTFGQTRLEIK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 64916 seqs, 12643201 residues

Total number of hits satisfying chosen parameters: 64916

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	522	88.5	112	7	US-11-239-308-12
2	511.5	86.7	113	7	US-11-239-308-2
3	511	86.6	113	6	US-10-506-063A-8
4	487	82.5	112	6	US-10-544-050-4
5	470	79.7	100	7	US-11-239-308-45
6	470	78.7	100	7	US-11-239-308-46
7	469	79.5	112	7	US-11-239-308-18
8	463	78.5	112	7	US-11-239-308-6
9	456.5	77.4	113	7	US-11-239-308-4
10	451	76.4	112	7	US-11-211-917-104
11	450	75.3	114	7	US-11-249-296-48
12	444	75.3	112	6	US-10-544-050-3
13	443	75.1	112	7	US-11-239-308-16
14	443	75.1	112	7	US-11-211-917-103
15	443	75.1	112	7	US-11-211-917-111
16	442.5	75.0	113	7	US-11-239-308-14
17	440	74.6	112	7	US-11-211-917-12
18	440	74.6	112	7	US-11-211-917-28
19	440	74.6	112	7	US-11-211-917-94
20	440	74.6	239	7	US-11-211-917-16
21	440	74.6	239	7	US-11-211-917-32
22	439	74.4	112	6	US-10-544-050-1
23	436	73.9	112	7	US-11-211-917-52
24	436	73.9	239	7	US-11-211-917-56
25	435	73.7	112	7	US-11-211-917-60

26	435	73.7	112	7	US-11-211-917-112
27	435	73.7	239	7	US-11-211-917-64
28	434	73.6	112	7	US-11-211-917-4
29	434	73.6	112	7	US-11-211-917-76
30	434	73.6	239	7	US-11-211-917-8
31	434	73.6	239	7	US-11-211-917-80
32	434	73.6	239	7	US-11-211-917-102
33	427	72.4	112	7	US-11-211-917-36
34	427	72.4	239	7	US-11-211-917-40
35	424	71.9	112	7	US-11-216-033-8
36	422	71.5	239	7	US-11-293-697-4028
37	417	70.7	100	7	US-11-239-308-50
38	415	70.3	100	7	US-11-239-308-47
39	415	70.3	148	1	US-09-784-950-36
40	409.5	69.4	113	7	US-11-254-679-54
41	399.5	67.7	101	7	US-11-239-308-44
42	397	67.3	148	1	US-09-784-950-24
43	396	67.1	100	7	US-11-239-308-48
44	391	66.3	100	7	US-11-239-308-49
45	376	63.7	143	1	US-09-784-950-32

ALIGNMENTS

RESULT 1
US-11-239-308-12
; Sequence 12, Application US/11239308
; Publication No. US2006008883A1
; GENERAL INFORMATION:
; APPLICANT: Smider, Vaughn
; APPLICANT: Larrick, James W.
; APPLICANT: Integrigen, Inc.
; TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses
; FILE REFERENCE: 021216-000310US
; CURRENT APPLICATION NUMBER: US/11/239,308
; PRIOR FILING DATE: 2005-09-28
; PRIOR APPLICATION NUMBER: US/10/683,733
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/417,979
; PRIOR FILING DATE: 2002-10-09
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-239-308-12

Query Match	88.5%	Score 522;	DB 7;	Length 112;
Best Local Similarity	88.4%	Pred. No. 2.2e-43;		
Matches	99;	Conservative	7;	Mismatches 6; Indels 0; Gaps 0;
QY	1	DVWMTQSPSLPVTILGPASISCKSSQSLSDGKFTLNWFOQRPGQSPRLIYLVSKLD	60	
DB	1	DVWMTQSPSLPVTILGPASISCKSSQSLSDGKFTLNWFOQRPGQSPRLIYLVSKND	60	
QY	61	SGVPRDFSGSGSGTDTFLTKISRVEADVGVIYCMQGTFFPVTFGGTRLEIK	112	
DB	61	SGVPRDFSGSGSGTDTFLTKISRVEADVGVIYCMQGTFFPVTFGGTRKVEIK	112	

RESULT 2
US-11-239-308-2
; Sequence 2, Application US/11239308
; Publication No. US2006008883A1
; GENERAL INFORMATION:
; APPLICANT: Smider, Vaughn
; APPLICANT: Larrick, James W.
; APPLICANT: Integrigen, Inc.
; TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses
; FILE REFERENCE: 021216-000310US
; CURRENT APPLICATION NUMBER: US/11/239,308

```
; CURRENT FILING DATE: 2005-09-28
; PRIOR APPLICATION NUMBER: US/10/683,733
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/417,979
; PRIOR FILING DATE: 2002-10-09
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-239-308-2

Query Match      86.7%; Score 511.5; DB 7; Length 113;
Best Local Similarity 87.6%; Pred. No. 2.2e-42;
Matches 99; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

QY 1 DVVMTQSLSPVTLGQPASISCKSSQSLDSDGKTFNLNWFQQRPGQSPRLIYLVSKLD 60
DB 1 DVVMTQSLSPVTLGQPASISCKSSQSLVSDGNTYLNWFQQRPGQSPRLIYKVSNRD 60
QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCWMQGTHF-PYTFQGQTRLEIK 112
DB 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCWMQGTHWPPWTFQGQTKVEIK 113

RESULT 3
US-10-506-063A-8
; Sequence 8, Application US/10506063A
; Publication No. US20060110771A1
; GENERAL INFORMATION:
; APPLICANT: KATAGIRI, Masanao
; APPLICANT: FUJIMOTO, Shigeru
; APPLICANT: GODA, Yasuhiro
; TITLE OF INVENTION: A protein binding to female hormones and a production thereof
; FILE REFERENCE: 2004-1363A/WMC/00279
; CURRENT APPLICATION NUMBER: US/10/506,063A
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: JP 2002-055669
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 59
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mouse
US-10-506-063A-8

Query Match      86.6%; Score 511; DB 6; Length 113;
Best Local Similarity 84.8%; Pred. No. 2.5e-42;
Matches 95; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 DVVMTQSLSPVTLGQPASISCKSSQSLDSDGKTFNLNWFQQRPGQSPRLIYLVSKLD 60
DB 1 DVLMTQTLLTSVTTLGQPASISCKSSQSLNSDGKTYLHLWLQRPQSPKRLIYLVSKLD 60
QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCWMQGTHF-PYTFQGQTRLEIK 112
DB 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCWMQVTHFPPLTFGAGTKLELK 112

RESULT 4
US-10-544-050-4
; Sequence 4, Application US/10544050
; Publication No. US20060110388A1
; GENERAL INFORMATION:
; APPLICANT: Davies Julian
; TITLE OF INVENTION: Abeta Binding Molecules
; FILE REFERENCE: X-16068
; CURRENT APPLICATION NUMBER: US/10/544,050
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/446380
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 76
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized heavy chain
US-10-544-050-4

Query Match      82.5%; Score 487; DB 6; Length 112;
Best Local Similarity 83.9%; Pred. No. 4.7e-40;
Matches 94; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 DVVMTQSLSPVTLGQPASISCKSSQSLDSDGKTFNLNWFQQRPGQSPRLIYLVSKLD 60
DB 1 DVVMTQSLSPVTLGQPASISCKSSQSLIYSDGNAYLHLWFQQRPGQSPRLIYKVSNR 60
QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCWMQGTHF-PYTFQGQTRLEIK 112
DB 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCSQSTHVPWTFGGTKVEIK 112

RESULT 5
US-11-239-308-45
; Sequence 45, Application US/11239308
; Publication No. US20060088883A1
; GENERAL INFORMATION:
; APPLICANT: Smider, Vaughn
; APPLICANT: Larrick, James W.
; APPLICANT: Integrigen, Inc.
; TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses
; FILE REFERENCE: 021216-000310US
; CURRENT APPLICATION NUMBER: US/11/239,308
; CURRENT FILING DATE: 2005-09-28
; PRIOR APPLICATION NUMBER: US/10/683,733
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/417,979
; PRIOR FILING DATE: 2002-10-09
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-239-308-45

Query Match      79.7%; Score 470; DB 7; Length 100;
Best Local Similarity 90.0%; Pred. No. 1.7e-38;
Matches 90; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 DVVMTQSLSPVTLGQPASISCKSSQSLDSDGKTFNLNWFQQRPGQSPRLIYLVSKLD 60
DB 1 DVVMTQSLSPVTLGQPASISCKSSQSLVSDGNTYLNWFQQRPGQSPRLIYKVSNRD 60
QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCWMQGTHF 100
DB 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCWMQGTHWP 100

RESULT 6
US-11-239-308-46
; Sequence 46, Application US/11239308
; Publication No. US20060088883A1
; GENERAL INFORMATION:
; APPLICANT: Smider, Vaughn
; APPLICANT: Larrick, James W.
; APPLICANT: Integrigen, Inc.
; TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses
; FILE REFERENCE: 021216-000310US
; CURRENT APPLICATION NUMBER: US/11/239,308
; CURRENT FILING DATE: 2005-09-28
; PRIOR APPLICATION NUMBER: US/10/683,733
; PRIOR FILING DATE: 2003-10-09
```

; PRIOR APPLICATION NUMBER: US 60/417,979
; PRIOR FILING DATE: 2002-10-09
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-239-308-46

Query Match 79.7%; Score 470; DB 7; Length 100;
Best Local Similarity 90.0%; Pred. No. 1.7e-38;
Matches 90; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWFOQRPGQSPRLIYLVSKLD 60
Db 1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWFOQRPGQSPRLIYLVSKLD 60
QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGVIYCMQGTTHP 100
Db 61 SGVPRFSGSGGTDTFTLKISRVEADVGVIYCMQGTTHP 100

RESULT 7

US-11-239-308-18
; Sequence 18, Application US/11239308
; Publication No. US2006008883A1
; GENERAL INFORMATION:
; APPLICANT: Smider, Vaughn
; APPLICANT: Larrick, James W.
; APPLICANT: Integrigen, Inc.
; TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses
; FILE REFERENCE: 021216-000310US
; CURRENT APPLICATION NUMBER: US/11/239,308
; CURRENT FILING DATE: 2005-09-28
; PRIOR APPLICATION NUMBER: US/10/683,733
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/417,979
; PRIOR FILING DATE: 2002-10-09
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-239-308-18

Query Match 79.5%; Score 469; DB 7; Length 112;
Best Local Similarity 78.6%; Pred. No. 2.4e-38;
Matches 88; Conservative 11; Mismatches 13; Indels 0; Gaps 0;
QY 1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWFOQRPGQSPRLIYLVSKLD 60
Db 1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWFOQRPGQSPRLIYLVSKLD 60
QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGVIYCMQGTTHP 112
Db 61 SGVPRFSGSGGTDTFTLKISRVEADVGVIYCMQGTTHP 112

RESULT 8

US-11-239-308-6
; Sequence 6, Application US/11239308
; Publication No. US2006008883A1
; GENERAL INFORMATION:
; APPLICANT: Smider, Vaughn
; APPLICANT: Larrick, James W.
; APPLICANT: Integrigen, Inc.
; TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses
; FILE REFERENCE: 021216-000310US
; CURRENT APPLICATION NUMBER: US/11/239,308
; CURRENT FILING DATE: 2005-09-28
; PRIOR APPLICATION NUMBER: US/10/683,733

; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/417,979
; PRIOR FILING DATE: 2002-10-09
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-239-308-6

Query Match 78.5%; Score 463; DB 7; Length 112;
Best Local Similarity 80.4%; Pred. No. 9e-38;
Matches 90; Conservative 8; Mismatches 14; Indels 0; Gaps 0;
QY 1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWFOQRPGQSPRLIYLVSKLD 60
Db 1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWFOQRPGQSPRLIYLVSKLD 60
QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGVIYCMQGTTHP 112
Db 61 SGVPRFSGSGGTDTFTLKISRVEADVGVIYCMQGTTHP 112

RESULT 9

US-11-239-308-4
; Sequence 4, Application US/11239308
; Publication No. US2006008883A1
; GENERAL INFORMATION:
; APPLICANT: Smider, Vaughn
; APPLICANT: Larrick, James W.
; APPLICANT: Integrigen, Inc.
; TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses
; FILE REFERENCE: 021216-000310US
; CURRENT APPLICATION NUMBER: US/11/239,308
; CURRENT FILING DATE: 2005-09-28
; PRIOR APPLICATION NUMBER: US/10/683,733
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/417,979
; PRIOR FILING DATE: 2002-10-09
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-239-308-4

Query Match 77.4%; Score 456.5; DB 7; Length 113;
Best Local Similarity 79.6%; Pred. No. 3.8e-37;
Matches 90; Conservative 9; Mismatches 13; Indels 1; Gaps 1;
QY 1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWFOQRPGQSPRLIYLVSKLD 60
Db 1 DVVMTQSPSLPVTLGQPASISCKSSQSLDSDGKTFLNWFOQRPGQSPRLIYLVSKLD 60
QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGVIYCMQGTTHP 112
Db 61 SGVPRFSGSGGTDTFTLKISRVEADVGVIYCMQGTTHP 112

RESULT 10

US-11-211-917-104
; Sequence 104, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US

```
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 104
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-104

Query Match 76.4%; Score 451; DB 7; Length 112;
Best Local Similarity 77.7%; Pred. No. 1.2e-36;
Matches 87; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 DVVMTQSLPLSVTLTGQPASISCKSSQSLSDSGKTFNLWFOQRPQSPRLIYLVSKLD 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIVMTQSLPLSVTPGEPASISCRSSQSLHSGNYLDWYLQKPGQPQLLIYLGSNRA 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGVPRFSGSGGTDFTLKISRVEAEDVGVYVCWQGTTHPPYTFGGGTGLEIK 112
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SGVPRFSGSGGTDFTLKISRVEAEDVGVYVCWQGTTHPPYTFGGGTGLEIK 112
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-11-249-296-48
; Sequence 48, Application US/11249296
; Publication No. US20060115428A1
; GENERAL INFORMATION:
; APPLICANT: Schering Aktiengesellschaft
; TITLE OF INVENTION: Identification and Characterization of Function-Blocking
; FILE OF INVENTION: Anti-ED-B-Fibronectin Antibodies
; FILE REFERENCE: 33042P DE (WWHC)
; CURRENT APPLICATION NUMBER: US/11/249,296
; CURRENT FILING DATE: 2005-10-14
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 48
; LENGTH: 114
; TYPE: PRT
; ORGANISM: human
US-11-249-296-48

Query Match 76.3%; Score 450; DB 7; Length 114;
Best Local Similarity 77.7%; Pred. No. 1.6e-36;
Matches 87; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 1 DVVMTQSLPLSVTLTGQPASISCKSSQSLSDSGKTFNLWFOQRPQSPRLIYLVSKLD 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIVMTQSLPLSVTPGEPASISCRSSQSLHSGNYTDLNWLQKPGQPQLLIYLGSYRA 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGVPRFSGSGGTDFTLKISRVEAEDVGVYVCWQGTTHPPYTFGGGTGLEIK 112
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SGVPRFSGSGGTDFTLKISRVEAEDVGVYVCWQGTTHPPYTFGGGTGLEIK 112
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-10-544-050-3
; Sequence 3, Application US/10544050
; Publication No. US20060110388A1
; GENERAL INFORMATION:
; APPLICANT: Davies Julian
; TITLE OF INVENTION: Abeta Binding Molecules
; FILE REFERENCE: X-16068
; CURRENT APPLICATION NUMBER: US/10/544,050
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/446380
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent In version 3.2
US-10-544-050-3

; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 104
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-103

Query Match 75.1%; Score 443; DB 7; Length 112;
Best Local Similarity 75.9%; Pred. No. 7.2e-36;
Matches 85; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 DVVMTQSLPLSVTLTGQPASISCKSSQSLSDSGKTFNLWFOQRPQSPRLIYLVSKLD 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIVMTQSLPLSVTPGEPASISCRSSQSLHSGNYLDWYLQKPGQPQLLIYLGSNRA 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGVPRFSGSGGTDFTLKISRVEAEDVGVYVCWQGTTHPPYTFGGGTGLEIK 112
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SGVPRFSGSGGTDFTLKISRVEAEDVGVYVCWQGTTHPPYTFGGGTGLEIK 112
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
US-11-211-917-103
; Sequence 103, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: PENG, XIAO
; TITLE OF INVENTION: ANTIODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
US-11-211-917-103
```

; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 103
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-103

Query Match 75.1%; Score 443; DB 7; Length 112;
Best Local Similarity 75.9%; Pred. No. 7.2e-36;
Matches 85; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 DVVMTQSPSLPVTIGQPASISCKSSQSLDSDGKTFLNWFOQRPQSPRLIYLVSKLD 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVMTQSPSLPVTIGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGVPRFSGSGSGTDFTLKISRVEADVGVYICMQALQTPWTFGQGTKEIK 112
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGVPRFSGSGSGTDFTLKISRVEADVGVYICMQALQTPWTFGQGTKEIK 112
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 15
US-11-211-917-111
; Sequence 111, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-111

Query Match 75.1%; Score 443; DB 7; Length 112;
Best Local Similarity 75.9%; Pred. No. 7.2e-36;
Matches 85; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 DVVMTQSPSLPVTIGQPASISCKSSQSLDSDGKTFLNWFOQRPQSPRLIYLVSKLD 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVMTQSPSLPVTIGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGVPRFSGSGSGTDFTLKISRVEADVGVYICMQALQTPWTFGQGTKEIK 112
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGVPRFSGSGSGTDFTLKISRVEADVGVYICMQALQTPWTFGQGTKEIK 112
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: June 10, 2006, 12:39:09
Job time : 3.86787 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 11:48:47 ; Search time 75.7162 Seconds
(without alignments)
706.511 Million cell updates/sec

Title: US-10-733-563-17

Perfect score: 620

Sequence: 1 EVQLVGGGLVPGGSLRL.....CTTFYGVNGVGGTLTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_8:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1980s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*
- 10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	620	100.0	117	4	Aae06954 Humanised
2	620	100.0	117	4	Aau09927 Humanised
3	620	100.0	117	5	Abg75536 Humanised
4	620	100.0	117	5	Aao14980 Humanised
5	620	100.0	117	5	Adf98240 Humanised
6	620	100.0	117	8	Adq89239 Humanised
7	620	100.0	117	9	Aeb09512 Humanised
8	620	100.0	117	9	Aec92171 Humanised
9	620	100.0	117	9	Aed43689 Humanised
10	620	100.0	119	4	Aae07034 Humanised
11	620	100.0	119	8	Adq89326 Humanised
12	620	100.0	119	9	Aeb09599 Humanised
13	613	98.9	117	4	Aae06955 Humanised
14	613	98.9	117	5	Abg75537 Humanised
15	613	98.9	117	5	Aao14981 Humanised
16	613	98.9	117	5	Adf98241 Humanised
17	613	98.9	117	8	Adq89240 Humanised
18	613	98.9	117	9	Aeb09513 Humanised
19	613	98.9	117	9	Aec92172 Humanised
20	613	98.9	117	9	Aed43690 Humanised
21	604	97.4	117	4	Aae06956 Humanised
22	604	97.4	117	4	Aau09929 Humanised
23	604	97.4	117	4	Aau09928 Humanised

ALIGNMENTS

RESULT 1

AAE06954

ID AAE06954 standard; protein; 117 AA.

XX

AC AAE06954;

XX

DT 11-SEP-2003 (revised)

DT 16-OCT-2001 (first entry)

XX

DE Humanised murine 1D9 antibody heavy chain variable region, 1D9RHA.

XX

Murine; humanised antibody; CC-Chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherosclerosis; arteriosclerosis; stenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; 1D9 antibody; neointimal hyperplasia; VH; heavy chain variable region; 1D9RHA.

XX Mus sp.

OS Homo sapiens.

OS Chimeric.

PH Key Location/Qualifiers

FT Region 27...35

FT /label= CDR1

FT /note= "Complementarity determining region 1"

FT Region 50...68

FT /label= CDR2

FT /note= "Complementarity determining region 2"

FT Region 101...106

FT /label= CDR3

FT /note= "Complementarity determining region 3"

PN WO200157226-A1.

PD 09-AUG-2001.

XX

PF 02-FEB-2001; 2001WO-US003537.

XX

PR 03-FEB-2000; 2000US-00497625.

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX

RESULT 3
 ABG75536
 ID ABG75536 standard; protein; 117 AA.
 XX
 AC ABG75536;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Humanised mouse mAb 1D9 heavy chain variable region, 1D9RHAHVH.
 XX
 KW Mouse; stenosis; restenosis; blood vessel; vascular injury; antibody;
 KW antigen binding fragment; cellular adhesion molecule; adhesion;
 KW recruitment; neutrophil; antagonist; CCR2; mononuclear cell; angioplasty;
 KW percutaneous transluminal coronary angioplasty; PTCA; stent;
 KW vascular by-pass surgery; vascular grafting; endarterectomy; atherectomy;
 KW endovascular stenting; prosthetic valve; transplantation;
 KW inflammatory disease; mastitis; vaginitis; cholecystitis;
 KW chronic bronchitis; asthma; graft-versus-host disease;
 KW chronic inflammatory disease; hypersensitivity pneumonitis;
 KW collagen disease; sarcoidosis; idiopathic; pancreatitis; HF-21/28;
 KW insulin dependent; diabetes mellitus; inflammatory bowel disease;
 KW Crohn's disease; allergic disease; psoriasis; atopic dermatitis; human;
 KW allergic rhinitis; autoimmune disease; arthritis; multiple sclerosis;
 KW graft rejection; atherosclerosis; myositis; therapy; 1D9; 1D9RHAHVH;
 KW heavy chain variable region; VH; complementarity determining region; CDR;
 KW mutant; mutein.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 XX Region 31..35 /note= "Mouse complementarity determining region 1
 XX (CDR1)"
 XX Region 50..68 /note= "Mouse complementarity determining region 2
 XX (CDR2)"
 XX Region 101..106 /note= "Mouse complementarity determining region 3
 XX (CDR3)"
 XX
 US2002106369-A1.
 XX
 08-AUG-2002.
 XX
 15-MAR-2001; 2001US-00809739.
 XX
 17-MAR-2000; 2000US-00528267.
 XX
 (MILL-) MILLENNIUM PHARM INC.
 XX
 Horvath CJ, Rao PE;
 XX
 WPI; 2002-697861/75.
 XX
 Inhibiting (re)stenosis of blood vessel following vascular injury, by
 PT administering first and second agents that inhibit adhesion and/or
 PT recruitment of neutrophils and mononuclear cells, respectively to site of
 PT vascular injury.
 XX
 Claim 32; Fig 18; 59pp; English.
 XX
 The invention discloses a method for inhibiting stenosis or restenosis of
 CC a blood vessel following vascular injury in a subject. The method
 CC involves administering to the subject a first therapeutic agent, which
 CC comprises an antibody or its antigen binding fragment which binds a
 CC cellular adhesion molecule, that inhibits the adhesion and/or recruitment
 CC of neutrophils to a site of vascular injury and a second therapeutic
 CC agent, which comprises an antagonist of CCR2 function, that inhibits
 CC adhesion and/or recruitment of mononuclear cells to a site of vascular
 CC injury. The vascular injury arises from a vascular intervention procedure

such as angioplasty (e.g. percutaneous transluminal coronary angioplasty
 (PTCA) or angioplasty including placement of a stent), vascular by-pass
 surgery, vascular grafting, endarterectomy, atherectomy, endovascular
 stenting, insertion of a prosthetic valve and transplantation of organs,
 tissues or cells. The method is also useful for treating inflammatory
 diseases or conditions mediated by early neutrophil activity and later
 mononuclear cell activity. Preferably, the method is useful for treating
 a subject having mastitis, vaginitis, cholecystitis, chronic bronchitis,
 asthma and graft-versus-host disease, chronic inflammatory disease of
 lung, hypersensitivity pneumonitis, collagen diseases, sarcoidosis and
 other idiopathic conditions, pancreatitis and insulin dependent diabetes
 mellitus. The method is also useful for treating inflammatory bowel
 disease, Crohn's disease, inflammatory or allergic rhinitis), autoimmune diseases
 (such as arthritis and multiple sclerosis), graft rejection,
 atherosclerosis and myositis. The method enables simultaneous inhibition
 of neutrophil and mononuclear cell participation in response to vascular
 injury or inhibition of neutrophil participation followed by inhibition
 of mononuclear cell participation, and thus provides superior therapy for
 inhibiting stenosis or restenosis following vascular injury. The sequence
 presented is the humanised mouse monoclonal antibody (mAb), 1D9, heavy
 chain variable region (VH), 1D9RHAHVH, which is comprised of the mouse 1D9
 mAb complementarity determining regions (CDR's) linked by human 4B4' CL
 MAB VH regions
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 620; DB 5; Length 117;
 Best Local Similarity 100.0%; Pred. No. 8.5e-48;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNWRQAPGKLEWVGRIKNNYAT 60
 DB 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNWRQAPGKLEWVGRIKNNYAT 60
 QY 61 YYADSVKDRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGNVWGQGLTVTSS 117
 DB 61 YYADSVKDRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGNVWGQGLTVTSS 117
 RESULT 4
 AAO14980
 ID AAO14980 standard; protein; 117 AA.
 XX
 AC AAO14980;
 XX
 DT 05-SEP-2002 (first entry)
 XX
 DE Humanised murine heavy chain variable region (1D9RHa Vh).
 XX
 KW Mouse; graft rejection; CC chemokine receptor 2 antagonist; mutant;
 KW CCR2 antagonist; anti-CCR2 antibody; kidney transplant; liver transplant;
 KW lung transplant; heart-lung transplant; pancreas transplant; mutein;
 KW bowel transplant; heart transplant; graft versus host disease;
 KW chronic graft rejection; antibody heavy chain variable region; 1D9RHa Vh.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 XX US2002042370-A1.
 XX
 PD 11-APR-2002.
 XX
 13-APR-2001; 2001US-00835087.
 XX
 14-APR-2000; 2000US-00549448.
 XX
 (MILL-) MILLENNIUM PHARM INC.
 XX
 Hancock WW;
 XX
 WPI; 2002-351265/38.
 XX

PT Inhibiting graft rejection, graft versus host disease or chronic
PT rejection of a transplanted graft, involves administering a CCR2
PT antagonist.

XX Claim 26; Fig 2; 16pp; English.

PS

CC The invention comprises a method of inhibiting graft rejection, graft
CC versus host disease or chronic rejection of a transplanted graft. The
CC method involves administering an antagonist of CC chemokine receptor 2
CC (CCR2) and optionally an immunosuppressive agent. The CCR2 antagonist may
CC be an anti-CCR2 antibody (i.e. containing light and heavy chain
CC complementarity determining regions from various non-human origins). CCR2
CC is known to be involved in the rejection of transplanted grafts. The
CC method of the invention is useful for inhibiting graft rejection -
CC particularly allografts such as kidney, liver, lung, heart-lung,
CC pancreas, bowel and heart. The method of the invention is also useful for
CC inhibiting graft versus host disease and for inhibiting chronic rejection
CC of a transplanted graft. The present amino acid sequence represents a
CC humanised murine antibody heavy chain variable region (1D9RHa Vh)

XX Sequence 117 AA;

SQ

Query Match 100.0%; Score 620; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 8.5e-48;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIITKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIITKNNYAT 60

Qy 61 YVADSVKDRFTISRDDSKNTLYLQMNSLKTEDTAVYCTTFYGVNGVWGQGLTLVTSS 117
Db 61 YVADSVKDRFTISRDDSKNTLYLQMNSLKTEDTAVYCTTFYGVNGVWGQGLTLVTSS 117

RESULT 6
ADQ89239

ID ADQ89239 standard; protein; 117 AA.

XX AC ADQ89239;

XX 21-OCT-2004 (first entry)

XX Humanised immunoglobulin protein #5.

XX Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;
XX inflammatory disease; autoimmune disorder; graft rejection;
XX HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;
XX anti-HIV; virucide; antiarteriosclerotic.

XX Synthetic.

XX US2004151721-A1.

XX 05-AUG-2004.

XX 10-DEC-2003; 2003US-00733563.

XX 19-OCT-2001; 2001US-0350166P.

XX 26-JUN-2002; 2002US-0392364P.

XX 17-OCT-2002; 2002US-00272899.

XX (OKEE/) O'KEEFE T.

XX (PONA/) PONATH P.

XX O'keefe T, Ponath P;

XX WPI; 2004-580175/56.

XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,
XX useful for diagnosing and/or treating inflammatory or autoimmune
XX diseases, and HIV infection.

XX Claim 1; SEQ ID NO 17; 128pp; English.

XX The invention relates to humanised immunoglobulin heavy and light chains
XX which have specificity for the CC-chemokine receptor 2 (CCR2) and an
XX immunoglobulin or its antigen binding fragment comprising the chains. The
XX humanised immunoglobulin or its antigen binding fragment preferably
XX comprises two heavy chains and two light chains. The humanised
XX immunoglobulin and its heavy and light chains are useful for the
XX diagnosis, prevention and/or treatment of diseases or conditions
XX associated with aberrant expression or activity of the CCR2 polypeptide,
XX such as inflammatory diseases, autoimmune disorders, graft rejection, HIV

CC infection and atherosclerosis. This sequence represents a humanised
 CC immunoglobulin protein of the invention.
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 620; DB 8; Length 117;
 Best Local Similarity 100.0%; Pred. No. 8.5e-48;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
 DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
 DB 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 7
 AEB09512
 ID AEB09512 standard; protein; 117 AA.
 XX
 AC AEB09512;

DT 08-SEP-2005 (first entry)
 XX
 DE Humanized 1D9 heavy chain variable region SEQ ID NO 17.
 XX
 KW antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;
 KW antibody engineering; therapeutic; diagnosis; inflammation;
 KW autoimmune disease; immune disorder; graft rejection; HIV infection;
 KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;
 KW heavy chain variable region.
 XX
 OS Synthetic.
 XX
 FN WO2005060368-A2.
 XX
 PD 07-JUL-2005.
 XX
 PF 10-DEC-2003; 2003WO-US039599.
 XX
 PR 10-DEC-2003; 2003WO-US039599.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Okeefe T, Ponath P;
 XX
 DR WPI; 2005-488561/49.
 XX
 PT New humanized immunoglobulin or its antigen binding portion having
 PT binding specificity for CC-chemokine receptor 2 and having a heavy chain
 PT and light chain, for treating inflammatory diseases, HIV, and autoimmune
 PT diseases.
 XX
 PS Claim 1; SEQ ID NO 17; 192pp; English.
 XX
 CC The invention describes a humanized immunoglobulin (I) or its antigen
 CC binding portion having binding specificity for CC-chemokine receptor 2
 CC (CCR2) and having a heavy chain and a light chain, where the heavy chain
 CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)
 CC sequence, given in specification or its portion, and the light chain
 CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given
 CC in specification. Also described are: a humanized immunoglobulin heavy
 CC chain, or its antigen binding fragment, having binding specificity for
 CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the
 CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized
 CC immunoglobulin light chain, or its antigen binding fragment, having
 CC binding specificity for CCR2 and comprising the amino acid sequence of
 CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)
 CC sequence, given in specification. The following are disclosed: isolated
 CC nucleic acid molecules comprising nucleic acid sequence encoding (I); a
 CC construct comprising nucleic acid molecule encoding (I); and host cell

CC comprising the nucleic acid molecule. (I) Is useful as a therapeutic
 CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus
 CC reducing inflammatory response, for use in the treatment of diseases
 CC associated with leukocyte infiltration of tissue, e.g. in the treatment
 CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV
 CC infection and monocyte-mediated disorders such as atherosclerosis. (I) Is
 CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.
 CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel
 CC fluid), and for modulating binding function and/or leukocyte trafficking
 CC modulated by CCR2. This is the amino acid sequence of a humanized 1D9
 CC heavy chain variable region used in the creation of a humanized anti-CCR2
 CC -antibody.
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 620; DB 9; Length 117;
 Best Local Similarity 100.0%; Pred. No. 8.5e-48;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
 DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
 DB 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 8
 AEC92171
 ID AEC92171 standard; protein; 117 AA.
 XX
 AC AEC92171;

DT 01-DEC-2005 (first entry)
 XX
 DE Humanized 1D9 mAb heavy chain variable region protein, 1D9RHA VH.
 XX
 KW Therapeutic; restenosis; vasotropic; cardiovascular disease; stenosis;
 KW pulmonary disease; respiratory-gen.; respiratory disease; stenosis;
 KW inflammatory bowel disease; antiinflammatory; gastrointestinal-gen.;
 KW gastrointestinal disease; inflammation; allergy; antiallergic;
 KW immune disorder; autoimmune disease; immunosuppressive; graft rejection;
 KW inflammation; antiinflammatory; 1D9; monoclonal antibody;
 KW humanized antibody; heavy chain variable region.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Synthetic.

PH Key Location/Qualifiers
 FT Region 31..35 /note= "Complementarity determining region (CDR) 1"
 FT Region 50..68 /note= "Complementarity determining region (CDR) 2"
 FT Region 101..106 /note= "Complementarity determining region (CDR) 3"
 FT
 XX US2005214299-A1.
 XX
 PD 29-SEP-2005.
 XX
 PF 12-SEP-2003; 2003US-00662061.
 XX
 PR 17-MAR-2000; 2000US-00528267.
 PR 15-MAR-2001; 2001US-00809739.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Horvath CJ, Rao PE;
 XX
 DR WPI; 2005-648726/66.
 XX

PT Inhibiting stenosis in a human blood vessel, by administering an anti-
 PT CD18 antibody, which binds specifically with the CD18 portion of a
 PT mammalian protein which comprises CD18, where stenosis is inhibited in
 PT the vessel.
 XX
 XX Disclosure; SEQ ID NO 20; 56pp; English.
 XX
 XX The invention relates to a method of inhibiting stenosis or restenosis of
 CC a blood vessel following vascular injury, wherein the recruitment and/or
 CC adhesion of neutrophils and the adhesion and/or recruitment of
 CC mononuclear cells to a site of vascular injury is inhibited. The methods
 CC of the invention are useful for inhibiting stenosis or restenosis in a
 CC human blood vessel, inhibiting interaction of a leukocyte having a CD18-
 CC containing cell-surface protein with vascular endothelium in a human,
 CC assessing the presence of leukocytes associated with vascular stenosis in
 CC blood obtained from a human and alleviating a disorder associated with
 CC stenosis in a blood vessel of a human. The invention is useful for
 CC treating mastitis, cholangitis and cholecystitis, chronic inflammatory
 CC diseases of the lungs such as interstitial lung disease and idiopathic
 CC pulmonary disease, hypersensitivity pneumonitis, pancreatitis, insulin-
 CC dependent diabetes mellitus, inflammatory bowel disease such as Crohn's
 CC disease, ulcerative colitis and sprue, inflammatory or allergic diseases
 CC including anaphylaxis, psoriasis, dermatitis, eczema, atopic dermatitis
 CC and allergic rhinitis, autoimmune diseases including arthritis, multiple
 CC sclerosis, myasthenia gravis, juvenile onset diabetes and autoimmune
 CC thyroiditis, graft rejection and other diseases or conditions in which
 CC undesirable inflammatory responses are to be inhibited including
 CC atherosclerosis or myositis. The present sequence is humanized murine 1D9
 CC monoclonal antibody (mAb; also termed as LS132.1D9, ID9-2-121-3-6) heavy
 CC chain variable region (VH) protein.

XX Sequence 117 AA;

Query Match 100.0%; Score 620; DB 9; Length 117;
 Best Local Similarity 100.0%; Pred. No. 8.5e-48;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
 DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
 QY 61 YYADSVKDRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
 DB 61 YYADSVKDRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 9
 AED43689
 ID AED43689 standard; protein; 117 AA.

AC AED43689;

XX 15-DEC-2005 (first entry)

XX Humanized murine 1D9 antibody heavy chain variable region 1D9RHA.

XX pharmaceutical; anticholinergic; CCR2 receptor; monoclonal antibody;
 KW respiratory-Gen.; antiinflammatory; inflammation; respiratory disease;
 KW antibody 1D9; humanized antibody.

XX Mus sp.

OS Homo sapiens.

OS Chimeric.

XX WO2005094798-A2.

XX 13-OCT-2005.

XX 22-MAR-2005; 2005WO-EP003005.

XX 30-MAR-2004; 2004EP-00007635.

XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.

(BOEH) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.

Pairret M;

WPI; 2005-714339/73.

XX New pharmaceutical composition containing one or more anticholinergics
 PT and a CCR2 receptor antagonist, and optionally together with an
 PT excipient, useful for treating inflammatory or obstructive diseases of
 PT the respiratory tract.

XX Claim 22; SEQ ID NO 8; 39pp; English.

XX The invention relates to a pharmaceutical composition containing one or
 CC more anticholinergics and a CCR2 receptor antagonist optionally in the
 CC form of individual optical isomers, their mixtures or racemates, addition
 CC salts, solvates or hydrates, and optionally together with an excipient.
 CC The pharmaceutical composition comprises the anticholinergic that is
 CC selected from tiotropium salts, oxitropium salts or ipratropium salts,
 CC preferably tiotropium salts. The anticholinergic is present in the form
 CC of the chloride, bromide, iodide, methanesulfonate or para-
 CC toluenesulfonate, preferably in the form of the bromide. The CCR2
 CC antagonist is an antibody, which can compete with the CCR2 binding of the
 CC monoclonal antibody 1D9 (ATCC HB-12549). The pharmaceutical composition
 CC is useful for preparing a medicament for treating inflammatory or
 CC obstructive diseases of the respiratory tract. The anticholinergic and
 CC CCR2 antagonist are useful for preparing the pharmaceutical composition.
 CC The present sequence represents the heavy chain variable region of a
 CC humanized murine 1D9 antibody.

XX Sequence 117 AA;

Query Match 100.0%; Score 620; DB 9; Length 117;
 Best Local Similarity 100.0%; Pred. No. 8.5e-48;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
 DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
 QY 61 YYADSVKDRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
 DB 61 YYADSVKDRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 10

AAE07034

ID AAE07034 standard; protein; 119 AA.

XX AAE07034;

XX 11-SEP-2003 (revised)

DT 16-OCT-2001 (first entry)

XX Humanised murine antibody heavy chain 1D9RHA protein.

XX Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotection; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherosclerosis; arteriosclerosis; restenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;
 KW inflammatory glomerulopathy; vascular intervention;
 KW necrotic hyperplasia; antibody 1D9 heavy chain; 1D9RHA.

XX Mus sp.

OS Homo sapiens.

OS Chimeric.

XX WO200157226-A1.

XX 09-AUG-2001.

XX 02-FEB-2001; 2001WO-US003537.
PF
XX
XX 03-FEB-2000; 2000US-00497625.
PR
XX
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;
PI
XX WPI; 2001-488888/53.
DR
XX N-PSDB; AAD13179.
DR
XX
XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated
PT disorder in a patient, comprises a binding specificity for CCR2, and a
PT non-human antigen binding region and human immunoglobulin.
PT
XX
XX Disclosure; Fig 23; 183pp; English.
PS
XX
XX The patent discloses a humanised antibody or its antigen-binding
CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),
CC comprising an antigen binding region of non-human origin and at least a
CC portion of an immunoglobulin of human origin. The humanised antibodies
CC are useful for inhibiting the interaction of a cell expressing CCR2. They
CC are useful for inhibiting or treating HIV infection. The proteins of the
CC invention are useful for inhibiting leukocyte trafficking, for treating
CC CCR2-mediated disorders such as inflammatory disorder, autoimmune
CC disorders such as rheumatoid arthritis and multiple sclerosis,
CC atherogenesis and atherosclerosis, and for inhibiting stenosis. They
CC are useful in therapy or diagnosis, and in the manufacture of a
CC medicament for treating CCR2 mediated disease. They are also useful for
CC treating allergy, anaphylaxis, malignancy, chronic and acute
CC inflammation, histamine and IgE-mediated allergic reaction, shock,
CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory
CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis
CC associated with vascular intervention, including angioplasty and/or stent
CC placement in a mammal. Humanised antibodies are also useful for
CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting
CC neointimal hyperplasia of a vessel in a mammal, preferably associated
CC with vascular intervention. The present sequence is humanised murine
CC antibody heavy chain region, 1D9RHA. 1D9RHA sequence consist of the
CC complementarity determining regions (CDRs) of the murine 1D9 antibody
CC heavy chain variable (VH) region genetically inserted into the framework
CC regions (FRs) of the human 4B4/CL antibody VH region. (Updated on 11-SEP-
CC 2003 to standardise OS field)
XX
XX Sequence 119 AA;
SQ
Query Match 100.0%; Score 620; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 8.7e-48;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNNYAT 60
QY 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVGGTGLTVSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVGGTGLTVSS 117
QY 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVGGTGLTVSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVGGTGLTVSS 117
RESULT 11
ADQ89326
ID ADQ89326 standard; protein; 119 AA.
XX
XX AC ADQ89326;
XX
XX 21-OCT-2004 (first entry)
DT
XX
XX Humanised immunoglobulin protein #9.
DE
XX Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;
KW inflammatory disease; autoimmune disorder; graft rejection;
KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;

KW anti-HIV; virucide; antiarteriosclerotic.
XX
XX Synthetic.
XX
XX US2004151721-A1.
PN
XX
XX 05-AUG-2004.
PD
XX
XX 10-DEC-2003; 2003US-00733563.
PF
XX
XX 19-OCT-2001; 2001US-0350166P.
PR
XX 26-JUN-2002; 2002US-0392364P.
PR
XX 17-OCT-2002; 2002US-00272899.
PR
XX
XX (OKEE/) O'KEEFE T.
PA
XX (PONA/) PONATH P.
PA
XX
XX O'keefe T, Ponath P;
PI
XX WPI; 2004-580175/56.
DR
XX N-PSDB; ADQ89319.
DR
XX
XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,
PT useful for diagnosing and/or treating inflammatory or autoimmune
PT diseases, and HIV infection.
PT
XX
XX Disclosure; SEQ ID NO 104; 128pp; English.
PS
XX
XX The invention relates to humanised immunoglobulin heavy and light chains
CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an
CC immunoglobulin or its antigen binding fragment comprising the chains. The
CC humanised immunoglobulin or its antigen binding fragment preferably
CC comprises two heavy chains and two light chains. The humanised
CC immunoglobulin and its heavy and light chains are useful for the
CC diagnosis, prevention and/or treatment of diseases or conditions
CC associated with aberrant expression or activity of the CCR2 polypeptide,
CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV
CC infection and atherosclerosis. This sequence represents a humanised
CC immunoglobulin protein of the invention.
XX
XX Sequence 119 AA;
SQ
Query Match 100.0%; Score 620; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 8.7e-48;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNNYAT 60
QY 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVGGTGLTVSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVGGTGLTVSS 117
RESULT 12
AEB09599
ID AEB09599 standard; protein; 119 AA.
XX
XX AC AEB09599;
XX
XX 08-SEP-2005 (first entry)
DT
XX
XX Humanized heavy chain 1D9RHA.
DE
XX
XX antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;
KW antibody engineering; therapeutic; diagnosis; inflammation;
KW autoimmune disease; immune disorder; graft rejection; HIV infection;
KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;
KW heavy chain variable region.
XX
XX Synthetic.
OS
XX

PN WO2005060368-A2.
 XX 07-JUL-2005.
 XX 10-DEC-2003; 2003WO-US039599.
 XX 10-DEC-2003; 2003WO-US039599.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX O'keefe T, Ponath P;
 XX WPI; 2005-488561/49.
 XX N-PSDB; AEB09592.
 XX New humanized immunoglobulin or its antigen binding portion having
 FT binding specificity for CC-chemokine receptor 2 and having a heavy chain
 FT and light chain, for treating inflammatory diseases, HIV, and autoimmune
 FT diseases.
 XX
 PS Disclosure; SEQ ID NO 104; 192pp; English.
 XX
 CC The invention describes a humanized immunoglobulin (I) or its antigen
 CC binding portion having binding specificity for CC-chemokine receptor 2
 CC (CCR2) and having a heavy chain and a light chain, where the heavy chain
 CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)
 CC sequences, given in specification or its portion, and the light chain
 CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given
 CC in specification. Also described are: a humanized immunoglobulin heavy
 CC chain, or its antigen binding fragment, having binding specificity for
 CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the
 CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized
 CC immunoglobulin light chain, or its antigen binding fragment, having
 CC binding specificity for CCR2 and comprising the amino acid sequence of
 CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)
 CC sequence, given in specification. The following are disclosed: isolated
 CC nucleic acid molecules comprising nucleic acid sequence encoding (I); a
 CC construct comprising nucleic acid molecule encoding (I); and host cell
 CC comprising the nucleic acid molecule. (I) Is useful as a therapeutic
 CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus
 CC reducing inflammatory response, for use in the treatment of diseases
 CC associated with leukocyte infiltration of tissue, e.g. in the treatment
 CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV
 CC infection and monocyte-mediated disorders such as atherosclerosis. (I) Is
 CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.
 CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel
 CC fluid), and for modulating binding function and/or leukocyte trafficking
 CC modulated by CCR2. This is the amino acid sequence of humanized heavy
 CC chain 1D9RHA.
 XX
 XX Sequence 119 AA;
 SQ
 Query Match 100.0%; Score 620; DB 9; Length 119;
 Best Local Similarity 100.0%; Pred. No. 8.7e-48;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANWVRQAPGKLEWVGRIKNNYAT 60
 DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANWVRQAPGKLEWVGRIKNNYAT 60
 QY 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYCTTFYGNVGWQGTLVTSS 117
 DB 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYCTTFYGNVGWQGTLVTSS 117
 RESULT 13
 AA06955
 ID AA06955 standard; protein; 117 AA.
 XX
 AC AA06955;
 XX
 DT 11-SEP-2003 (revised)
 DT 16-OCT-2001 (first entry)

XX Humanised murine 1D9 antibody heavy chain variable region, 1D9RHB.
 DE
 XX Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;
 KW inflammatory glomerulopathy; vascular intervention; 1D9 antibody;
 KW necrotic hyperplasia; VH; heavy chain variable region; 1D9RHB.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 XX Key Location/Qualifiers
 FH Region 27..35
 FT /label= CDR1
 FT /note= "Complementarity determining region 1"
 FT 50..68
 FT /label= CDR2
 FT /note= "Complementarity determining region 2"
 FT 101..106
 FT /label= CDR3
 FT /note= "Complementarity determining region 3"
 XX
 XX WO200157226-A1.
 PN 09-AUG-2001.
 XX
 PF 02-FEB-2001; 2001WO-US003537.
 PR
 XX 03-FEB-2000; 2000US-00497625.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX
 XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;
 XX WPI; 2001-488888/53.
 DR
 XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated
 PT disorder in a patient, comprises a binding specificity for CCR2, and a
 PT non-human antigen binding region and human immunoglobulin.
 XX
 PS Claim 62; Fig 12; 183pp; English.
 XX
 CC The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),
 CC comprising an antigen binding region of non-human origin and at least a
 CC portion of an immunoglobulin of human origin. The humanised antibodies
 CC are useful for inhibiting the interaction of a cell expressing CCR2. They
 CC are useful for inhibiting or treating HIV infection. The proteins of the
 CC invention are useful for inhibiting leukocyte trafficking, for treating
 CC CCR2-mediated disorders such as inflammatory disorder, autoimmune
 CC disorders such as rheumatoid arthritis and multiple sclerosis.
 CC atherogenesis and atherosclerosis, and for inhibiting restenosis. They
 CC are useful in therapy or diagnosis, and in the manufacture of a
 CC medicament for treating CCR-2 mediated disease. They are also useful for
 CC treating allergy, anaphylaxis, malignancy, chronic and acute
 CC inflammation, histamine and IGE-mediated allergic reaction, shock,
 CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory
 CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis
 CC associated with vascular intervention, including angioplasty and/or stent
 CC placement in a mammal. Humanised antibodies are also useful for
 CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting
 CC neointimal hyperplasia of a vessel in a mammal, preferably associated
 CC with vascular intervention. The present sequence is humanised murine 1D9
 CC antibody heavy chain variable (VH) region, 1D9RHB. (Updated on 11-SEP-
 XX 2003 to standardise OS field)
 XX Sequence 117 AA;


```

Query Match      98.9%; Score 613; DB 4; Length 117;
Best Local Similarity 98.3%; Pred. No. 3.6e-47;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRIRTKNNYAT 60
DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRIRTKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
DB 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 14
ID ABG75537 standard; protein; 117 AA.
XX
AC ABG75537;
XX
DT 16-APR-2003 (first entry)
XX
DE Humanised mouse mAb 1D9 heavy chain variable region, 1D9RHBVH.
XX
KW Mouse; stenosis; restenosis; blood vessel; vascular injury; antibody;
KW antigen binding fragment; cellular adhesion molecule; adhesion;
KW recruitment; neutrophil; antagonist; CCR2; mononuclear cell; angioplasty;
KW percutaneous transluminal coronary angioplasty; PTCA; stent;
KW vascular by-pass surgery; vascular grafting; endarterectomy; atherosclerosis;
KW endovascular stenting; prosthetic valve; transplantation;
KW inflammatory disease; mastitis; vaginitis; cholecystitis;
KW chronic bronchitis; asthma; graft-versus-host disease;
KW chronic inflammatory disease; hypersensitivity pneumonitis;
KW collagen disease; sarcoidosis; idiopathic; pancreatitis; HF-21/28;
KW insulin dependent; diabetes mellitus; inflammatory bowel disease;
KW Crohn's disease; allergic disease; psoriasis; atopic dermatitis; human;
KW allergic rhinitis; autoimmune disease; arthritis; multiple sclerosis;
KW graft rejection; atherosclerosis; myositis; therapy; 1D9; 1D9RHBVH;
KW heavy chain variable region; VH; complementarity determining region; CDR;
KW mutant; mutein.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
XX
Key Location/Qualifiers
XX
FT Misc-difference 28
FT /note= "Thr derived from the mouse 1D9 mAb sequence"
FT
FT Misc-difference 30
FT /note= "Ser derived from the mouse 1D9 mAb sequence"
FT
FT Region 31..35
FT /note= "Mouse complementarity determining region 1
FT (CDR1)"
FT
FT Region 50..68
FT /note= "Mouse complementarity determining region 2
FT (CDR2)"
FT
FT Region 101..106
FT /note= "Mouse complementarity determining region 3
FT (CDR3)"
FT
XX
US2002106369-A1.
XX
XX 08-AUG-2002.
XX
XX 15-MAR-2001; 2001US-00809739.
XX
XX 17-MAR-2000; 2000US-00528267.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Horvath CJ, Rao PE;
XX
XX WPI; 2002-697861/75.
XX

```

```

XX
PT Inhibiting (re)stenosis of blood vessel following vascular injury, by
PT administering first and second agents that inhibit adhesion and/or
PT recruitment of neutrophils and mononuclear cells, respectively to site of
PT vascular injury.
XX
XX Claim 32; Fig 18; 59pp; English.
XX
XX The invention discloses a method for inhibiting stenosis or restenosis of
XX a blood vessel following vascular injury in a subject. The method
XX involves administering to the subject a first therapeutic agent, which
XX comprises an antibody or its antigen binding fragment which binds a
XX cellular adhesion molecule, that inhibits the adhesion and/or recruitment
XX of neutrophils to a site of vascular injury and a second therapeutic
XX agent, which comprises an antagonist of CCR2 function, that inhibits
XX adhesion and/or recruitment of mononuclear cells to a site of vascular
XX injury. The vascular injury arises from a vascular intervention procedure
XX such as angioplasty (e.g. percutaneous transluminal coronary angioplasty
XX (PTCA) or angioplasty including placement of a stent), vascular by-pass
XX surgery, vascular grafting, endarterectomy, atherectomy, endovascular
XX stenting, insertion of a prosthetic valve and transplantation of organs,
XX tissues or cells. The method is also useful for treating inflammatory
XX diseases or conditions mediated by early neutrophil activity and later
XX mononuclear cell activity. Preferably, the method is useful for treating
XX a subject having mastitis, vaginitis, cholecystitis, chronic bronchitis,
XX asthma and graft-versus-host disease, chronic inflammatory disease of
XX lung, hypersensitivity pneumonitis, collagen diseases, sarcoidosis and
XX other idiopathic conditions, pancreatitis and insulin dependent diabetes
XX mellitus. The method is also useful for treating inflammatory bowel
XX disease, Crohn's disease, inflammatory or allergic diseases (such as
XX psoriasis, atopic dermatitis and allergic rhinitis), autoimmune diseases
XX (such as arthritis and multiple sclerosis), graft rejection,
XX atherosclerosis and myositis. The method enables simultaneous inhibition
XX of neutrophil and mononuclear cell participation in response to vascular
XX injury or inhibition of neutrophil participation followed by inhibition
XX of mononuclear cell participation, and thus provides superior therapy for
XX inhibiting stenosis or restenosis following vascular injury. The sequence
XX presented is the humanised mouse monoclonal antibody (mAb), 1D9, heavy
XX chain variable region (VH), 1D9RHBVH, which is comprised of the mouse 1D9
XX mAb complementarity determining regions (CDR's) linked by human 4B4'CL
XX mAb VH regions with a mouse derived Thr at position 28 and Ser at
XX position 30
XX
SQ Sequence 117 AA;

```

```

Query Match      98.9%; Score 613; DB 5; Length 117;
Best Local Similarity 98.3%; Pred. No. 3.6e-47;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRIRTKNNYAT 60
DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRIRTKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
DB 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 15
AAO14981
ID AAO14981 standard; protein; 117 AA.
XX
AC AAO14981;
XX
DT 05-SEP-2002 (first entry)
XX
DE Humanised murine heavy chain variable region (1D9RHB VH).
XX
KW Mouse; graft rejection; CC chemokine receptor 2 antagonist; mutant;
KW CCR2 antagonist; anti-CCR2 antibody; kidney transplant; liver transplant;
KW lung transplant; heart-lung transplant; pancreas transplant; mutein;
KW bowel transplant; heart transplant; graft versus host disease;
KW chronic graft rejection; antibody heavy chain variable region; 1D9RHB VH.
KW

```

XX Mus musculus.
OS Synthetic.
XX US2002042370-A1.
XX 11-APR-2002.
XX
PF 13-APR-2001; 2001US-00835087.
XX
PR 14-APR-2000; 2000US-00549448.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
FI Hancock WW;
XX
DR WPI; 2002-351265/38.
XX
XX Inhibiting graft rejection, graft versus host disease or chronic
PT rejection of a transplanted graft, involves administering a CCR2
FT antagonist.
XX
XX Claim 26; Fig 2; 16pp; English.
XX
CC The invention comprises a method of inhibiting graft rejection, graft
CC versus host disease or chronic rejection of a transplanted graft. The
CC method involves administering an antagonist of CC chemokine receptor 2
CC (CCR2) and optionally an immunosuppressive agent. The CCR2 antagonist may
CC be an anti-CCR2 antibody (i.e. containing light and heavy chain
CC complementarity determining regions from various non-human origins). CCR2
CC is known to be involved in the rejection of transplanted grafts. The
CC method of the invention is useful for inhibiting graft rejection -
CC particularly allografts such as kidney, liver, lung, heart-lung,
CC pancreas, bowel and heart. The method of the invention is also useful for
CC inhibiting graft versus host disease and for inhibiting chronic rejection
CC of a transplanted graft. The present amino acid sequence represents a
CC humanised murine antibody heavy chain variable region (1D9RHb Vh)
XX
SQ Sequence 117 AA;

Query Match 98.9%; Score 613; DB 5; Length 117;
Best Local Similarity 98.3%; Pred. No. 3.6e-47;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIRTKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117

Search completed: June 10, 2006, 11:56:18
Job time : 76.7162 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 11:56:42 ; Search time 12.473 Seconds
(without alignments)
902.540 Million cell updates/sec

Title: US-10-733-563-17

Perfect score: 620

Sequence: 1 EVQLVESGGGLVPGGSLRL.....CTTFYGVNGVGGTFLVTSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	492.5	79.4	137	2 S42467	Ig heavy chain V r
2	490	79.0	121	2 S31106	Ig heavy chain - h
3	485	78.2	127	2 S58213	Ig heavy chain V r
4	483	77.9	121	2 H36005	Ig heavy chain V r
5	482	77.7	117	2 S31109	Ig heavy chain - h
6	480	77.4	121	2 A41940	Ig heavy chain V r
7	479.5	77.3	141	2 I32513	Ig heavy chain pre
8	478	77.1	123	2 A36006	Ig heavy chain V r
9	477	76.9	138	2 A30561	Ig heavy chain pre
10	474	76.5	139	2 S31678	Ig heavy chain V r
11	472.5	76.2	126	2 S44107	Ig heavy chain V-D
12	467	75.3	160	2 S05271	Ig heavy chain pre
13	463.5	74.8	122	2 S30533	Ig heavy chain V r
14	463.5	74.8	147	2 I37780	Ig variable region
15	463	74.7	123	2 S26794	Ig heavy chain V r
16	463	74.7	140	2 S31588	Ig heavy chain V r
17	461	74.4	119	2 C36005	Ig heavy chain V r
18	460	74.2	115	1 AVMS06	Ig heavy chain V-I
19	460	74.2	119	2 S31107	Ig heavy chain - h
20	459.5	74.1	120	2 E49590	Ig heavy chain V r
21	458	73.9	138	2 S31666	Ig heavy chain V r
22	457.5	73.8	120	2 S48798	Ig heavy chain V r
23	456	73.5	119	2 S31108	Ig heavy chain - h
24	456	73.5	143	2 S23624	Ig heavy chain V r
25	454.5	73.3	122	2 E36005	Ig heavy chain V r
26	454.5	73.3	124	2 S20775	Ig heavy chain V r
27	454.5	73.3	124	2 S20782	Ig heavy chain V r
28	454	73.2	119	2 D36005	Ig heavy chain V r
29	454	73.2	123	2 S34009	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S42467

Ig heavy chain V region precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C;Accession: S42467

R;Shiyanov, P.A.; Beepalov, I.A.; Terletskaya, H.N.; Deyev, S.M.

submitted to the EMBL Data Library, March 1994

A;Reference number: S42466

A;Accession: S42467

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-137 <SH1>

A;Cross-references: UNIPARC:UPI00001161DB; EMBL:X78107; NID:g460798; PIDN:CAAS4997.1; PIR

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-119/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 492.5; DB 2; Length 137;

Best Local Similarity 79.2%; Pred. No. 3.9e-37;

Matches 95; Conservative 11; Mismatches 9; Indels 5; Gaps 2;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60

DB 20 EVQLVESGGGLVQPKGSLKLSCAASGFTFTYAMNVRQAPGKLEWVAIRSKNNYAT 79

QY 61 YYADSVKDRFTISRDSKNTLYIQMNSLKTEDTAVYYCTTFYGN---GVWGQGTFLVTSS 117

DB 80 YYGNSVKDRFTISRDSQSMLYLQMNILKTEDTAMYVCV--YGNFGFAYWGQGTFLVTSA 137

RESULT 2

S31106

Ig heavy chain - human

C;Species: Homo sapiens (man)

C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C;Accession: S31106

R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman,

Eur. J. Immunol. 22, 247-251, 1992

A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple

A;Reference number: S31104; MUID:92111633; PMID:1730252

A;Accession: S31106

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA

A;Residues: 1-121 <RAA>

A;Cross-references: UNIPARC:UPI0000176C8E; EMBL:X62954

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-100/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 490; DB 2; Length 121;

```
Best Local Similarity 81.0%; Pred. No. 5.8e-37;
Matches 98; Conservative 5; Mismatches 14; Indels 4; Gaps 1;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
   |||||
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSNAMSVWRQAPGKLEWVGRIKSKTDGGTT 60
   |||||

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTT-----FYGNGVWGQTLTVTS 116
   |||||
Db 61 DYAAPVKGRTISRDDSKNTLYLQMSLKTEDTAVYYCTTVIDYYGMDVWGQTTVTVS 120
   |||||

Qy 117 S 117
Db 121 S 121

RESULT 3
S58213
IG heavy chain V region (anti-F(ab')2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1996 #sequence_revision 12-Apr-1996 #text_change 23-Jul-1999
C;Accession: S58213; S58212
R;Welschhof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling,
submitted to the EMBL Data Library, July 1995
A;Description: Characterization of heavy and light chain immunoglobulin variable region
A;Reference number: S58206
A;Accession: S58213
A;Molecule type: mRNA
A;Residues: 1-127 <WEL>
A;Cross-references: UNIPARC:UPI000003PEA8; EMBL:X89055; NID:9929638; PIDN:CAA61442.1; PI
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMV>

Query Match 78.2%; Score 485; DB 2; Length 127;
Best Local Similarity 75.6%; Pred. No. 1.7e-36;
Matches 96; Conservative 7; Mismatches 14; Indels 10; Gaps 1;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
   |||||
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSGSTMHWVRQASGKLEWVGRIKNDNSYAT 60
   |||||

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTT-----FYGNGVWGQ 110
   |||||
Db 61 AYASVKGRTISRDDSENTAYLQMSLKIEDTAVYYCTTRGSSWVRGVNGYGMVWGQ 120
   |||||

Qy 111 TLTVSS 117
Db 121 TTVTSS 127

RESULT 4
H36005
IG heavy chain V region (M85) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C;Accession: H36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: H36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <SCH>
A;Cross-references: UNIPARC:UPI0000176C28; GB:M34032
C;Genetics:
A;Gene: GDB:IGH@; IGHY1
A;Gene-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMV>
```

```
Query Match 77.9%; Score 483; DB 2; Length 121;
Best Local Similarity 81.0%; Pred. No. 2.4e-36;
Matches 98; Conservative 3; Mismatches 16; Indels 4; Gaps 1;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
   |||||
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSNAMSVWRQAPGKLEWVGRIKSKTDGGTT 60
   |||||

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFFYNG-----VWGQTLTVTS 116
   |||||
Db 61 DYAAPVKGRTISRDDSKNTLYLQMSLKTEDTAVYYCTTDRGSSQGDYWGQTLTVTS 120
   |||||

Qy 117 S 117
Db 121 S 121

RESULT 5
S31109
IG heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31109
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman,
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31109
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-117 <RAA>
A;Cross-references: UNIPARC:UPI0000176DCA; EMBL:X62960
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMV>

Query Match 77.7%; Score 482; DB 2; Length 117;
Best Local Similarity 82.1%; Pred. No. 2.9e-36;
Matches 96; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
   |||||
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSNAMSVWRQAPGKLEWVGRIKSKTDGGTT 60
   |||||

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFFYNGVWGQTLTVSS 117
   |||||
Db 61 DYAAPVKGRTISRDDSKNTLYLQMSLKTEDTAVYYCTATYYFDYWGQTLTVSS 117
   |||||

RESULT 6
A41940
IG heavy chain V region G2b, autoantibody BV04-01 - mouse (fragment)
N;Alternate names: anti-DNA autoantibody BV04-01, heavy chain V region
C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 07-May-1999
C;Accession: A41940; PLO201
R;Herron, J.N.; He, X.M.; Ballard, D.W.; Blier, P.R.; Pace, P.E.; Bothwell, A.L.; Voss J;
Proteins 11, 159-175, 1991
A;Title: An autoantibody to single-stranded DNA: comparison of the three-dimensional str
A;Reference number: A41940; MUID:92086633; PMID:1749770
A;Accession: A41940
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-121 <HER>
A;Cross-references: UNIPARC:UPI0000176D34
A;Note: sequence extracted from NCBI backbone (NCBIP:70715)
R;Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from NZ
A;Reference number: PLO198; MUID:90309768; PMID:2114528
A;Accession: PLO201
```

A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: A36006
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-123 <SCH>
A:Cross-references: UNIPARC:UPI000003FEBD; GB:M34023
C:Genetics:
A:Gene: GDB:IGH@; IGHDIY1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 478; DB 2; Length 123;
Best Local Similarity 78.9%; Pred. No. 6.9e-36;
Matches 97; Conservative 4; Mismatches 16; Indels 6; Gaps 1;

Qy 1 EVQLVESGGLVKPGGSLRLSCAASGFTTSAYAMNWVRQAPGKLEWVGRIETKNNVAT 60
| | | | | | | | | | | | | | | | | | | | | | : | | | | |
Db 1 EVQLVESGGLVKPGGSLRLSCAASGFTTSANAWMSWRQAPGKLEWVGRIKSKTDGGTT 60
| | | | | | | | | | | | | | | | | | | | | | : | | | | |

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTT-----FYGNCGVWGQGTILVT 114
| | | | | | | | | | | | | | | | | | | | | | : | | | | |
Db 61 DYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTSPGIAGVAGTDYWGGQTLVT 120
| | | | | | | | | | | | | | | | | | | | | | : | | | | |

Qy 115 VSS 117
| | |
Db 121 VSS 123
| | |

RESULT 9
A30561
Ig heavy chain precursor V-IIJ region (4B4) - human (fragment)
N:Alternate names: Ig heavy chain V region (DP-38)
C:Species: Homo sapiens (man)
C>Date: 23-Mar-1989 #sequence revision 23-Mar-1989 #text_change 23-Jul-1999
C:Accession: A30561; S26931; S34008
R:Sanz, I.; Dang, H.; Takei, M.; Talal, N.; Capra, J.D.
J. Immunol. 142, 883-887, 1989
A>Title: V-H sequence of a human anti-Sm autoantibody. Evidence that autoantibodies can
A:Reference number: A30561; MUID:89110065; PMID:2492331
A:Accession: A30561
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-138 <SAN>
A:Cross-references: UNIPARC:UPI0000176C80
R:Tominson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A>Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26931
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 20-119 <TOM>
A:Cross-references: UNIPARC:UPI000011640B; EMBL:Z12338; NID:g32896; PIDN:CAA78208.1; PID
R:Marieite, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A>Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A:Reference number: S34001; MUID:93209281; PMID:7681398
A:Accession: S34008
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 20-119 <MAR>
A:Cross-references: UNIPARC:UPI000011640B
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 477; DB 2; Length 138;
Best Local Similarity 81.5%; Pred. No. 9.5e-36;
Matches 97; Conservative 5; Mismatches 15; Indels 2; Gaps 1;

THIS PAGE BLANK (USPTO)

Result No.	Query			ID	Description
	Score	Match	Length		
1	490	79.0	123	Q2VT26_MOUSE	Q2vt26 mus musculu
2	487	78.5	123	Q2VT28_MOUSE	Q2vt28 mus musculu
3	482	77.7	123	Q2VR03_MOUSE	Q2vr03 mus musculu
4	478.5	77.2	124	Q2VT24_MOUSE	Q2vt24 mus musculu
5	477.5	77.0	471	Q66K04_MOUSE	Q66k04 mus musculu
6	463	74.7	464	Q6MZU6_HUMAN	Q6mzu6 homo sapien
7	460	74.2	115	HV32_MOUSE	P01801 mus musculu
8	453	73.1	113	Q9UL90_HUMAN	Q9ul90 homo sapien
9	453	73.1	131	Q9UL88_HUMAN	Q9ul88 homo sapien
10	452	72.9	240	Q6SZC9_HUMAN	Q6szc9 homo sapien
11	450	72.6	113	HV27_MOUSE	P01796 mus musculu
12	450	72.6	113	HV30_MOUSE	P01799 mus musculu
13	450	72.6	115	HV33_MOUSE	P01802 mus musculu
14	447	72.1	597	Q96BB9_HUMAN	Q96bb9 homo sapien
15	446.5	72.0	494	Q96K68_HUMAN	Q96k68 homo sapien
16	446.5	72.0	613	Q8WUK3_HUMAN	Q8wuk1 homo sapien
17	446	71.9	121	Q9UL71_HUMAN	Q9ul71 homo sapien
18	444	71.6	113	HV28_MOUSE	P01797 mus musculu
19	444	71.6	487	Q8OZ17_MOUSE	Q8oz17 mus musculu
20	443	71.5	116	Q9UL93_HUMAN	Q9ul93 homo sapien
21	442.5	71.4	606	Q6GMW2_HUMAN	Q6gmw2 homo sapien
22	442	71.3	113	HV31_MOUSE	P01800 mus musculu
23	440.5	71.0	118	Q9UL91_HUMAN	Q9ul91 homo sapien
24	440	71.0	113	HV29_MOUSE	P01798 mus musculu
25	439	70.8	468	Q569B4_RAT	Q569b4 rattus norv
26	437	70.5	458	Q65ZQ1_HUMAN	Q65zq1 homo sapien
27	436.5	70.4	469	Q569F4_HUMAN	Q569f4 homo sapien
28	436	70.3	472	Q6N089_HUMAN	Q6n089 homo sapien
29	434	70.0	478	Q6P181_HUMAN	Q6p181 homo sapien
30	432.5	69.8	122	HV33_MOUSE	P01768 mus musculu
31	432.5	69.8	573	Q8WU38_HUMAN	Q8wu38 homo sapien


```
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 07-MAR-2006, entry version 38.
DE Ig heavy chain V-III region J606.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=8209361; PubMed=6798111;
RA Johnson N., Slankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
RT binding proteins.";
RL J. Immunol. 128:302-307(1982).
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC binds inulin.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR PIR; C92811; AVMS06.
DR HSP; P01852; INFD.
DR Ensembl; ENSMUSG00000045097; Mus musculus.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT CHAIN 1 >115
FT DOMAIN 1 114
FT DISULFID 22 98
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12810 MW; B67AD6638A121A5F CRC64;

Query Match 74.2%; Score 460; DB 1; Length 115;
Best Local Similarity 73.5%; Pred. No. 1.7e-41;
Matches 86; Conservative 15; Mismatches 14; Indels 2; Gaps 1;

QY 1 EVLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIRTKNNYAT 60
DB 1 EVKLEESGGGLVQPGGSKLSCVSGFTFSYNNWVRQSPKGLWVAIRLKSNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYQMNSLKTEDTAVYYCTTFYNGVWGQGLTVTVSS 117
DB 61 HYAESVKGRTFTISRDDSKSYLQMNLRADETGIYYCTT--GFAVWGQGLTVTVA 115

RESULT 8
Q9UL90_HUMAN PRELIMINARY; PRT; 113 AA.
ID Q9UL90_HUMAN
AC Q9UL90;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=98277139; PubMed=6614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Placental alkaline phosphatase has a binding site for the human
RA immunoglobulin-G Fc portion.";
```

```
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92111633; PubMed=1730252;
RA Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA Schuurman R.K.;
RT "Restricted utilization of germ-line VH3 genes and short diverse third
RT complementarity-determining regions (CDR3) in human fetal B lymphocyte
RT immunoglobulin heavy chain rearrangements.";
RL Eur. J. Immunol. 22:247-251(1992).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF035024; AAD56260.1; -; mRNA.
DR PIR; S78486; S78486.
DR HSP; P01772; 2PB4.
DR SMR; Q9UL90; 1-113.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin domain.
FT NON TER 1 1
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 73.1%; Score 453; DB 2; Length 113;
Best Local Similarity 77.8%; Pred. No. 9.4e-41;
Matches 91; Conservative 7; Mismatches 15; Indels 4; Gaps 2;

QY 1 EVLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIRTKNNYAT 60
DB 1 EVLVESGGGVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAFIRYDGSN--K 58

QY 61 YYADSVKDRFTISRDDSKNTLYQMNSLKTEDTAVYYCTTFYNGVWGQGLTVTVSS 117
DB 59 YYADSVKGRFTISRDNKNTLYQMNSLRADETAVYYCAK--DLNVWGQGLTVTVSS 113

RESULT 9
Q9UL88_HUMAN PRELIMINARY; PRT; 131 AA.
ID Q9UL88_HUMAN
AC Q9UL88;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP PROTEIN SEQUENCE.
RX MEDLINE=92209522; PubMed=1555592;
RA Makiya R., Stigbrand T.;
RT "Placental alkaline phosphatase has a binding site for the human
RT immunoglobulin-G Fc portion.";
```

```

RL Eur. J. Biochem. 205:341-345(1992).
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: AF03026; AAD56262.1; -, mRNA.
DR PIR: S21205; S21205.
DR PIR: S30533; S30533.
DR HSSP: P01852; INF.
DR SMR: Q9UL88; 1-131.
DR LinkHub; Q9UL88; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 131
FT NON_TER 131
SQ SEQUENCE 131 AA; 14142 MW; 96E7D668E375DEA0 CRC64;

Query Match 73.1%; Score 453; DB 2; Length 131;
Best Local Similarity 69.6%; Pred. No. 1.1e-40;
Matches 94; Conservative 6; Mismatches 13; Indels 22; Gaps 2;

QY 1 EVQLVSGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRIKNNYAT 60
DB 1 EVQLVSGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRIKNNYAT 60
QY 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYNGV----- 106
DB 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYNGV----- 106
QY 107 -----WGQGLTLVTSS 117
DB 117 SFYWGQGLTLVTSS 131

RESULT 10
Q652C9 HUMAN PRELIMINARY; PRT; 240 AA.
ID Q652C9
AC Q652C9
DT 11-OCT-2004, integrated into UniprotKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C1q/7;
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: Y13056; CAA73499.1; -, mRNA.
DR LinkHub; Q652C9; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.

Query Match 72.6%; Score 450; DB 1; Length 113;
Best Local Similarity 73.0%; Pred. No. 2e-40;
Matches 84; Conservative 15; Mismatches 14; Indels 2; Gaps 1;

QY 1 EVQLVSGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRIKNNYAT 60

```

```

DR PROSITE; PS50835; IG LIKE; 2.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 72.9%; Score 452; DB 2; Length 240;
Best Local Similarity 74.8%; Pred. No. 3e-40;
Matches 89; Conservative 12; Mismatches 14; Indels 4; Gaps 2;

QY 1 EVQLVSGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRIKNNYAT 60
DB 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFSYGHVVRQAPGKGLVWVIVSDGSN--K 58
QY 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYNGV--WGQGLTLVTSS 117
DB 59 YYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDWGDGLDPWCKGLTLVTSS 117

RESULT 11
HV27 MOUSE STANDARD; PRT; 113 AA.
ID HV27 MOUSE
AC P01736;
DT 21-JUL-1986, integrated into UniprotKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 07-MAR-2006, entry version 39.
DE Ig heavy chain V-III region A4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -! MISCELLANEOUS: This chain was isolated from a myeloma protein that
binds inulin.
CC -! SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR PIR: A93818; AVMSAB.
DR HSSP; P01783; IIGC.
DR SMR; P01796; 1-113.
DR Ensembl; ENSMUSG00000045097; Mus musculus.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT CHAIN 1 >113
FT DOMAIN 1 >113
FT DISULFID 22 98
FT NON_TER 113
SQ SEQUENCE 113 AA; 12675 MW; 76658C121C598285 CRC64;

Query Match 72.6%; Score 450; DB 1; Length 113;
Best Local Similarity 73.0%; Pred. No. 2e-40;
Matches 84; Conservative 15; Mismatches 14; Indels 2; Gaps 1;

QY 1 EVQLVSGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRIKNNYAT 60

```

```
Db 1 EVKLEESGGGLVPGGSKMLSCVASGFTFSGNYMNMVVRQSPKGLWVAIRLKSHNYAT 60
QY 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYCTTFYGNVGWQGLTLTV 115
Db 61 HYAESVKGRTISRDDSKSVYLQMNLRADTGIYYCTT--GFAYWGQGLTLTV 113

RESULT 12
HV30_MOUSE STANDARD; PRT; 113 AA.
AC HV30_MOUSE
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 07-MAR-2006, entry version 38.
DE Ig heavy chain V-III region ABE-47N.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN PROTEIN SEQUENCE.
RP MEDLINE=77134726; PubMed=402936;
RA Vrana M., Rudikoff S., Potter M.;
RT "Heavy-chain variable-region sequence from an inulin-binding myeloma
protein.";
RL Biochemistry 16:1170-1175(1977).
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC binds inulin.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
-----
DR PIR; A90400; AVMSB7.
DR HSSP; P01810; 2FBJ.
DR SMR; P01799; 1-113.
DR Ensembl; ENSMUSG00000045097; Mus musculus.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT CHAIN 1 >113
FT DOMAIN 1 >113
FT DISULFID 22 98
FT NON_TER 113 113
FT SEQUENCE 113 AA; 12675 MW; 76658C16C779845E CRC64;

Query Match 72.6%; Score 450; DB 1; Length 113;
Best Local Similarity 73.08; Pred. No. 2e-40;
Matches 84; Conservative 16; Mismatches 13; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVPGGSKRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIPTKNNYAT 60
Db 1 EVKLEESGGGLVPGGSKMLSCVASGFTFSGNYMNMVVRQSPKGLWVAIRLKSHNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYCTTFYGNVGWQGLTLTV 115
Db 61 HYAESVKGRTISRDDSKSVYLQMNLRADTGIYYCTT--GFAYWGQGLTLTV 113

RESULT 13
HV33_MOUSE STANDARD; PRT; 115 AA.
ID HV33_MOUSE
AC P01802;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
```

```
DT 21-JUL-1986, sequence version 1.
DT 07-MAR-2006, entry version 39.
DE Ig heavy chain V-III region W3082.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN PROTEIN SEQUENCE.
RP MEDLINE=8209361; PubMed=6798111;
RA Johnson N., Slankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
binding proteins.";
RL J. Immunol. 128:302-307(1982).
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC binds inulin.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
-----
DR PIR; D92811; AVMS82.
DR HSSP; P01852; 1NFD.
DR SMR; P01802; 1-115.
DR Ensembl; ENSMUSG00000045097; Mus musculus.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT CHAIN 1 >115
FT DOMAIN 1 114
FT DISULFID 22 98
FT NON_TER 115 115
FT SEQUENCE 115 AA; 12887 MW; 9B4517648C121C5A CRC64;

Query Match 72.6%; Score 450; DB 1; Length 115;
Best Local Similarity 71.8%; Pred. No. 2e-40;
Matches 84; Conservative 17; Mismatches 14; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVPGGSKRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIPTKNNYAT 60
Db 1 EVKLEESGGGLVPGGSKMLSCVASGFTFSGNYMNMVVRQSPKGLWVAIRLKSHNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYCTTFYGNVGWQGLTLTVSS 117
Db 61 HYAESVKGRTISRDDSKSVYLQMNLRADTGIYYCTT--GFAYWGQGLTLTVSA 115

RESULT 14
Q96BB9_HUMAN PRELIMINARY; PRT; 597 AA.
ID Q96BB9_HUMAN
AC Q96BB9;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Primary B-Cells;
```


GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 12:05:52 ; Search time 20.2027 Seconds
(without alignments)
506.917 Million cell updates/sec

Title: US-10-733-563-17
Perfect score: 620
Sequence: 1 EVQLVESGGGLVPGGSLRL.....CTTFYGNVGWGQGLTVTVSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Issued Patents AA.*
- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep.*
 - 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep.*
 - 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep.*
 - 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep.*
 - 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep.*
 - 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep.*
 - 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	620	100.0	117	2	US-09-809-739-20
2	620	100.0	117	2	US-09-840-459-17
3	620	100.0	117	2	US-09-497-625A-17
4	620	100.0	119	2	US-09-840-459-104
5	620	100.0	119	2	US-09-497-625A-104
6	613	98.9	117	2	US-09-809-739-21
7	613	98.9	117	2	US-09-840-459-18
8	613	98.9	117	2	US-09-497-625A-18
9	604	97.4	117	2	US-09-809-739-22
10	604	97.4	117	2	US-09-840-459-19
11	604	97.4	117	2	US-09-497-625A-19
12	599	96.6	117	2	US-09-809-739-23
13	599	96.6	117	2	US-09-840-459-20
14	599	96.6	117	2	US-09-497-625A-20
15	548	88.4	117	2	US-09-809-739-12
16	548	88.4	117	2	US-09-840-459-10
17	548	88.4	117	2	US-09-497-625A-10
18	548	88.4	148	2	US-09-840-459-100
19	548	88.4	148	2	US-09-497-625A-100
20	488.5	80.4	444	3	US-09-674-716B-53
21	488.5	78.8	116	1	US-08-428-197-10
22	488.5	78.8	116	5	PCT-US93-10555-10
23	487	78.5	123	2	US-09-097-055B-87
24	487	78.5	123	2	US-09-893-615-87
25	485	78.2	125	1	US-08-428-197-9
26	485	78.2	125	5	PCT-US93-10555-9

Sequence 71, Appl
Sequence 71, Appl
Sequence 74, Appl
Sequence 74, Appl
Sequence 36, Appl
Sequence 83, Appl
Sequence 73, Appl
Sequence 70, Appl
Sequence 93, Appl
Sequence 70, Appl
Sequence 93, Appl
Sequence 7, Appl
Sequence 94, Appl
Sequence 11, Appl
Sequence 19, Appl
Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-809-739-20
; Sequence 20, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-20

Query Match 100.0%; Score 620; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.2e-54;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIRTKNNYAT 60
Qy 61 YYADSVKDRFTISRDSDSKNTLYLQMSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
Db 61 YYADSVKDRFTISRDSDSKNTLYLQMSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117

RESULT 2
US-09-840-459-17
; Sequence 17, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND


```
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized heavy chain
US-09-497-625A-104

Query Match      100.0%; Score 620; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.2e-54;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 6
US-09-809-739-21
; Sequence 21, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: Restenosis
; CURRENT APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-21

Query Match      98.9%; Score 613; DB 2; Length 117;
Best Local Similarity 98.3%; Pred. No. 6.1e-54;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 7
US-09-840-459-18
; Sequence 18, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012

Query Match      98.9%; Score 613; DB 2; Length 117;
Best Local Similarity 98.3%; Pred. No. 6.1e-54;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 8
US-09-497-625A-18
; Sequence 18, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; PRIOR FILING DATE: 2000-02-03
; PRIOR FILING DATE: 1999-07-22
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-18

Query Match      98.9%; Score 613; DB 2; Length 117;
Best Local Similarity 98.3%; Pred. No. 6.1e-54;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
```

```
Db      61 YYADSVKDRFTISRDDSKNTLYLQMNLSKLTEDTAVYYCTTFYGNVGWVGQGLTVTVSS 117

RESULT 9
US-09-809-739-22
; Sequence 22, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-22

Query Match      97.4%; Score 604; DB 2; Length 117;
Best Local Similarity 96.6%; Pred. No. 4.8e-53;
Matches 113; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 EVLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIRTKNNYAT 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 EVLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIRTKNNYAT 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy      61 YYADSVKDRFTISRDDSKNTLYLQMNLSKLTEDTAVYYCTTFYGNVGWVGQGLTVTVSS 117
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 YYADSVKDRYTI SRDDSKNTLYLQMNLSKLTEDTAVYYCTTFYGNVGWVGQGLTVTVSS 117
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10
US-09-840-459-19
; Sequence 19, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-19

Query Match      97.4%; Score 604; DB 2; Length 117;
Best Local Similarity 96.6%; Pred. No. 4.8e-53;
Matches 113; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 EVLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIRTKNNYAT 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 EVLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIRTKNNYAT 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy      61 YYADSVKDRFTISRDDSKNTLYLQMNLSKLTEDTAVYYCTTFYGNVGWVGQGLTVTVSS 117
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 YYADSVKDRYTI SRDDSKNTLYLQMNLSKLTEDTAVYYCTTFYGNVGWVGQGLTVTVSS 117
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
US-09-497-625A-19
; Sequence 19, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-19

Query Match      97.4%; Score 604; DB 2; Length 117;
Best Local Similarity 96.8%; Pred. No. 4.8e-53;
Matches 113; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 EVLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIRTKNNYAT 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 EVLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIRTKNNYAT 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy      61 YYADSVKDRFTISRDDSKNTLYLQMNLSKLTEDTAVYYCTTFYGNVGWVGQGLTVTVSS 117
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 YYADSVKDRYTI SRDDSKNTLYLQMNLSKLTEDTAVYYCTTFYGNVGWVGQGLTVTVSS 117
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
US-09-809-739-23
; Sequence 23, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 23
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
; US-09-809-739-23

Query Match          96.6%; Score 599; DB 2; Length 117;
Best Local Similarity 95.7%; Pred. No. 1.5e-52;
Matches 112; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFSFNAYAMNVRQAPGKLEWVARIRTKNNYAT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 YYADSVKDRYTIISRDSSKNTLYLQMSLKTEDTAVYYCVTFYGVNGVWGQGLTVTVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 13
US-09-840-459-20
; Sequence 20, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
; US-09-840-459-20

Query Match          96.6%; Score 599; DB 2; Length 117;
Best Local Similarity 95.7%; Pred. No. 1.5e-52;
Matches 112; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFSFNAYAMNVRQAPGKLEWVARIRTKNNYAT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 YYADSVKDRYTIISRDSSKNTLYLQMSLKTEDTAVYYCVTFYGVNGVWGQGLTVTVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
US-09-497-625A-20
; Sequence 20, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
```

```
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
; US-09-497-625A-20

Query Match          96.6%; Score 599; DB 2; Length 117;
Best Local Similarity 95.7%; Pred. No. 1.5e-52;
Matches 112; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFSFNAYAMNVRQAPGKLEWVARIRTKNNYAT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 YYADSVKDRYTIISRDSSKNTLYLQMSLKTEDTAVYYCVTFYGVNGVWGQGLTVTVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 15
US-09-809-739-12
; Sequence 12, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(117)
; OTHER INFORMATION: Murine mAb 1D9 heavy chain variable region
; NAME/KEY: SITE
; LOCATION: (31)...(35)
; OTHER INFORMATION: CDR1
; NAME/KEY: SITE
; LOCATION: (50)...(68)
; OTHER INFORMATION: CDR2
; NAME/KEY: SITE
; LOCATION: (101)...(106)
; OTHER INFORMATION: CDR3
; OTHER INFORMATION: Mouse
; US-09-809-739-12
```


GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 12:31:52 ; Search time 66.4054 Seconds
(without alignments)
816.140 Million cell updates/sec

Title: US-10-733-563-17

Perfect score: 620

Sequence: 1 EVQLVESGGGLVPGGSLRL.....CTTFYGNVGWGQGLTVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	620	100.0	117	3	US-09-835-087-10
2	620	100.0	117	3	US-09-809-739-20
3	620	100.0	117	3	US-09-840-459-17
4	620	100.0	117	4	US-10-766-773-17
5	620	100.0	117	4	US-10-766-610-17
6	620	100.0	117	4	US-10-733-563-17
7	620	100.0	117	5	US-10-662-061-20
8	620	100.0	117	6	US-11-075-184A-8
9	620	100.0	119	3	US-09-840-459-104
10	620	100.0	119	4	US-10-766-773-104
11	620	100.0	119	4	US-10-766-610-104
12	620	100.0	119	4	US-10-733-563-104
13	613	98.9	117	3	US-09-835-087-11
14	613	98.9	117	3	US-09-809-739-21
15	613	98.9	117	3	US-09-840-459-18
16	613	98.9	117	4	US-10-766-773-18
17	613	98.9	117	4	US-10-766-610-18
18	613	98.9	117	4	US-10-733-563-18
19	613	98.9	117	5	US-10-662-061-21
20	613	98.9	117	6	US-11-075-184A-9
21	604	97.4	117	3	US-09-835-087-12
22	604	97.4	117	3	US-09-809-739-22
23	604	97.4	117	3	US-09-840-459-19
24	604	97.4	117	4	US-10-766-773-19
25	604	97.4	117	4	US-10-766-610-19
26	604	97.4	117	4	US-10-733-563-19
27	604	97.4	117	5	US-10-662-061-22

28	604	97.4	117	6	US-11-075-184A-10	Sequence 10, Appl
29	599	96.6	117	3	US-09-835-087-13	Sequence 13, Appl
30	599	96.6	117	3	US-09-809-739-23	Sequence 23, Appl
31	599	96.6	117	3	US-09-840-459-20	Sequence 20, Appl
32	599	96.6	117	4	US-10-766-773-20	Sequence 20, Appl
33	599	96.6	117	4	US-10-766-610-20	Sequence 20, Appl
34	599	96.6	117	4	US-10-733-563-20	Sequence 20, Appl
35	599	96.6	117	5	US-10-662-061-23	Sequence 23, Appl
36	599	96.6	117	6	US-11-075-184A-11	Sequence 11, Appl
37	548	88.4	117	3	US-09-835-087-8	Sequence 8, Appl
38	548	88.4	117	3	US-09-809-739-12	Sequence 12, Appl
39	548	88.4	117	3	US-09-840-459-10	Sequence 10, Appl
40	548	88.4	117	4	US-10-766-773-10	Sequence 10, Appl
41	548	88.4	117	4	US-10-766-610-10	Sequence 10, Appl
42	548	88.4	117	4	US-10-733-563-10	Sequence 10, Appl
43	548	88.4	117	5	US-10-662-061-12	Sequence 12, Appl
44	548	88.4	117	6	US-11-075-184A-2	Sequence 2, Appl
45	548	88.4	125	4	US-10-272-899A-84	Sequence 84, Appl

ALIGNMENTS

RESULT 1
US-09-835-087-10
; Sequence 10, Application US/09835087
; Patent No. US20020042370A1
; GENERAL INFORMATION:
; APPLICANT: Wayne W. Hancock
; TITLE OF INVENTION: Method of Treating Graft Rejection Using
; FILE OF INVENTION: Inhibitors of CCR2 Function
; FILE REFERENCE: 1855.2008-003
; CURRENT APPLICATION NUMBER: US/09/835,087
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/549,448
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-835-087-10

Query Match	100.0%	Score 620;	DB 3;	Length 117;
Best Local Similarity	100.0%;	Pred. No. 1.9e-49;		
Matches 117;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRI	TNNNYAT	60
Db	1	EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRI	TNNNYAT	60
Qy	61	YYADSVKDRFTISRDSDSKNTLYLQMNLSKTEDTAVYCTTFFYGNVGW	QGLTVTVSS	117
Db	61	YYADSVKDRFTISRDSDSKNTLYLQMNLSKTEDTAVYCTTFFYGNVGW	QGLTVTVSS	117

RESULT 2
US-09-809-739-20
; Sequence 20, Application US/09809739
; Patent No. US20020106369A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia B.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17

```
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-20

Query Match      100.0%; Score 620; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.9e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIITKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIITKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVWGQGTFLVTVSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVWGQGTFLVTVSS 117

RESULT 3
US-09-840-459-17
; Sequence 17, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-17

Query Match      100.0%; Score 620; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.9e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIITKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIITKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVWGQGTFLVTVSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVWGQGTFLVTVSS 117

RESULT 4
US-10-766-773-17
; Sequence 17, Application US/10766773
```

```
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-10-766-773-17

Query Match      100.0%; Score 620; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.9e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIITKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIITKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVWGQGTFLVTVSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVWGQGTFLVTVSS 117

RESULT 5
US-10-766-610-17
; Sequence 17, Application US/10766610
; Publication No. US20040132980A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-029
; CURRENT APPLICATION NUMBER: US/10/766,610
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/840,459
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 117
; TYPE: PRT
```



```

RESULT 7
US-10-662-061-20
; Sequence 20, Application US/10662061
; Publication No. US20050214299A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/10/662,061
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15

```

RESULT 9
US-09-840-459-104
; Sequence 104, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Lakosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.

; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized heavy chain
; US-09-840-459-104

Query Match 100.0%; Score 620; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.9e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVOLVESGGGLVPGGSLRLSCLASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
|
Db 1 EVOLVESGGGLVPGGSLRLSCLASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
|
Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
|
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
|

RESULT 10

US-10-766-773-104
; Sequence 104, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized heavy chain
; US-10-766-773-104

Query Match 100.0%; Score 620; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.9e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVOLVESGGGLVPGGSLRLSCLASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
|
Db 1 EVOLVESGGGLVPGGSLRLSCLASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
|
Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
|
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
|

RESULT 11

US-10-766-610-104
; Sequence 104, Application US/10766610
; Publication No. US20040132980A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-029
; CURRENT APPLICATION NUMBER: US/10/766,610
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/840,459
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized heavy chain
; US-10-766-610-104

Query Match 100.0%; Score 620; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.9e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVOLVESGGGLVPGGSLRLSCLASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
|
Db 1 EVOLVESGGGLVPGGSLRLSCLASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
|
Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
|
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
|

RESULT 12

US-10-733-563-104
; Sequence 104, Application US/10733563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Ponath, Paul
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; METHODS OF USE THEREFOR
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364

; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized heavy chain
US-10-733-563-104

Query Match 100.0%; Score 620; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.9e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
Db 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVWGQGTLLTVSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVWGQGTLLTVSS 117

RESULT 13
US-09-835-087-11
; Sequence 11, Application US/09835087
; Patent No. US20020042370A1
; GENERAL INFORMATION:
; APPLICANT: Wayne W. Hancock
; TITLE OF INVENTION: Method of Treating Graft Rejection Using
; TITLE OF INVENTION: Inhibitors of CCR2 Function
; FILE REFERENCE: 1855.2008-003
; CURRENT APPLICATION NUMBER: US/09/835,087
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/549,448
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-835-087-11

Query Match 98.9%; Score 613; DB 3; Length 117;
Best Local Similarity 98.3%; Pred. No. 8.2e-49;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
Db 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVWGQGTLLTVSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVWGQGTLLTVSS 117

RESULT 14
US-09-809-739-21
; Sequence 21, Application US/09809739
; Patent No. US20020106369A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1089-003
; CURRENT APPLICATION NUMBER: US/09/809,739

; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-21

Query Match 98.9%; Score 613; DB 3; Length 117;
Best Local Similarity 98.3%; Pred. No. 8.2e-49;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
Db 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVWGQGTLLTVSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVWGQGTLLTVSS 117

RESULT 15
US-09-840-459-18
; Sequence 18, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-18

Query Match 98.9%; Score 613; DB 3; Length 117;
Best Local Similarity 98.3%; Pred. No. 8.2e-49;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60
Db 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVWGQGTLLTVSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVWGQGTLLTVSS 117

Search completed: June 10, 2006, 12:38:41
Job time : 66.4054 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: June 10, 2006, 12:32:32 ; Search time 4.04054 Seconds
(without alignments)
366.103 Million cell updates/sec
Title: US-10-733-563-17
Perfect score: 620
Sequence: 1 EVQLVESGGGLVPGGSLRL.....CTTFYGNVGWGQGLTVTVSS 117
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 64916 seqs, 12643201 residues
Total number of hits satisfying chosen parameters: 64916

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Published_Applications_AA_New.*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
1	490.5	79.1	112 6	US-10-544-050-5 Sequence 5, Appli
2	479.5	77.3	120 7	US-11-075-891-33 Sequence 33, Appl
3	479.5	77.3	254 7	US-11-075-891-6 Sequence 6, Appli
4	479.5	77.3	254 7	US-11-075-891-12 Sequence 12, Appl
5	479.5	77.3	254 7	US-11-075-891-18 Sequence 18, Appl
6	474.5	76.5	120 7	US-11-075-891-34 Sequence 34, Appl
7	474.5	76.5	254 7	US-11-075-891-8 Sequence 8, Appli
8	474.5	76.5	254 7	US-11-075-891-14 Sequence 14, Appl
9	474.5	76.5	254 7	US-11-075-891-20 Sequence 20, Appl
10	470.5	75.9	120 7	US-11-075-891-35 Sequence 35, Appl
11	470.5	75.9	254 7	US-11-075-891-10 Sequence 10, Appl
12	470.5	75.9	254 7	US-11-075-891-16 Sequence 16, Appl
13	470.5	75.9	254 7	US-11-075-891-22 Sequence 22, Appl
14	464.5	74.9	116 7	US-11-249-296-76 Sequence 76, Appl
15	464	74.8	291 7	US-11-154-103-1 Sequence 1, Appli
16	464	74.8	291 7	US-11-154-103-2 Sequence 2, Appli
17	462	74.5	113 7	US-11-219-121-24 Sequence 24, Appl
18	461.5	74.4	448 7	US-11-219-121-28 Sequence 28, Appl
19	461	74.4	288 6	US-10-539-403-2 Sequence 2, Appli
20	459.5	74.1	126 6	US-10-994-679-64 Sequence 64, Appl
21	458.5	74.0	116 7	US-11-249-296-82 Sequence 82, Appl
22	458	73.9	113 7	US-11-249-296-46 Sequence 46, Appl
23	457.5	73.8	116 7	US-11-249-296-30 Sequence 30, Appl
24	457.5	73.8	116 7	US-11-249-296-80 Sequence 80, Appl
25	457.5	73.8	116 7	US-11-249-296-86 Sequence 86, Appl

26	457.5	73.8	116 7	US-11-249-296-88 Sequence 88, Appl
27	456.5	73.6	122 7	US-11-254-679-36 Sequence 36, Appl
28	455.5	73.5	116 7	US-11-249-296-84 Sequence 84, Appl
29	455	73.4	119 7	US-11-254-182-6 Sequence 6, Appli
30	455	73.4	119 7	US-11-254-182-30 Sequence 30, Appl
31	455	73.4	119 7	US-11-300-563-11 Sequence 11, Appl
32	455	73.4	119 7	US-11-106-762-13 Sequence 13, Appl
33	455	73.4	570 1	US-09-784-950-18 Sequence 18, Appl
34	454.5	73.3	112 6	US-10-544-050-6 Sequence 6, Appli
35	454	73.2	123 7	US-11-211-917-117 Sequence 117, App
36	453	73.1	123 7	US-11-219-563-69 Sequence 69, Appl
37	452.5	73.0	116 7	US-11-249-296-10 Sequence 10, Appl
38	452.5	73.0	116 7	US-11-249-296-34 Sequence 34, Appl
39	451	72.7	123 7	US-11-211-917-115 Sequence 115, App
40	450.5	72.7	116 7	US-11-249-296-22 Sequence 22, Appl
41	450.5	72.7	122 7	US-11-254-679-72 Sequence 72, Appl
42	450.5	72.7	124 7	US-11-211-917-50 Sequence 50, Appl
43	450.5	72.7	124 7	US-11-211-917-96 Sequence 96, Appl
44	450.5	72.7	469 7	US-11-211-917-54 Sequence 54, Appl
45	450	72.6	123 7	US-11-211-917-116 Sequence 116, App

ALIGNMENTS

RESULT 1
US-10-544-050-5
; Sequence 5, Application US/10544050
; Publication No. US20060110388A1
; GENERAL INFORMATION:
; APPLICANT: Davies Julian
; TITLE OF INVENTION: Abeta Binding Molecules
; FILE REFERENCE: X-16068
; CURRENT APPLICATION NUMBER: US/10/544,050
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/446380
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized light chain
US-10-544-050-5

Query Match 79.1%; Score 490.5; DB 6; Length 112;
Best Local Similarity 82.9%; Pred. No. 2.6e-40;
Matches 97; Conservative 6; Mismatches 9; Indels 5; Gaps 2;
QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSYAMNVRQAPGKLEWVGRITKNNVAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSYMSWVRQAPGKLEWVGQINSVGN--ST 58
QY 61 YYADSVKDRFTISRDSDSKNTLYLQMSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
Db 59 YYPDVKGRFTISRDSDSKNTLYLQMSLKTEDTAVYYCTT---GDYWGQGLTVTVSS 112

RESULT 2
US-11-075-891-33
; Sequence 33, Application US/11075891
; Publication No. US20060088521A1
; GENERAL INFORMATION:
; APPLICANT: MAHADEVAN, DARUKA
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT
; FILE REFERENCE: 263922US96
; CURRENT APPLICATION NUMBER: US/11/075,891
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: US 60/557,258
; PRIOR FILING DATE: 2004-03-27
; NUMBER OF SEQ ID NOS: 36

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-075-891-33

Query Match      77.3%; Score 479.5; DB 7; Length 120;
Best Local Similarity 78.3%; Pred. No. 3.1e-39;
Matches 94; Conservative 7; Mismatches 16; Indels 3; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVGVGRIRTKNNYAT 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVGVGRIRTKSDNYGA 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTT---FYGNGVWGOGTLVTYSS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 KYAESVGRGFTISRDDSKNSLYLQNSLKTEDTAVYYCARTPWVYAMDCWGOGTLVTYSS 120

RESULT 3
US-11-075-891-6
; Sequence 6, Application US/11075891
; Publication No. US20060088521A1
; GENERAL INFORMATION:
; APPLICANT: MAHADEVAN, DARUKA
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT
; FILE REFERENCE: 263922US96
; CURRENT APPLICATION NUMBER: US/11/075,891
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: US 60/557,258
; PRIOR FILING DATE: 2004-03-27
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-075-891-6

Query Match      77.3%; Score 479.5; DB 7; Length 254;
Best Local Similarity 78.3%; Pred. No. 6.7e-39;
Matches 94; Conservative 7; Mismatches 16; Indels 3; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVGVGRIRTKNNYAT 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 EVQLVESGGGLVQPGGSLRLSCAASGFTFSNRYRMHWVRQAPGKGLVGVGRITVKSDNYGA 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTT---FYGNGVWGOGTLVTYSS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 KYAESVGRGFTISRDDSKNSLYLQNSLKTEDTAVYYCARTPWVYAMDCWGOGTLVTYSS 121

RESULT 4
US-11-075-891-12
; Sequence 12, Application US/11075891
; Publication No. US20060088521A1
; GENERAL INFORMATION:
; APPLICANT: MAHADEVAN, DARUKA
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT
; FILE REFERENCE: 263922US96
; CURRENT APPLICATION NUMBER: US/11/075,891
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: US 60/557,258
; PRIOR FILING DATE: 2004-03-27
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-075-891-12

Query Match      77.3%; Score 479.5; DB 7; Length 254;
Best Local Similarity 78.3%; Pred. No. 6.7e-39;
Matches 94; Conservative 7; Mismatches 16; Indels 3; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVGVGRIRTKNNYAT 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 EVQLVESGGGLVQPGGSLRLSCAASGFTFSNRYRMHWVRQAPGKGLVGVGRITVKSDNYGA 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTT---FYGNGVWGOGTLVTYSS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 KYAESVGRGFTISRDDSKNSLYLQNSLKTEDTAVYYCARTPWVYAMDCWGOGTLVTYSS 121

RESULT 5
US-11-075-891-18
; Sequence 18, Application US/11075891
; Publication No. US20060088521A1
; GENERAL INFORMATION:
; APPLICANT: MAHADEVAN, DARUKA
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT
; FILE REFERENCE: 263922US96
; CURRENT APPLICATION NUMBER: US/11/075,891
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: US 60/557,258
; PRIOR FILING DATE: 2004-03-27
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-075-891-18

Query Match      77.3%; Score 479.5; DB 7; Length 254;
Best Local Similarity 78.3%; Pred. No. 6.7e-39;
Matches 94; Conservative 7; Mismatches 16; Indels 3; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVGVGRIRTKNNYAT 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 EVQLVESGGGLVQPGGSLRLSCAASGFTFSNRYRMHWVRQAPGKGLVGVGRITVKSDNYGA 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTT---FYGNGVWGOGTLVTYSS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 KYAESVGRGFTISRDDSKNSLYLQNSLKTEDTAVYYCARTPWVYAMDCWGOGTLVTYSS 121

RESULT 6
US-11-075-891-34
; Sequence 34, Application US/11075891
; Publication No. US20060088521A1
; GENERAL INFORMATION:
; APPLICANT: MAHADEVAN, DARUKA
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT
; FILE REFERENCE: 263922US96
; CURRENT APPLICATION NUMBER: US/11/075,891
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: US 60/557,258
; PRIOR FILING DATE: 2004-03-27
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-075-891-34
```

; OTHER INFORMATION: Synthetic Peptide
US-11-075-891-34

Query Match 76.5%; Score 474.5; DB 7; Length 120;
Best Local Similarity 76.7%; Pred. No. 9.2e-39;
Matches 92; Conservative 8; Mismatches 17; Indels 3; Gaps 1;

QY 1 EVLVESGGGLVKPGSLRLSCAASGFTFSAYAMNVRQAPKGLEWVGRIRTKNNYAT 60
DB 1 EVLVESGGGLVQPGSLRLSCATSGFTFSNRYRMHWVRQAPKGLEWIGVITVKSDNYGA 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTT---FYGNMGWGQGLTVTVSS 117
DB 61 KYAESVGRGFTISRDDSKNSLYLQNSLKTEDTAVYYCARTPWVYAMDCWGQGLTVTVSS 120

RESULT 7
US-11-075-891-8
; Sequence 8, Application US/11075891
; Publication No. US20060088521A1
; GENERAL INFORMATION:
; APPLICANT: MAHADEVAN, DARUKA
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT
; CURRENT APPLICATION NUMBER: US/11/075,891
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: US 60/557,258
; PRIOR FILING DATE: 2004-03-27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-075-891-8

Query Match 76.5%; Score 474.5; DB 7; Length 254;
Best Local Similarity 76.7%; Pred. No. 2e-38;
Matches 92; Conservative 8; Mismatches 17; Indels 3; Gaps 1;

QY 1 EVLVESGGGLVKPGSLRLSCAASGFTFSAYAMNVRQAPKGLEWVGRIRTKNNYAT 60
DB 2 EVLVESGGGLVQPGSLRLSCATSGFTFSNRYRMHWVRQAPKGLEWIGVITVKSDNYGA 61

QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTT---FYGNMGWGQGLTVTVSS 117
DB 62 KYAESVGRGFTISRDDSKNSLYLQNSLKTEDTAVYYCARTPWVYAMDCWGQGLTVTVSS 121

RESULT 8
US-11-075-891-14
; Sequence 14, Application US/11075891
; Publication No. US20060088521A1
; GENERAL INFORMATION:
; APPLICANT: MAHADEVAN, DARUKA
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT
; CURRENT APPLICATION NUMBER: US/11/075,891
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: US 60/557,258
; PRIOR FILING DATE: 2004-03-27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-075-891-14

Query Match 76.5%; Score 474.5; DB 7; Length 254;
Best Local Similarity 76.7%; Pred. No. 2e-38;
Matches 92; Conservative 8; Mismatches 17; Indels 3; Gaps 1;

QY 1 EVLVESGGGLVKPGSLRLSCAASGFTFSAYAMNVRQAPKGLEWVGRIRTKNNYAT 60
DB 2 EVLVESGGGLVQPGSLRLSCATSGFTFSNRYRMHWVRQAPKGLEWIGVITVKSDNYGA 61

QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTT---FYGNMGWGQGLTVTVSS 117
DB 62 KYAESVGRGFTISRDDSKNSLYLQNSLKTEDTAVYYCARTPWVYAMDCWGQGLTVTVSS 121

RESULT 9
US-11-075-891-20
; Sequence 20, Application US/11075891
; Publication No. US20060088521A1
; GENERAL INFORMATION:
; APPLICANT: MAHADEVAN, DARUKA
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT
; CURRENT APPLICATION NUMBER: US/11/075,891
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: US 60/557,258
; PRIOR FILING DATE: 2004-03-27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-075-891-20

Query Match 76.5%; Score 474.5; DB 7; Length 254;
Best Local Similarity 76.7%; Pred. No. 2e-38;
Matches 92; Conservative 8; Mismatches 17; Indels 3; Gaps 1;

QY 1 EVLVESGGGLVKPGSLRLSCAASGFTFSAYAMNVRQAPKGLEWVGRIRTKNNYAT 60
DB 2 EVLVESGGGLVQPGSLRLSCATSGFTFSNRYRMHWVRQAPKGLEWIGVITVKSDNYGA 61

QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTT---FYGNMGWGQGLTVTVSS 117
DB 62 KYAESVGRGFTISRDDSKNSLYLQNSLKTEDTAVYYCARTPWVYAMDCWGQGLTVTVSS 121

RESULT 10
US-11-075-891-35
; Sequence 35, Application US/11075891
; Publication No. US20060088521A1
; GENERAL INFORMATION:
; APPLICANT: MAHADEVAN, DARUKA
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT
; CURRENT APPLICATION NUMBER: US/11/075,891
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: US 60/557,258
; PRIOR FILING DATE: 2004-03-27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-075-891-35

Query Match 75.9%; Score 470.5; DB 7; Length 120;
Best Local Similarity 75.8%; Pred. No. 2.2e-38;
Matches 91; Conservative 9; Mismatches 17; Indels 3; Gaps 1;

RESULT 15
US-11-154-103-1
; Sequence 1, Application US/11154103
; Publication No. US20060099205A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; FILE REFERENCE: 407T-000420US
; CURRENT APPLICATION NUMBER: US/11/154,103
; PRIOR FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US10/406,830
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic antibody.
US-11-154-103-1

Query Match 74.8%; Score 464; DB 7; Length 291;
Best Local Similarity 76.0%; Pred. No. 2.3e-37;
Matches 92; Conservative 8; Mismatches 15; Indels 6; Gaps 2;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTPSAYAMNVRQAPGKLEWVGRIRTKNNYAT 60
Db 23 QVQLVESGGGLVPGGSLRLSCAASGFTPSYAMSWVRQAPGKLEWWSAISGRGDN--T 80
Qy 61 YYADSVKORFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYNG-----VWGQGLTVTS 116
Db 81 YYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKMTSNAPFDYWGQGLTVTS 140
Qy 117 S 117
Db 141 S 141

Search completed: June 10, 2006, 12:39:10
Job time : 4.04054 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 12, 2006, 17:04:30 ; Search time 213.707 Seconds
(without alignments)
706.020 Million cell updates/sec

Title: US-10-733-563-110

Perfect score: 1765

Sequence: 1 ASTKGPSVFPLAPSSKSTSG.....MHEALHNYTKQSLSLSPGK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : A_Geneseq_8.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*
- 10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1765	100.0	330	8	ADQ89332 Human imm
2	1765	100.0	330	9	AEB09605 Human Igg
3	1765	100.0	333	8	ADJ95914 Human Igg
4	1765	100.0	333	8	ADQ89336 Human imm
5	1765	100.0	333	9	AEB09609 Human Igg
6	1765	100.0	356	8	ADJ95974 Human Igg
7	1765	100.0	444	3	AAV32263 Humanised
8	1765	100.0	448	8	ADP88447 Human imm
9	1765	100.0	448	8	ADP88431 Antibody
10	1765	100.0	448	10	AEB27216 Anti-CD4
11	1765	100.0	448	10	AEB27200 Anti-CD4
12	1765	100.0	450	9	AED19177 Humanized
13	1765	100.0	462	9	AEB08800 Anti-NOGO
14	1765	100.0	467	6	ADA47334 TRX1 heav
15	1765	100.0	467	6	ADA47336 TRX1 heav
16	1765	100.0	467	8	ADP88446 Antibody
17	1765	100.0	467	8	ADP88430 Antibody
18	1765	100.0	467	8	ADQ87966 Heavy cha
19	1765	100.0	467	8	ADQ87974 Heavy cha
20	1765	100.0	467	10	AEB27213 Anti-CD4
21	1765	100.0	467	10	AEB27197 Anti-CD4
22	1765	100.0	467	10	AEB27215 Anti-CD4
23	1765	100.0	467	10	AEB27199 Anti-CD4

24	1765	100.0	473	5	ABC70743	Abg70743	Mouse/hum
25	1765	100.0	475	8	ADL23051	Adl23051	Mouse/hum
26	1765	100.0	475	8	ADL23054	Adl23054	Humanised
27	1765	100.0	475	8	ADS88803	Ads88803	Humanised
28	1765	100.0	475	8	ADS88792	Ads88792	A mouse/h
29	1758	99.6	469	7	ADL23199	Adl23199	Human ant
30	1756	99.5	330	4	AAB04071	Aab04071	Zcytor 10
31	1756	99.5	330	5	AAM47856	Aam47856	Human Ig-
32	1756	99.5	330	5	AAE21960	Aae21960	Human dea
33	1756	99.5	330	5	ABB81641	Abb81641	Human Igg
34	1756	99.5	330	5	ABB05736	Abb05736	Human imm
35	1756	99.5	330	6	ABP71856	Abp71856	Human Igg
36	1756	99.5	330	6	AAE32915	Aae32915	Human imm
37	1756	99.5	330	6	AAE32627	Aae32627	Human imm
38	1756	99.5	330	6	ABR82103	Abr82103	Human DR6
39	1756	99.5	330	6	AAO31102	Aao31102	Human A2-
40	1756	99.5	330	6	ABE55836	Abr55836	Anti-Ang-
41	1756	99.5	330	6	AAO30893	Aao30893	Human imm
42	1756	99.5	330	7	ADF11389	Adf11389	Anti-OpGL
43	1756	99.5	330	7	ADF97351	Adf97351	Human Igg
44	1756	99.5	330	7	ADF83605	Adf83605	Cytokine
45	1756	99.5	330	7	ADF75001	Adf75001	Human Ig
46	1756	99.5	330	8	ADM41537	Adm41537	Anti-inte
47	1756	99.5	330	8	ADM68911	Adm68911	Human Igg
48	1756	99.5	330	8	ADR43460	Adr43460	Heavy cha
49	1756	99.5	330	8	ADR31605	Adr31605	Human Igg
50	1756	99.5	330	8	ADS87909	Ads87909	Anti-IFN-
51	1756	99.5	330	8	ADN33230	Adn33230	IgG1-CH h
52	1756	99.5	330	8	ADS94906	Ad94906	Anti-IFN-
53	1756	99.5	330	8	ADS33309	Ads33309	Human Igg
54	1756	99.5	330	8	ADT88869	Adt88869	Human Igg
55	1756	99.5	330	8	ADT51577	Adt51577	Heavy cha
56	1756	99.5	330	8	ADT51581	Adt51581	Heavy cha
57	1756	99.5	330	8	ADT51724	Adt51724	Human Hui
58	1756	99.5	330	8	ADU68015	Adu68015	Mouse ant
59	1756	99.5	330	9	ADW08868	Adw08868	IGF-IR an
60	1756	99.5	330	9	ADM86657	Adm86657	Human imm
61	1756	99.5	330	9	ADX97894	Adx97894	Human Ig
62	1756	99.5	330	9	ADX98273	Adx98273	Human ant
63	1756	99.5	330	9	ADY51253	Ady51253	Human Igg
64	1756	99.5	330	9	ADY58147	Ady58147	Human Igg
65	1756	99.5	330	9	ADY26687	Ady26687	Human ant
66	1756	99.5	330	9	AEA12531	Aea12531	Human Igg
67	1756	99.5	330	9	AEA25942	Aea25942	Human imm
68	1756	99.5	330	9	AEA48148	Aea48148	Human Igg
69	1756	99.5	330	9	ABE86186	Aeb86186	Amino aci
70	1756	99.5	330	9	ASC08181	Aec08181	Heavy cha
71	1756	99.5	330	9	AEC81727	Aec81727	Human imm
72	1756	99.5	330	9	AED12326	Aed12326	Human Igg
73	1756	99.5	330	9	AED08855	Aed08855	Human imm
74	1756	99.5	330	9	AED41916	Aed41916	Deimmuniz
75	1756	99.5	330	9	AED28069	Aed28069	Human gam
76	1756	99.5	330	9	AED28067	Aed28067	Human Igg
77	1756	99.5	330	10	AEBF11770	Aef11770	Human Scf
78	1756	99.5	330	10	AEBF16289	Aef16289	Humanized
79	1756	99.5	330	10	AEBF16285	Aef16285	Human OST
80	1756	99.5	330	10	AEF51200	Aef51200	Human imm
81	1756	99.5	330	10	AEF82207	Aef82207	Human imm
82	1756	99.5	330	10	AEG11432	Aeg11432	Immunoglo
83	1756	99.5	332	8	ADL35095	Adl35095	Human Igg
84	1756	99.5	332	8	ADM07455	Adm07455	Human Igg
85	1756	99.5	333	8	ADJ95912	Adj95912	Human Igg
86	1756	99.5	333	8	ADL22761	Adl22761	Human ant
87	1756	99.5	335	9	AEC22665	Aec22665	Secreted
88	1756	99.5	351	2	AAE43685	Aae43685	Human kap
89	1756	99.5	356	8	ADJ95976	Adj95976	Immunoglo
90	1756	99.5	371	1	AAP91918	Aap91918	Sequence
91	1756	99.5	442	6	ABR39465	Abr39465	Humanised
92	1756	99.5	442	6	ABR39474	Abr39474	Humanised
93	1756	99.5	442	6	ABU08311	Abu08311	Humanised
94	1756	99.5	442	6	ABU08320	Abu08320	Humanised
95	1756	99.5	442	6	ABR39793	Abr39793	Humanised
96	1756	99.5	442	6	ABB80113	Abb80113	Deglycosy

97	1756	99.5	442	6	ABB80109	Abb80109 Heavy cha	170	1756	99.5	461	4	AAU07745	Aau07745 Humanised
98	1756	98.5	442	7	AD894066	Ad894066 Humanised	171	1756	99.5	461	6	ABR39844	AbR39844 Hu266 N56
99	1756	99.5	442	7	AD894075	Ad894075 Humanised	172	1756	99.5	461	6	ABR39847	AbR39847 Hu266 N56
100	1756	99.5	442	8	ADN61714	Adn61714 Humanised	173	1756	99.5	461	6	ABR39843	AbR39843 Hu266 N56
101	1756	99.5	444	6	AAE35327	Aae35327 Humanised	174	1756	99.5	461	6	ABR39848	AbR39848 Hu266 N56
102	1756	99.5	444	6	AAE34876	Aae34876 BIWA4/8 a	175	1756	99.5	462	9	ABO08804	Aeb08804 Reference
103	1756	99.5	444	8	ADL15443	Adl15443 Humanised	176	1756	99.5	463	8	ADM72025	Adm72025 Chimeric
104	1756	98.5	444	8	AD000851	Ado00851 Humanised	177	1756	99.5	463	10	AEF50991	Aef50991 Variable
105	1756	99.5	444	9	ABE29789	Abe29789 Humanised	178	1756	99.5	464	8	ADU68011	Adu68011 Mouse ant
106	1756	99.5	444	9	ABE29780	Abe29780 Humanised	179	1756	99.5	464	9	AEA41072	Aea41072 Human ant
107	1756	99.5	445	6	AAO31101	Aao31101 Human A2-	180	1756	99.5	464	9	AEA41918	Aea41918 Deimmuniz
108	1756	99.5	445	7	ADFL11421	Adfl11421 2E11 anti	181	1756	99.5	464	9	AEAD41912	Aead41912 Deimmuniz
109	1756	99.5	445	7	ADFL11429	Adfl11429 18B2 anti	182	1756	99.5	464	9	AEAD41920	Aead41920 Deimmuniz
110	1756	98.5	445	9	ADY74778	Ady74778 Rat anti-	183	1756	99.5	464	9	AEAD41924	Aead41924 Deimmuniz
111	1756	99.5	445	10	AEF11768	Aef11768 Human SCF	184	1756	99.5	464	8	ADU68011	Adu68011 Mouse ant
112	1756	99.5	446	7	ADFL11425	Adfl11425 2D8 anti-	185	1756	99.5	465	4	ABE72228	Abe72228 Humanised
113	1756	99.5	446	7	ADFL11437	Adfl11437 9H7 anti-	186	1756	99.5	465	4	ABE72228	Abe72228 Humanised
114	1756	99.5	446	7	ADFL11433	Adfl11433 16E1 anti	187	1756	99.5	465	9	ADX83744	Adx83744 Human Igg
115	1756	99.5	446	7	ADFL11417	Adfl11417 22B3 anti	188	1756	99.5	467	2	AAE22759	Aae22759 Reshaped
116	1756	99.5	447	2	ADY31669	Ady31669 Human Igg	189	1756	99.5	467	2	AAE22758	Aae22758 Reshaped
117	1756	99.5	447	8	ADQ31274	Adq31274 Humanised	190	1756	99.5	467	7	ADM05608	Adm05608 Human pro
118	1756	99.5	447	8	ADQ31271	Adq31271 Murine 11	191	1756	99.5	467	8	ADM41567	Adm41567 Anti-inte
119	1756	99.5	447	8	ADQ31276	Adq31276 Humanised	192	1756	99.5	467	9	ADY30112	Ady30112 Human Igg
120	1756	99.5	447	8	ADS87928	Ads87928 Anti-IFN-	193	1756	99.5	468	5	AAE27928	Aae27928 Human cDN
121	1756	99.5	447	8	ADS87924	Ads87924 Anti-IFN-	194	1756	99.5	468	6	ABB82837	Abb82837 Antibody
122	1756	99.5	447	8	ADS87926	Ads87926 Anti-IFN-	195	1756	99.5	468	6	ABP58275	Abp58275 Humanised
123	1756	99.5	447	8	ADS87939	Ads87939 Anti-IFN-	196	1756	99.5	468	8	ADR46819	Adr46819 Human ant
124	1756	99.5	447	8	ADS94936	Ads94936 Anti-IFN-	197	1756	99.5	468	9	ADY91369	Ady91369 Anti-KID3
125	1756	99.5	447	8	ADS94923	Ads94923 Anti-IFN-	198	1756	99.5	468	10	AAE99093	Aae99093 RSV antib
126	1756	99.5	447	8	ADS94921	Ads94921 Anti-IFN-	199	1756	99.5	469	8	ADM41555	Adm41555 Anti-inte
127	1756	99.5	447	8	ADS94925	Ads94925 Anti-IFN-	200	1756	99.5	469	8	ADM41561	Adm41561 Anti-inte
128	1756	99.5	447	9	ABE12291	Abe12291 Human Igg	201	1756	99.5	469	10	AAE99092	Aae99092 RSV antib
129	1756	99.5	448	9	AAW49203	Aaw49203 Humanised	202	1756	99.5	470	2	AAE22757	Aae22757 Reshaped
130	1756	99.5	448	9	ADZ99442	Adz99442 Humanized	203	1756	99.5	470	2	AAE22757	Aae22757 Reshaped
131	1756	99.5	448	10	AEQ01544	Aeq01544 Kallikrei	204	1756	99.5	470	3	AAU77289	Aau77289 Protein #
132	1756	99.5	449	2	AAW43339	Aaw43339 Compleet	205	1756	99.5	470	3	AAU77289	Aau77289 Protein #
133	1756	99.5	449	2	AAW49816	Aaw49816 Amino aci	206	1756	99.5	470	7	ADB65576	Adb65576 Human pro
134	1756	99.5	449	6	ABP58273	Abp58273 Humanised	207	1756	99.5	470	8	ADM72031	Adm72031 Chimeric
135	1756	99.5	449	6	AD135159	Adi35159 Humanised	208	1756	99.5	470	8	ADM72031	Adm72031 Chimeric
136	1756	99.5	449	8	ADZ80769	Adz80769 Amino aci	209	1756	99.5	470	10	AEF50993	Aef50993 Variable
137	1756	99.5	449	9	ADZ99434	Adz99434 Humanised	210	1756	99.5	470	10	AEF50993	Aef50993 Variable
138	1756	99.5	450	6	ABG74713	Abg74713 Murine hu	211	1756	99.5	471	7	ADM05609	Adm05609 Human pro
139	1756	99.5	450	6	ABR83153	AbR83153 Hu007 ant	212	1756	99.5	471	8	ADM72029	Adm72029 Chimeric
140	1756	99.5	450	7	ABR83153	AbR83153 Hu007 ant	213	1756	99.5	471	8	ADM72029	Adm72029 Chimeric
141	1756	99.5	450	8	ADS18704	Ads18704 Protein s	214	1756	99.5	471	8	ADR09218	Adr09218 Human pro
142	1756	99.5	450	8	ADS18706	Ads18706 Protein s	215	1756	99.5	471	9	AEF50996	Aef50996 Variable
143	1756	99.5	450	8	ADS18710	Ads18710 Protein s	216	1756	99.5	471	10	AEF50996	Aef50996 Variable
144	1756	99.5	450	8	ADS18702	Ads18702 Protein s	217	1756	99.5	472	6	ABP58289	Abp58289 Humanised
145	1756	99.5	450	8	ADS18708	Ads18708 Protein s	218	1756	99.5	472	8	ADQ66377	Adq66377 Novel hum
146	1756	99.5	450	9	AED19128	Aed19128 Humanized	219	1756	99.5	472	8	ADQ66377	Adq66377 Novel hum
147	1756	99.5	450	10	AEF80308	Aef80308 Antibody	220	1756	99.5	472	8	ADS88783	Ads88783 Sequence
148	1756	99.5	450	10	AEF80304	Aef80304 Antibody	221	1756	99.5	472	8	ADS88783	Ads88783 Sequence
149	1756	99.5	451	4	AAE12715	Aae12715 Human rec	222	1756	99.5	473	4	AAE64475	Aae64475 Human typ
150	1756	99.5	451	6	ABU58807	Abu58807 Mucin 1 (223	1756	99.5	473	4	AAE64475	Aae64475 Human typ
151	1756	99.5	451	8	ADL92469	Adl92469 Antibody	224	1756	99.5	473	4	AAE64475	Aae64475 Human typ
152	1756	99.5	451	8	ADP88494	Adp88494 Humanised	225	1756	99.5	473	7	ADM05599	Adm05599 Human pro
153	1756	99.5	451	8	ADU68151	Adu68151 Novel var	226	1756	99.5	473	8	ADM97513	Adm97513 CD1d-IgG-
154	1756	99.5	451	8	ADU80279	Adu80279 CD20 bind	227	1756	99.5	473	9	ADM05597	Adm05597 Human pro
155	1756	99.5	451	9	AED19166	Aed19166 Humanized	228	1756	99.5	474	9	ADM05597	Adm05597 Human pro
156	1756	99.5	451	10	AAE27225	Aae27225 Humanized	229	1756	99.5	474	9	AEF50993	Aef50993 Variable
157	1756	99.5	452	2	AAV30201	Aav30201 Heavy cha	230	1756	99.5	475	2	AAE220057	Aae220057 Heavy cha
158	1756	99.5	452	9	AEF34780	Aef34780 Chimeric	231	1756	99.5	475	2	AAE220057	Aae220057 Heavy cha
159	1756	99.5	453	6	ABP58287	Abp58287 Humanised	232	1756	99.5	475	2	AAE220057	Aae220057 Heavy cha
160	1756	99.5	453	6	ABP56295	Abp56295 4AS-3.1.1	233	1756	99.5	475	4	AAE63640	Aae63640 Amino aci
161	1756	99.5	453	6	ADT55443	Adt55443 Anti IGE	234	1756	99.5	475	4	AAE63640	Aae63640 Amino aci
162	1756	99.5	453	8	ADT55443	Adt55443 Anti IGE	235	1756	99.5	475	8	ADL23053	Adl23053 Mouse ant
163	1756	99.5	453	8	ADT55443	Adt55443 Anti-NGF-	236	1756	99.5	475	8	ADL23056	Adl23056 Humanised
164	1756	99.5	453	9	ABE56309	Abe56309 Anti-IGF	237	1756	99.5	475	8	ADL23056	Adl23056 Humanised
165	1756	99.5	455	10	AEF18982	Aef18982 Humanized	238	1756	99.5	475	8	ADS88805	Ads88805 A mouse/h
166	1756	99.5	455	10	AEF18981	Aef18981 Humanized	239	1756	99.5	476	2	AAE31023	Aae31023 Antibody
167	1756	99.5	455	10	AEF18984	Aef18984 Humanized	240	1756	99.5	476	2	AAE31023	Aae31023 Antibody
168	1756	99.5	457	9	AEF18983	Aef18983 Humanized	241	1756	99.5	476	2	AAE31023	Aae31023 Antibody
169	1756	99.5	461	2	AAE16143	Aae16143 Human ant	242	1756	99.5	476	2	AAE31023	Aae31023 Antibody
					AAE42162	AAe42162 Anti-HIV-							

243	1756	99.5	477	7	ADM05604	Adm05604 Human pro	316	1753	99.3	470	9	ADZ51043	Adz51043 Amino aci
244	1756	99.5	477	8	ADQ65990	Novel hum	317	1753	99.3	476	9	AED19758	Aed19758 Chimeric
245	1756	99.5	477	8	ADL10018	Human pro	318	1753	99.3	480	9	AED19756	Aed19756 Chimeric
246	1756	99.5	477	9	AEC88534	Human CDN	319	1753	99.3	713	8	ADN97491	Adn97491 Artificia
247	1756	99.5	478	8	ADQ67023	Novel hum	320	1753	99.3	715	8	ADN97489	Adn97489 Artificia
248	1756	99.5	481	2	AAR24442	Sequence	321	1752	99.3	329	2	AAR91806	Aar91806 Human imm
249	1756	99.5	485	9	ADX83727	Human IGG	322	1752	99.3	329	2	ADP56389	Adp56389 Human PRO
250	1756	99.5	502	8	ADN97493	CD1d-IGG-	323	1752	99.3	329	10	AEF72978	Aef72978 Human IGG
251	1756	99.5	534	2	AAR26531	Sequence	324	1752	99.3	330	9	ADZ69645	Adz69645 Human IGG
252	1756	99.5	541	5	AAE29077	Human IL-	325	1752	99.3	330	9	ADZ69654	Adz69654 Human IGG
253	1756	99.5	541	8	ADS31713	Soluble I	326	1752	99.3	330	9	ADZ69615	Adz69615 Human IGG
254	1756	99.5	541	8	ADZ92715	IL-22RA s	327	1752	99.3	330	9	ADZ69623	Adz69623 Human IGG
255	1756	99.5	547	4	AAH85279	Human IL-	328	1752	99.3	446	8	ADP19328	Adp19328 Chimeric
256	1756	99.5	547	5	ABG67210	Interleuk	329	1752	99.3	448	8	ADP84969	Adp84969 Chimeric
257	1756	99.5	547	5	AAE23362	Human IL-	330	1752	99.3	451	8	ADL92472	Adl92472 Antibody
258	1756	99.5	547	8	ADJ83334	Human IL-	331	1752	99.3	451	8	ADU68154	Adu68154 Novel var
259	1756	99.5	547	9	ADG64569	IL-20RA a	332	1752	99.3	451	10	AEF51206	Aef51206 Human ant
260	1756	99.5	551	9	AEC05756	Homo-cont	333	1752	99.3	451	10	AEF51206	Aef51206 Human ant
261	1756	99.5	551	9	AEC05755	Homo-cont	334	1752	99.3	468	9	AEI29408	Aei29408 Human mon
262	1756	99.5	557	9	AEC05753	Homo-cont	335	1752	99.3	468	9	AEA18640	Aea18640 Amino aci
263	1756	99.5	557	9	AEC05752	Homo-cont	336	1752	99.3	470	3	AAV44721	Aav44721 Human imm
264	1756	99.5	557	9	AEC05754	Homo-cont	337	1752	99.3	470	5	AAE27923	Aae27923 Human C2B
265	1756	99.5	558	5	AAE29076	Human IL-	338	1752	99.3	470	6	ABB2832	Abb2832 Antibody
266	1756	99.5	567	5	AAE13733	Human Zai	339	1752	99.3	470	10	AEH86008	Aeh86008 Anthrax t
267	1756	99.5	571	4	AAH85278	Human IL-	340	1752	99.3	471	7	ADM05600	Adm05600 Human pro
268	1756	99.5	571	5	AAU04065	Human IL-	341	1752	99.3	471	9	AEC88530	Aec88530 Human CDN
269	1756	99.5	571	5	ABG67209	Interleuk	342	1752	99.3	475	2	AAW11641	Aaw11641 Human ant
270	1756	99.5	571	8	AAE23359	Human IL-	343	1752	99.3	475	2	AAW11639	Aaw11639 Human ant
271	1756	99.5	571	8	ADJ83333	Human IL-	344	1752	99.3	475	2	ADQ65032	Adq65032 Novel hum
272	1756	99.5	571	9	ADG64568	IL-20RA a	345	1752	99.3	476	2	AAW01818	Aaw01818 Primatise
273	1756	99.5	581	4	AAH81972	Human IL-	346	1752	99.3	476	2	AAW63761	Aaw63761 Macaque p
274	1756	99.5	582	4	AAH81987	Ganglios	347	1752	99.3	476	2	AAW63761	Aaw63761 Macaque p
275	1756	99.5	582	4	AAH81991	Ganglios	348	1752	99.3	476	2	AAW63765	Aaw63765 Macaque p
276	1756	99.5	583	4	AAH83156	Ganglios	349	1752	99.3	476	5	AAU11539	Aau11539 Protein s
277	1756	99.5	595	2	AAW86003	Anti-5T4	350	1752	99.3	476	5	AAU11646	Aau11646 Protein s
278	1756	99.5	613	8	ADR46827	Human bet	351	1752	99.3	476	6	AAE37360	Aae37360 Monkey 7C
279	1756	99.5	649	8	ADM97531	CD1d-IGG	352	1752	99.3	477	2	AAE47453	Aae47453 chIT84.12
280	1756	99.5	652	2	AAW48650	Heavy cha	353	1752	99.3	478	2	AAW63763	Aaw63763 Macaque p
281	1756	99.5	659	8	ADZ75345	Chimeric	354	1752	99.3	478	5	AAU11644	Aau11644 Protein s
282	1756	99.5	690	3	AAV92195	Human IL-	355	1751	99.2	329	8	ADS85004	AdS85004 Human OST
283	1756	99.5	729	1	AAE93008	Genetic c	356	1751	99.2	330	8	ADP51717	AdP51717 Human OST
284	1756	99.5	729	3	AAV59168	CD4-Ig fu	357	1751	99.2	330	9	ADY74806	AdY74806 Human IGG
285	1756	99.5	731	4	AAW52156	Humanised	358	1751	99.2	330	9	ADZ69637	AdZ69637 Human IGG
286	1756	99.5	741	4	AAW52159	Humanised	359	1751	99.2	330	9	ADZ69616	AdZ69616 Human IGG
287	1756	99.5	951	2	AAW70798	Human gp1	360	1751	99.2	330	9	ADZ69650	AdZ69650 Human IGG
288	1756	99.5	951	3	AAW92186	Human gp1	361	1751	99.2	330	9	ADZ69642	AdZ69642 Human IGG
289	1756	99.5	951	7	ABW02166	Human gp1	362	1751	99.2	330	9	ADZ69620	AdZ69620 Human IGG
290	1756	99.5	961	3	AAV92187	Human gp1	363	1751	99.2	330	9	ADZ69600	AdZ69600 Human IGG
291	1756	99.5	972	3	ADG87101	Glucosamyl	364	1751	99.2	330	9	ADZ69611	AdZ69611 Human IGG
292	1756	99.5	975	7	ADG87102	Glucosamyl	365	1751	99.2	330	9	ADZ69619	AdZ69619 Human IGG
293	1754	99.4	330	9	ADZ69626	Human IGG	366	1751	99.2	330	9	ADZ69634	AdZ69634 Human IGG
294	1754	99.4	330	4	ADZ69628	Human IGG	367	1751	99.2	330	10	AEF16352	Aef16352 Human IGG
295	1754	99.4	592	4	AAH83838	Amino aci	368	1751	99.2	445	8	ADJ11308	AdJ11308 BHA10 VH#
296	1753	99.3	330	8	ADN97485	Artificia	369	1751	99.2	447	6	AAE33524	Aae33524 Human AOC
297	1753	99.3	330	8	ADT51725	Human Hul	370	1751	99.2	447	6	AAE33522	Aae33522 Human AOC
298	1753	99.3	330	8	ADT51718	Human OST	371	1751	99.2	447	9	AEI13531	Aei13531 Mature ch
299	1753	99.3	330	9	ADZ69635	Human IGG	372	1751	99.2	448	6	ABR55871	Abr55871 Human imm
300	1753	99.3	330	9	ADZ69647	Human IGG	373	1751	99.2	448	8	ADN49728	Adn49728 Human imm
301	1753	99.3	330	10	AEF16353	Human IGG	374	1751	99.2	448	8	ADU74404	AdU74404 Human imm
302	1753	99.3	446	8	ADT51688	Daclizuma	375	1751	99.2	448	9	AED12731	Aed12731 Heavy cha
303	1753	99.3	446	10	AEF16403	Humanized	376	1751	99.2	449	5	AAO18400	Aao18400 Mature hu
304	1753	99.3	447	8	ADT51699	Humanized	377	1751	99.2	449	9	AEA36337	Aea36337 Human CBE
305	1753	99.3	447	10	AEF16414	Fontolizu	378	1751	99.2	449	9	AEC92138	Aec92138 Anti-t-huPR
306	1753	99.3	448	8	AEF171908	Humanized	379	1751	99.2	452	2	AAE42066	Aae42066 Human ant
307	1753	99.3	464	9	ADT19760	Chimeric	380	1751	99.2	464	4	AAE72232	Aae72232 Humanised
308	1753	99.3	465	7	ADL23152	Mouse/hum	381	1751	99.2	464	8	ADJ11354	AdJ11354 BHA10 VH#
309	1753	99.3	465	7	ADL23135	Mouse/hum	382	1751	99.2	470	3	AAH08026	Aah08026 A dimeric
310	1753	99.3	465	7	ADL23150	Mouse/hum	383	1751	99.2	470	7	ADM05607	Adm05607 Human pro
311	1753	99.3	465	9	ADW48323	Anti-epit	384	1751	99.2	470	9	AEC88537	Aec88537 Human CDN
312	1753	99.3	465	9	ADW48340	Anti-epit	385	1751	99.2	476	8	ADP09212	Adp09212 Human pro
313	1753	99.3	465	9	ADW48338	Anti-epit	386	1751	99.2	697	8	AQO07403	Aqo07403 hCBE11/hB
314	1753	99.3	469	8	ADU17617	Human ant	387	1751	99.2	697	8	AQD12180	Aqd12180 Heavy cha
315	1753	99.3	469	8	ADU17474	Human ant	388	1751	99.2	701	8	ADQ07409	Adq07409 hCBE11 mo

389	1751	99.2	701	8	AD012186	Adn12186 Heavy cha	462	1750	99.2	451	8	ADN07039	Adn07039 Anti-IGE
390	1751	99.2	701	9	AE692142	Aee92142 Mature He	463	1750	99.2	451	8	ADN07035	Adn07035 Anti-IGE
391	1751	99.2	729	4	AAW52158	Aam52158 Humanized	464	1750	99.2	451	8	ADT55442	Adt55442 Anti-IGE
392	1751	99.2	739	4	AAW52161	Aam52161 Humanized	465	1750	99.2	451	8	ADT55441	Adt55441 Anti-IGE
393	1750	99.2	330	2	AAW50153	Aay50153 Human hea	466	1750	99.2	451	9	ADW00659	Adw00659 Human ant
394	1750	99.2	330	6	ABE98756	Abb98756 Human hea	467	1750	99.2	451	9	ADW00661	Adw00661 Human ant
395	1750	99.2	330	8	ADG91427	Adg91427 Amino aci	468	1750	99.2	451	9	ADW00657	Adw00657 Human ant
396	1750	99.2	330	8	ADG92917	Adg92917 Human IGG	469	1750	99.2	451	9	ADW79894	Adw79894 Anti-IGE
397	1750	99.2	330	8	ADT511716	Adt511716 Human OST	470	1750	99.2	451	9	ABE56308	Aeb56308 Anti-IGE
398	1750	99.2	330	8	ADT511715	Adt511715 Human OST	471	1750	99.2	451	9	ABE56307	Aeb56307 Anti-IGE
399	1750	99.2	330	8	ADT511714	Adt511714 Human OST	472	1750	99.2	451	9	ABE89918	Aeb89918 Anti-IGE
400	1750	99.2	330	9	ADW86658	Adw86658 Human Imm	473	1750	99.2	451	9	ABE89920	Aeb89920 Anti-IGE
401	1750	99.2	330	9	ADZ69610	Adz69610 Human IGG	474	1750	99.2	451	9	AEF89916	Aef89916 Anti-IGE
402	1750	99.2	330	9	ADZ69612	Adz69612 Human IGG	475	1750	99.2	451	10	AE605002	Aeg05002 Anti-CD20
403	1750	99.2	330	9	ADZ69646	Adz69646 Human IGG	476	1750	99.2	452	2	AY29458	Aay29458 Recombina
404	1750	99.2	330	9	ADZ69603	Adz69603 Human IGG	477	1750	99.2	452	3	AY77766	Aay77766 Humanized
405	1750	99.2	330	9	ADZ69639	Adz69639 Human IGG	478	1750	99.2	452	3	AAAB30322	Aab30322 Humanized
406	1750	99.2	330	9	ADZ69655	Adz69655 Human IGG	479	1750	99.2	452	6	ABU13799	Abu13799 Humanized
407	1750	99.2	330	9	ADZ69651	Adz69651 Human IGG	480	1750	99.2	452	6	ABU13799	Abu13799 Humanized
408	1750	99.2	330	9	ADZ69601	Adz69601 Human IGG	481	1750	99.2	452	7	ABU59512	Abu59512 Humanized
409	1750	99.2	330	9	ADZ69602	Adz69602 Human IGG	482	1750	99.2	452	7	AAE33094	Aae33094 Protein #
410	1750	99.2	330	9	ADZ69602	Adz69602 Human IGG	483	1750	99.2	452	8	ADZ33304	Adz33304 Anti-CD20
411	1750	99.2	330	9	ADZ69632	Adz69632 Human IGG	484	1750	99.2	452	9	ADW03410	Adw03410 Humanized
412	1750	99.2	330	9	ADZ69608	Adz69608 Human IGG	485	1750	99.2	452	9	ABE27728	Aeb27728 Humanized
413	1750	99.2	330	9	ADZ69613	Adz69613 Human IGG	486	1750	99.2	452	9	ABE18927	Aeb18927 Humanized
414	1750	99.2	330	9	ADZ69656	Adz69656 Human IGG	487	1750	99.2	452	9	ABE18960	Aeb18960 Humanized
415	1750	99.2	330	9	ADZ69607	Adz69607 Human IGG	488	1750	99.2	452	9	ABE18946	Aeb18946 Humanized
416	1750	99.2	330	9	ADZ69614	Adz69614 Human IGG	489	1750	99.2	452	10	ABE26246	Aee26246 Humanized
417	1750	99.2	330	9	ADZ69609	Adz69609 Human IGG	490	1750	99.2	452	10	ABE64957	Aee64957 Mature 2H
418	1750	99.2	330	9	ADZ69631	Adz69631 Human IGG	491	1750	99.2	452	10	ABE10478	Aee10478 Humanized
419	1750	99.2	330	9	ADZ69631	Adz69631 Human IGG	492	1750	99.2	452	10	ABE70764	Aee70764 Humanized
420	1750	99.2	330	9	ADZ69633	Adz69633 Human IGG	493	1750	99.2	452	10	AEF05020	Aef05020 Humanized
421	1750	99.2	330	9	ADZ69627	Adz69627 Human IGG	494	1750	99.2	452	10	AEF64241	Aef64241 Humanized
422	1750	99.2	330	9	ADZ69652	Adz69652 Human IGG	495	1750	99.2	453	2	AY50151	Aay50151 Antibody
423	1750	99.2	330	9	ADZ69653	Adz69653 Human IGG	496	1750	99.2	454	10	ABE99266	Aee99266 Heavy cha
424	1750	99.2	330	9	ADZ70836	Adz70836 Human will	497	1750	99.2	454	10	ABE99306	Aee99306 Heavy cha
425	1750	99.2	330	9	ADZ70837	Adz70837 Human ina	498	1750	99.2	467	10	ABE99284	Aee99284 Heavy cha
426	1750	99.2	330	9	ABE28909	Aeb28909 Human imm	499	1750	99.2	468	8	ADU23622	Adu23622 Human Imm
427	1750	99.2	330	9	ABE28908	Aeb28908 Human imm	500	1750	99.2	470	5	ABE81109	Abb81109 Anti-tiss
428	1750	99.2	330	9	ABE05749	Aec05749 Human IGG	501	1750	99.2	470	6	ABP72748	Adp72748 Anti-tiss
429	1750	99.2	330	10	ABF16349	Aef16349 Human IGG	502	1750	99.2	470	8	ADU14123	Ado14123 Plasmid p
430	1750	99.2	330	10	ABF16351	Aef16351 Human IGG	503	1750	99.2	470	8	ADU14137	Ado14137 Plasmid p
431	1750	99.2	330	10	ABF16350	Aef16350 Human IGG	504	1750	99.2	470	8	ADU14126	Ado14126 Plasmid p
432	1750	99.2	330	10	ABF90631	Aef90631 Human IGG	505	1750	99.2	471	8	ADP79584	Adp79584 2H7 v16 H
433	1750	99.2	371	1	ABP93558	Abp93558 Linked	506	1750	99.2	471	9	ADW03399	Adw03399 Human ant
434	1750	99.2	446	8	ADT51687	Adt51687 Dacilizuma	507	1750	99.2	471	9	ADW21319	Adw21319 Mouse ant
435	1750	99.2	446	8	ADT51686	Adt51686 Dacilizuma	508	1750	99.2	471	9	ADX00805	Adx00805 Humanized
436	1750	99.2	446	10	ABF16401	Aef16401 Humanized	509	1750	99.2	471	9	ABE18945	Aee18945 Humanized
437	1750	99.2	446	10	ABF16402	Aef16402 Humanized	510	1750	99.2	471	10	ABE26245	Aee26245 Humanized
438	1750	99.2	447	8	ADT51697	Adt51697 Fontolizu	511	1750	99.2	471	8	ADQ90735	Adq90735 Anti-IGE
439	1750	99.2	447	8	ADT51698	Adt51698 Fontolizu	512	1750	99.2	474	8	ADQ90734	Adq90734 Anti-IGE
440	1750	99.2	447	10	ABF16412	Aef16412 Humanized	513	1750	99.2	474	8	ADQ90736	Adq90736 Anti-VEGF
441	1750	99.2	447	10	ABF16413	Aef16413 Humanized	514	1750	99.2	476	5	ABE81110	Abb81110 Plasmid p
442	1750	99.2	449	10	ABF03142	Aef03142 Pertuzuma	515	1750	99.2	476	8	ADU14129	Ado14129 Plasmid p
443	1750	99.2	449	10	ABF27312	Aef27312 Humanized	516	1750	99.2	476	8	ADQ90736	Adq90736 Anti-VEGF
444	1750	99.2	450	3	AEA11269	Aea11269 Lys450-mo	517	1750	99.2	476	8	ADQ90733	Adq90733 Anti-VEGF
445	1750	99.2	450	3	AEA11270	Aea11270 Asp102Ieo	518	1750	99.2	479	8	ADU14132	Ado14132 Plasmid p
446	1750	99.2	451	2	AAW95659	Aaw95659 Mus muscu	519	1750	99.2	479	8	ADQ90737	Adq90737 Anti-VEGF
447	1750	99.2	451	2	AAW95663	Aaw95663 Mus muscu	520	1750	99.2	479	8	ADQ90732	Adq90732 Anti-VEGF
448	1750	99.2	451	2	AAW95661	Aaw95661 Mus muscu	521	1750	99.2	479	8	ADQ90729	Adq90729 Anti-VEGF
449	1750	99.2	451	2	AAW50031	Aay50031 Human B27	522	1750	99.2	479	8	ADQ90731	Adq90731 Anti-VEGF
450	1750	99.2	451	3	AAW85201	Aay85201 Light cha	523	1750	99.2	479	9	ADX85585	Adx85585 Human IGF
451	1750	99.2	451	3	AAW07473	Abw07473 Amino aci	524	1750	99.2	487	8	ADX98576	Adx98576 Protein f
452	1750	99.2	451	4	AAW47088	Aab47088 Anti-IGE	525	1750	99.2	548	9	ABE05751	Aec05751 Homo-cont
453	1750	99.2	451	4	AAW76952	Aab76952 Full leng	526	1750	99.2	557	9	ABE05750	Aec05750 Homo-cont
454	1750	99.2	451	4	AAW76948	Aab76948 Full leng	527	1750	99.2	564	9	ABE05758	Aec05758 Hetero-co
455	1750	99.2	451	4	AAW76950	Aab76950 Full leng	528	1750	99.2	666	9	ABE38766	Aeb38766 Humanized
456	1750	99.2	451	4	AAW74212	Aab74212 E27 anti-	529	1750	99.2	666	9	ABE53760	Aeb53760 Amino aci
457	1750	99.2	451	6	ABU62798	Abu62798 E27 anti-	530	1750	99.2	667	9	ABE38764	Aeb38764 Humanized
458	1750	99.2	451	7	ADP29039	Adp29039 Human ant	531	1750	99.2	667	9	ABE53758	Aeb53758 Amino aci
459	1750	99.2	451	7	ADP29039	Adp29039 Anti-IGE	532	1750	99.2	695	9	ABE38765	Aeb38765 Humanized
460	1750	99.2	451	8	ADF11670	Adf11670 anti-CD11	533	1750	99.2	695	9	ABE53759	Aeb53759 Amino aci
461	1750	99.2	451	8	ADN07037	Adn07037 Anti-IGE	534	1749	99.1	330	8	ADN36570	Adn36570 Chemokine

535	1749	99.1	330	9	ADZ69625	Adz69625 Human Igg	608	1747	99.0	449	7	ABR82262	AbR82262 Chimeric
536	1749	99.1	330	9	ADZ69630	Adz69630 Human Igg	609	1747	99.0	449	8	ADH34585	AdH34585 0011 heav
537	1749	99.1	330	9	ADZ69648	Adz69648 Human Igg	610	1747	99.0	449	8	ADP84137	ADP84137 Anti-mono
538	1749	99.1	330	9	ADZ69605	Adz69605 Human Igg	611	1747	99.0	449	8	ADP84131	ADP84131 Anti-mono
539	1749	99.1	330	9	ADZ69629	Adz69629 Human Igg	612	1747	99.0	449	8	ADZ23346	ADZ23346 Human CD7
540	1749	99.1	330	9	ADZ69606	Adz69606 Human Igg	613	1747	99.0	449	8	ADS31793	ADs31793 Chimeric
541	1749	99.1	330	9	ADZ69604	Adz69604 Human Igg	614	1747	99.0	449	10	ABE73924	Aee73924 Human ant
542	1749	99.1	330	9	ADZ69617	Adz69617 Human Igg	615	1747	99.0	450	4	AAE10521	AAe10521 Humanised
543	1749	99.1	330	9	ADZ69622	Adz69622 Human Igg	616	1747	99.0	450	4	AAE10525	AAe10525 Humanised
544	1749	99.1	330	9	ADZ69618	Adz69618 Human Igg	617	1747	99.0	450	4	AAE10513	AAe10513 Humanised
545	1749	99.1	330	9	ADZ69641	Adz69641 Human Igg	618	1747	99.0	450	4	AAE10515	AAe10515 Humanised
546	1749	99.1	330	9	ADZ69649	Adz69649 Human Igg	619	1747	99.0	450	4	AAE10517	AAe10517 Humanised
547	1749	99.1	330	9	ADZ69644	Adz69644 Human Igg	620	1747	99.0	450	4	AAE10523	AAe10523 Humanised
548	1749	99.1	330	10	AEF51211	Aef51211 Human imm	621	1747	99.0	450	4	AAE10519	AAe10519 Humanised
549	1749	99.1	400	7	ADD13790	Add13790 Plasmid p	622	1747	99.0	450	4	AAE10509	AAe10509 Humanised
550	1749	99.1	447	8	ADP19327	Adp19327 Chimeric	623	1747	99.0	450	4	AAE10511	AAe10511 Humanised
551	1748	99.0	330	5	ABG31479	Abg31479 Aglycosyl	624	1747	99.0	450	5	ABP66572	ABp66572 Human RSV
552	1748	99.0	330	9	ADZ69643	Adz69643 Human Igg	625	1747	99.0	450	5	ABP66578	ABp66578 Human RSV
553	1748	99.0	330	9	ADZ69621	Adz69621 Human Igg	626	1747	99.0	450	5	ABP66576	ABp66576 Human RSV
554	1748	99.0	330	9	ADZ69640	Adz69640 Human Igg	627	1747	99.0	450	5	ABP66582	ABp66582 Human RSV
555	1748	99.0	330	9	ADZ69624	Adz69624 Human Igg	628	1747	99.0	450	5	ABP66608	ABp66608 Human RSV
556	1748	99.0	330	10	AEF95114	Aef95114 Human Igg	629	1747	99.0	450	5	ABP66590	ABp66590 Human RSV
557	1748	99.0	448	8	ADP88439	Adp88439 Antibody	630	1747	99.0	450	5	ABP66610	ABp66610 Human RSV
558	1748	99.0	448	8	ADP88455	Adp88455 Antibody	631	1747	99.0	450	5	ABP66588	ABp66588 Human RSV
559	1748	99.0	448	10	AEF27208	Aef27208 Anti-CD4	632	1747	99.0	450	5	ABP66596	ABp66596 Human RSV
560	1748	99.0	448	10	AEF27224	Aef27224 Anti-CD4	633	1747	99.0	450	5	ABP66602	ABp66602 Human RSV
561	1748	99.0	449	3	AAV68810	Aav68810 A rat hea	634	1747	99.0	450	5	ABP66606	ABp66606 Human RSV
562	1748	99.0	451	9	ADW79892	Adw79892 Anti-IgE	635	1747	99.0	450	5	ABP66604	ABp66604 Human RSV
563	1748	99.0	467	6	ADA47341	Ada47341 TRX1 agly	636	1747	99.0	450	5	ABP66586	ABp66586 Human RSV
564	1748	99.0	467	6	ADA47342	Ada47342 TRX1 agly	637	1747	99.0	450	5	ABP66594	ABp66594 Human RSV
565	1748	99.0	467	8	ADP88454	Adp88454 Antibody	638	1747	99.0	450	5	ABP66598	ABp66598 Human RSV
566	1748	99.0	467	8	ADP88438	Adp88438 Antibody	639	1747	99.0	450	5	ABP66564	ABp66564 Human RSV
567	1748	99.0	467	8	ADQ87970	Adq87970 Heavy cha	640	1747	99.0	450	5	ABP66566	ABp66566 Human RSV
568	1748	99.0	467	10	AEF27207	Aef27207 Anti-CD4	641	1747	99.0	450	5	ABP66580	ABp66580 Human RSV
569	1748	99.0	467	10	AEF27264	Aef27264 Anti-CD4	642	1747	99.0	450	5	ABP66592	ABp66592 Human RSV
570	1748	99.0	467	10	AEF27205	Aef27205 Anti-CD4	643	1747	99.0	450	5	ABP66600	ABp66600 Human RSV
571	1748	99.0	467	10	AEF27223	Aef27223 Anti-CD4	644	1747	99.0	450	5	ABP66574	ABp66574 Human RSV
572	1748	99.0	467	10	AEF27221	Aef27221 Anti-CD4	645	1747	99.0	450	5	ABP66562	ABp66562 Human RSV
573	1748	99.0	468	8	ADQ07413	Adq07413 Mature CB	646	1747	99.0	450	5	ABP66568	ABp66568 Human RSV
574	1748	99.0	468	8	ADQ12196	Adq12196 CBE11 pen	647	1747	99.0	450	5	ABP66570	ABp66570 Human RSV
575	1748	99.0	469	7	ADM05602	Adm05602 Human pro	648	1747	99.0	450	6	ABU69427	ABu69427 Respirato
576	1748	99.0	469	9	AEC88532	Aec88532 Human cDN	649	1747	99.0	450	6	ABU69443	ABu69443 Respirato
577	1748	99.0	472	7	ADM05610	Adm05610 Human pro	650	1747	99.0	450	6	ABU69437	ABu69437 Respirato
578	1748	99.0	472	9	AEC88540	Aec88540 Human cDN	651	1747	99.0	450	6	ABU69467	ABu69467 Respirato
579	1748	99.0	477	8	ADL10091	Adl10091 Human pro	652	1747	99.0	450	6	ABU69471	ABu69471 Respirato
580	1747	99.0	330	8	ADT51720	Adt51720 Human OSt	653	1747	99.0	450	6	ABU69435	ABu69435 Respirato
581	1747	99.0	330	9	AE886185	Aeb86185 Amino aci	654	1747	99.0	450	6	ABU69451	ABu69451 Respirato
582	1747	99.0	330	10	AEF16358	Aef16358 Human Igg	655	1747	99.0	450	6	ABU69455	ABu69455 Respirato
583	1747	99.0	330	10	AEF09132	Aeg09132 Tie recep	656	1747	99.0	450	6	ABU69459	ABu69459 Respirato
584	1747	99.0	434	7	ADZ35960	Adz35960 SYNAGIS a	657	1747	99.0	450	6	ABU69429	ABu69429 Respirato
585	1747	99.0	445	9	ADX02218	Adx02218 SIRS coro	658	1747	99.0	450	6	ABU69457	ABu69457 Respirato
586	1747	99.0	446	8	ADT51689	Adt51689 Daclizuma	659	1747	99.0	450	6	ABU69439	ABu69439 Respirato
587	1747	99.0	446	9	ADX01861	Adx01861 SIRS coro	660	1747	99.0	450	6	ABU69453	ABu69453 Respirato
588	1747	99.0	446	10	AEF16404	Aef16404 Humanized	661	1747	99.0	450	6	ABU69463	ABu69463 Respirato
589	1747	99.0	447	8	AEF51700	Adf51700 Fontolizu	662	1747	99.0	450	6	ABU69473	ABu69473 Respirato
590	1747	99.0	447	9	AE846954	Aeb46954 CD1a spec	663	1747	99.0	450	6	ABU69425	ABu69425 Respirato
591	1747	99.0	447	9	AE846964	Aeb46964 CD1a spec	664	1747	99.0	450	6	ABU69441	ABu69441 Respirato
592	1747	99.0	447	9	AE846962	Aeb46962 CD1a spec	665	1747	99.0	450	6	ABU69445	ABu69445 Respirato
593	1747	99.0	447	10	AEF16415	Aef16415 Humanized	666	1747	99.0	450	6	ABU69433	ABu69433 Respirato
594	1747	99.0	448	5	ABE99224	ABe99224 Chimeric	667	1747	99.0	450	6	ABU69465	ABu69465 Respirato
595	1747	99.0	448	8	ADF71916	Adf71916 Hu3G8VH-2	668	1747	99.0	450	6	ABU69431	ABu69431 Respirato
596	1747	99.0	448	8	ADF71912	Adf71912 Hu3G8VH-5	669	1747	99.0	450	6	ABU69461	ABu69461 Respirato
597	1747	99.0	448	8	ADR23352	Adr23352 Human CD7	670	1747	99.0	450	6	ABU69449	ABu69449 Respirato
598	1747	99.0	448	8	ADR23354	Adr23354 Human CD7	671	1747	99.0	450	6	ABU69469	ABu69469 Respirato
599	1747	99.0	448	9	ADW11298	Adw11298 Human C-t	672	1747	99.0	450	6	ABG75662	ABg75662 Synagis h
600	1747	99.0	448	9	ADW11296	Adw11296 Human C-t	673	1747	99.0	450	7	ADE35928	AdE35928 SYNAGIS a
601	1747	99.0	448	9	ADW11294	Adw11294 Human C-t	674	1747	99.0	450	7	ADE35948	AdE35948 SYNAGIS a
602	1747	99.0	448	9	ADW90319	Adw90319 Phage scF	675	1747	99.0	450	7	ADE35920	AdE35920 SYNAGIS a
603	1747	99.0	448	9	ADX01871	Adx01871 SIRS coro	676	1747	99.0	450	7	ADE35926	AdE35926 SYNAGIS a
604	1747	99.0	448	9	ADY80252	Ady80252 Amino aci	677	1747	99.0	450	7	ADE35934	AdE35934 SYNAGIS a
605	1747	99.0	448	9	AE846960	Aeb46960 CD1a spec	678	1747	99.0	450	7	ADE35932	AdE35932 SYNAGIS a
606	1747	99.0	448	9	AE846958	Aeb46958 CD1a spec	679	1747	99.0	450	7	ADE35936	AdE35936 SYNAGIS a
607	1747	99.0	448	9	AE846956	Aeb46956 CD1a spec	680	1747	99.0	450	7	ADE35940	AdE35940 SYNAGIS a

681	1747	99.0	450	7	AD335952	AD335952	SYNAGIS a	754	1747	99.0	450	9	ABC76855	Aec76855	SYNAGIS-d
682	1747	99.0	450	7	AD335938	AD335938	SYNAGIS a	755	1747	99.0	450	9	ABC76843	Aec76843	SYNAGIS-d
683	1747	99.0	450	7	AD335956	AD335956	SYNAGIS a	756	1747	99.0	450	9	ABC76871	Aec76871	SYNAGIS-d
684	1747	99.0	450	7	AD335968	AD335968	SYNAGIS a	757	1747	99.0	450	9	ABC76877	Aec76877	SYNAGIS-d
685	1747	99.0	450	7	AD335946	AD335946	SYNAGIS a	758	1747	99.0	450	9	ABC76839	Aec76839	SYNAGIS a
686	1747	99.0	450	7	AD335966	AD335966	SYNAGIS a	759	1747	99.0	450	9	ABC76859	Aec76859	SYNAGIS-d
687	1747	99.0	450	7	AD335964	AD335964	SYNAGIS a	760	1747	99.0	450	9	ABC76885	Aec76885	SYNAGIS-d
688	1747	99.0	450	7	AD335930	AD335930	SYNAGIS a	761	1747	99.0	450	9	ABC76845	Aec76845	SYNAGIS-d
689	1747	99.0	450	7	AD335962	AD335962	SYNAGIS a	762	1747	99.0	450	9	ABC76847	Aec76847	SYNAGIS-d
690	1747	99.0	450	7	AD335958	AD335958	SYNAGIS a	763	1747	99.0	450	9	ABC76865	Aec76865	SYNAGIS-d
691	1747	99.0	450	7	AD335954	AD335954	SYNAGIS a	764	1747	99.0	450	9	ABC76875	Aec76875	SYNAGIS-d
692	1747	99.0	450	7	AD335922	AD335922	SYNAGIS a	765	1747	99.0	450	9	ABC76887	Aec76887	SYNAGIS-d
693	1747	99.0	450	7	AD335924	AD335924	SYNAGIS a	766	1747	99.0	450	9	ABC76879	Aec76879	SYNAGIS-d
694	1747	99.0	450	7	AD335944	AD335944	SYNAGIS a	767	1747	99.0	450	9	ABC76883	Aec76883	SYNAGIS-d
695	1747	99.0	450	7	AD335950	AD335950	SYNAGIS a	768	1747	99.0	450	9	ABC76857	Aec76857	SYNAGIS-d
696	1747	99.0	450	8	ADH34587	ADH34587	023 heavy	769	1747	99.0	450	9	ABC76869	Aec76869	SYNAGIS-d
697	1747	99.0	450	9	ADW20110	ADW20110	RSV antiG	770	1747	99.0	450	9	ABC76851	Aec76851	SYNAGIS-d
698	1747	99.0	450	9	ADW20082	ADW20082	RSV antiG	771	1747	99.0	450	9	ABC76881	Aec76881	SYNAGIS-d
699	1747	99.0	450	9	ADW20072	ADW20072	RSV antiG	772	1747	99.0	451	5	ABP66584	Human RSV	
700	1747	99.0	450	9	ADW20096	ADW20096	RSV antiG	773	1747	99.0	451	6	ABU69447	Respirato	
701	1747	99.0	450	9	ADW20100	ADW20100	RSV antiG	774	1747	99.0	451	7	AD335942	AD335942	SYNAGIS a
702	1747	99.0	450	9	ADW20104	ADW20104	RSV antiG	775	1747	99.0	451	8	ADH34584	008 heavy	
703	1747	99.0	450	9	ADW20064	ADW20064	RSV antiG	776	1747	99.0	451	8	ADH34586	ADH34586	021 heavy
704	1747	99.0	450	9	ADW20068	ADW20068	RSV antiG	777	1747	99.0	451	8	ADR23348	Human CD7	
705	1747	99.0	450	9	ADW20080	ADW20080	RSV antiG	778	1747	99.0	451	8	ADR23350	Human CD7	
706	1747	99.0	450	9	ADW20090	ADW20090	RSV antiG	779	1747	99.0	451	8	ADR23344	Human CD7	
707	1747	99.0	450	9	ADW20094	ADW20094	RSV antiG	780	1747	99.0	451	9	ADW20084	RSV antiG	
708	1747	99.0	450	9	ADW20062	ADW20062	RSV antiG	781	1747	99.0	451	9	ADX01865	SARS coro	
709	1747	99.0	450	9	ADW20102	ADW20102	RSV antiG	782	1747	99.0	451	9	ABE07066	RSV-speci	
710	1747	99.0	450	9	ADW20070	ADW20070	RSV antiG	783	1747	99.0	451	9	AEC76861	SYNAGIS-d	
711	1747	99.0	450	9	ADW20098	ADW20098	RSV antiG	784	1747	99.0	452	9	ADX01863	SARS coro	
712	1747	99.0	450	9	ADW20106	ADW20106	RSV antiG	785	1747	99.0	452	9	ADY70962	Human mon	
713	1747	99.0	450	9	ADW20108	ADW20108	RSV antiG	786	1747	99.0	452	10	ABE73716	ABE73716	Human ant
714	1747	99.0	450	9	ADW20076	ADW20076	RSV antiG	787	1747	99.0	455	9	ADY70958	Human mon	
715	1747	99.0	450	9	ADW20092	ADW20092	RSV antiG	788	1747	99.0	457	9	ADY70954	Human mon	
716	1747	99.0	450	9	ADW20078	ADW20078	RSV antiG	789	1747	99.0	457	10	ABE73712	ABE73712	Human ant
717	1747	99.0	450	9	ADW20074	ADW20074	RSV antiG	790	1747	99.0	466	10	ABE17836	Aec17836	Heavy cha
718	1747	99.0	450	9	ADW20086	ADW20086	RSV antiG	791	1747	99.0	467	9	AEC20875	Low risk	
719	1747	99.0	450	9	ADW20066	ADW20066	RSV antiG	792	1747	99.0	467	9	AEC20877	Low + mod	
720	1747	99.0	450	9	ADW20088	ADW20088	RSV antiG	793	1747	99.0	468	7	AD664201	MN14HCF p	
721	1747	99.0	450	9	ADX02216	ADX02216	SARS coro	794	1747	99.0	468	7	ADF60815	HMN-14 he	
722	1747	99.0	450	9	ADX01867	ADX01867	SARS coro	795	1747	99.0	468	8	ADS14299	EGFR anti	
723	1747	99.0	450	9	ADX01869	ADX01869	SARS coro	796	1747	99.0	468	10	ABE86004	Aec86004	Anthrax t
724	1747	99.0	450	9	AEB07080	AEB07080	RSV-speci	797	1747	99.0	469	7	ABR61529	Humanised	
725	1747	99.0	450	9	AEB07050	AEB07050	RSV-speci	798	1747	99.0	469	7	ABR61527	Humanised	
726	1747	99.0	450	9	AEB07072	AEB07072	RSV-speci	799	1747	99.0	469	9	ADY86264	Anti-huma	
727	1747	99.0	450	9	AEB07058	AEB07058	RSV-speci	800	1747	99.0	469	9	AEA12650	Variant h	
728	1747	99.0	450	9	AEB07048	AEB07048	RSV-speci	801	1747	99.0	469	9	AEA18906	Variant h	
729	1747	99.0	450	9	AEB07056	AEB07056	RSV-speci	802	1747	99.0	469	9	AEA18546	Variant h	
730	1747	99.0	450	9	AEB07062	AEB07062	RSV-speci	803	1747	99.0	469	9	AEA10639	Human ant	
731	1747	99.0	450	9	AEB07064	AEB07064	RSV-speci	804	1747	99.0	469	9	AE225712	Monoclonal	
732	1747	99.0	450	9	AEB07082	AEB07082	RSV-speci	805	1747	99.0	469	9	AE224413	Human CHI	
733	1747	99.0	450	9	AEB07084	AEB07084	RSV-speci	806	1747	99.0	469	9	AE225978	Ant-CD40	
734	1747	99.0	450	9	AEB07086	AEB07086	RSV-speci	807	1747	99.0	470	2	AAW83036	Ant1-Fas	
735	1747	99.0	450	9	AEB07078	AEB07078	RSV-speci	808	1747	99.0	470	2	AAW83037	Ant1-Fas	
736	1747	99.0	450	9	AEB07060	AEB07060	RSV-speci	809	1747	99.0	470	3	AAW814779	Humanised	
737	1747	99.0	450	9	AEB07068	AEB07068	RSV-speci	810	1747	99.0	470	3	AAW814776	Humanised	
738	1747	99.0	450	9	AEB07076	AEB07076	RSV-speci	811	1747	99.0	470	3	AAW90926	Humanised	
739	1747	99.0	450	9	AEB07070	AEB07070	RSV-speci	812	1747	99.0	470	3	AAW90934	Humanised	
740	1747	99.0	450	9	AEB07046	AEB07046	RSV-speci	813	1747	99.0	470	3	AAW90935	Humanised	
741	1747	99.0	450	9	AEB07044	AEB07044	RSV-speci	814	1747	99.0	470	3	AAW90933	Humanised	
742	1747	99.0	450	9	AEB07054	AEB07054	RSV-speci	815	1747	99.0	470	3	AAW90936	Humanised	
743	1747	99.0	450	9	AEB07090	AEB07090	RSV-speci	816	1747	99.0	470	3	AAW90929	Humanised	
744	1747	99.0	450	9	AEB07092	AEB07092	RSV-speci	817	1747	99.0	470	5	ABB74941	Humanised	
745	1747	99.0	450	9	AEB07052	AEB07052	RSV-speci	818	1747	99.0	470	5	ABB74944	Humanised	
746	1747	99.0	450	9	AEB07074	AEB07074	RSV-speci	819	1747	99.0	470	5	ABB74945	Humanised	
747	1747	99.0	450	9	AEB07088	AEB07088	RSV-speci	820	1747	99.0	470	5	ABB74898	Humanised	
748	1747	99.0	450	9	AEC76849	AEC76849	SYNAGIS-d	821	1747	99.0	470	5	ABB74904	Mouse hum	
749	1747	99.0	450	9	AEC76863	AEC76863	SYNAGIS-d	822	1747	99.0	470	5	ABB74902	Humanised	
750	1747	99.0	450	9	AEC76841	AEC76841	SYNAGIS-d	823	1747	99.0	470	5	ABB74903	Mouse hum	
751	1747	99.0	450	9	AEC76867	AEC76867	SYNAGIS-d	824	1747	99.0	470	5	ABB74895	Humanised	
752	1747	99.0	450	9	AEC76873	AEC76873	SYNAGIS-d	825	1747	99.0	470	9	ABE48573	Human igG	
753	1747	99.0	450	9	AEC76853	AEC76853	SYNAGIS-d	826	1747	99.0	472	2	AAV50157	Chimeric	

827	1747	99.0	473	4	AAB36206	Aab36206 Human imm	900	1745	98.9	544	8	ADR66914	Adr66914 Human pro
828	1747	99.0	473	7	ADM05996	Adm05996 Human pro	901	1745	98.9	544	8	ADU66016	Adu66016 Human pro
829	1747	99.0	473	7	AEC88926	Aec88926 Human cDN	902	1745	98.9	545	8	ADU06496	Adu06496 Novel bro
830	1747	99.0	474	4	AAU14177	Aau14177 Human nov	903	1745	98.9	730	4	AAU52157	Aau52157 Humanised
831	1747	99.0	474	5	AAO14065	Aao14065 Heavy cha	904	1745	98.9	740	4	AAW52160	Aaw52160 Humanised
832	1747	99.0	474	6	ABU08017	Abu08017 Human mon	905	1744	98.8	329	8	ADH75410	Adh75410 Human Igg
833	1747	99.0	474	7	ADF65775	Adf65775 Human pro	906	1744	98.8	332	7	ABR63190	Abr63190 Mutated a
834	1747	99.0	474	7	ADM05955	Adm05955 Human pro	907	1744	98.8	332	7	ABR63190	Abr63190 Mutated a
835	1747	99.0	474	8	ADJ92515	Adj92515 Human SOJ	908	1744	98.8	469	9	AEA12649	Aea12649 Heavy cha
836	1747	99.0	474	9	AEA12653	Aea12653 Heavy cha	909	1744	98.8	469	9	AEA18905	Aea18905 Heavy cha
837	1747	99.0	474	9	AEA18909	Aea18909 Variant h	910	1744	98.8	469	9	AEA18545	Aea18545 Heavy cha
838	1747	99.0	474	9	AEA18549	Aea18549 Variant o	911	1744	98.8	469	9	AEA10638	Aea10638 Human ant
839	1747	99.0	474	9	AEA10642	Aea10642 Human ant	912	1744	98.8	469	9	AED25711	Aed25711 Monoclonal
840	1747	99.0	474	9	AEA10642	Aea10642 Human ant	912	1744	98.8	469	9	AED25711	Aed25711 Monoclonal
841	1747	99.0	474	9	AED25715	Aed25715 Monoclonal	913	1744	98.8	469	9	AED25715	Aed25715 Monoclonal
842	1747	99.0	474	9	AEC88885	Aec88885 Human cDN	914	1744	98.8	469	9	AED25977	Aed25977 Ant-CD40
843	1747	99.0	474	9	AED24416	Aed24416 Human CHI	915	1744	98.8	474	8	ADR72764	Adr72764 Human mon
844	1747	99.0	474	9	AED25981	Aed25981 Ant-CD40	916	1744	98.8	474	8	ADS98007	Ads98007 Protein f
845	1747	99.0	474	10	AEE23615	Aee23615 Novel hum	917	1744	98.8	474	9	AEA12652	Aea12652 Heavy cha
846	1747	99.0	475	9	AE848567	Aeb48567 Human Igg	918	1744	98.8	474	9	AEA18908	Aea18908 Heavy cha
847	1747	99.0	476	6	ABU08022	Abu08022 Monoclonal	919	1744	98.8	474	9	AEA18548	Aea18548 Heavy cha
848	1747	99.0	476	7	ADF65788	Adf65788 Human ant	920	1744	98.8	474	9	AEA10641	Aea10641 Human ant
849	1747	99.0	476	8	ADJ92523	Adj92523 Human SOJ	921	1744	98.8	474	9	AED25714	Aed25714 Monoclonal
850	1747	99.0	476	9	ADV99723	Adv99723 Human rab	922	1744	98.8	474	9	AED25980	Aed25980 Ant-CD40
851	1747	99.0	477	4	AAU14288	Aau14288 Human nov	923	1744	98.8	556	5	AAE29073	Aae29073 Human IL-
852	1747	99.0	477	10	AEE23726	Aee23726 Novel hum	924	1744	98.8	559	4	AAE29073	Aae29073 Human IL-
853	1747	99.0	478	7	ADB65658	Adb65658 Human pro	925	1744	98.8	559	5	ABG67217	Abg67217 IL-20RA e
854	1747	99.0	489	7	ADB65175	Adb65175 Human pro	926	1744	98.8	559	5	AAE23361	Aae23361 Human IL-
855	1747	99.0	526	9	AE848561	Aeb48561 Human Igg	927	1744	98.8	559	8	ADJ83342	Adj83342 Human IL-
856	1747	99.0	579	6	ADG87073	Aeg87073 Glucoamyl	928	1744	98.8	559	9	ADW64577	Adw64577 IL-20RA a
857	1746	98.9	472	2	AAW01820	Aaw01820 Anti-rhes	930	1744	98.8	559	9	AEA28863	Aea28863 Human IL-
858	1746	98.9	478	2	AAW01820	Aaw01820 Primatise	931	1744	98.8	573	5	AAE29072	Aae29072 Human IL-
859	1746	98.9	667	9	AEA38767	Aea38767 Humanized	932	1744	98.8	594	4	AAH85274	Aah85274 Human IL-
860	1746	98.9	667	9	AEA38769	Aea38769 Humanized	933	1744	98.8	594	4	AAU04062	Aau04062 Human IL-
861	1746	98.9	667	9	AED53761	Aed53761 Amino aci	934	1744	98.8	594	5	ABG67205	Abg67205 IL-20RA e
862	1746	98.9	667	9	AED53763	Aed53763 Amino aci	935	1744	98.8	594	5	AAE23358	Aae23358 Human IL-
863	1746	98.9	729	3	AA515078	Aay51078 Human fus	936	1744	98.8	594	8	ADJ83303	Adj83303 Human IL-
864	1745	98.9	333	6	ADW42733	Adw42733 Anti-tiss	937	1744	98.8	594	9	ADW64540	Adw64540 IL-20RA a
865	1745	98.9	339	9	ADW42733	Adw42733 Anti-tiss	938	1744	98.8	594	9	AEA50124	Aea50124 Human IL-
866	1745	98.9	339	9	ADW42743	Adw42743 Human var	939	1744	98.8	594	9	AEA28862	Aea28862 Human IL-
867	1745	98.9	339	9	ADW20894	Adw20894 Mammalian	940	1743	98.8	329	8	ADH75387	Adh75387 Human Igg
868	1745	98.9	339	9	ADZ08810	Adz08810 Mammalian	941	1743	98.8	329	8	ADT99194	Adt99194 Human rec
869	1745	98.9	339	9	ADZ44467	Adz44467 Human imm	942	1743	98.8	359	9	AED85880	Aed85880 Igg1 expr
870	1745	98.9	339	9	AEA16542	Aea16542 Human MCP	943	1743	98.8	467	10	AEF38712	Aef38712 Monoclonal
871	1745	98.9	339	9	AEF72777	Aeb72777 Anti-Lfai	944	1743	98.8	472	9	ADM05606	Adm05606 Human cDN
872	1745	98.9	339	9	AEC94905	Aec94905 Anti-IL-1	945	1743	98.8	472	9	ADM05606	Adm05606 Human cDN
873	1745	98.9	339	9	AED21951	Aed21951 GLP-1 CHI	946	1743	98.8	474	10	AEF17112	Aef17112 B. brevis
874	1745	98.9	339	9	AED49127	Aed49127 Heavy cha	947	1743	98.8	474	10	AEF17109	Aef17109 B. brevis
875	1745	98.9	329	10	AEF57797	Aef57797 Anti-IL-1	948	1743	98.8	474	10	AEF18357	Aef18357 Outer wal
876	1745	98.9	330	8	ADT51719	Adt51719 Human OST	949	1743	98.8	474	10	AEF18354	Aef18354 Outer wal
877	1745	98.9	330	10	AEF16357	Aef16357 Human Igg	950	1743	98.8	476	8	AQO90730	Aqo90730 Anti-VEGF
878	1745	98.9	402	9	AEC22861	Aec22861 Membrane	951	1743	98.8	729	3	AAH19507	Aah19507 CD4-IgG1
879	1745	98.9	446	8	ADT51690	Adt51690 Daclizuma	952	1742	98.7	330	7	ADJ94620	Adj94620 Human Igg
880	1745	98.9	446	10	AEF16405	Aef16405 Humanized	953	1742	98.7	465	7	ADW64199	Adw64199 IL2HCF pr
881	1745	98.9	447	6	AEC33523	Aec33523 Human AQC	954	1742	98.7	470	7	ADM05506	Adm05506 Human pro
882	1745	98.9	447	6	ADT51701	Adt51701 Fontolizu	955	1742	98.7	470	9	AEC88436	Aec88436 Human cDN
883	1745	98.9	448	10	AEF16416	Aef16416 Humanized	956	1742	98.7	575	8	ADP42961	Adp42961 Humanised
884	1745	98.9	448	10	AEF27304	Aef27304 Humanized	957	1742	98.7	669	9	ADY97271	Ady97271 Exemplary
885	1745	98.9	449	3	AEA11268	Aea11268 Aspi02iso	958	1741	98.6	443	9	AEH43843	Aeh43843 Human Hul
886	1745	98.9	449	3	AEA11271	Aea11271 Aspi02suc	959	1741	98.6	446	2	AAW05829	Aaw05829 Humanised
887	1745	98.9	449	3	AEA11266	Aea11266 Humanized	960	1741	98.6	451	10	AEQ04998	Aeq04998 Anti-IL-8
888	1745	98.9	449	7	ADH85320	Adh85320 Heavy cha	961	1741	98.6	452	2	AAW69316	Aaw69316 Heavy cha
889	1745	98.9	449	8	ADP11668	Adp11668 anti-HER2	962	1741	98.6	452	9	EBI17638	Eeb17638 Heavy cha
890	1745	98.9	449	8	ADH34511	Adh34511 Heavy cha	963	1741	98.6	454	2	AAH30774	Aah30774 H52H4-160
891	1745	98.9	449	8	ADM31929	Adm31929 Humanized	964	1741	98.6	466	2	AAH24812	Aah24812 Sequence
892	1745	98.9	449	9	ADH80642	Adh80642 Trastuzum	965	1741	98.6	473	7	ADM05593	Adm05593 Human pro
893	1745	98.9	449	9	AED20674	Aed20674 Trastuzum	966	1741	98.6	473	9	AEC88523	Aec88523 Human cDN
894	1745	98.9	449	10	AEF03140	Aef03140 Trastuzum	967	1741	98.6	476	6	AAE37364	Aae37364 Monkey 16
895	1745	98.9	449	10	AEF27302	Aef27302 Humanized	968	1741	98.6	479	7	ADG87079	Adg87079 Fusion pr
896	1745	98.9	451	10	AEF64965	Aef64965 Mature 2H	969	1741	98.6	479	7	ADG87079	Adg87079 Fusion pr
897	1745	98.9	451	10	AEF10486	Aef10486 Humanized	970	1740.5	98.6	451	5	AAH47726	Aah47726 Heavy cha
898	1745	98.9	467	10	AEF27306	Aef27306 Humanized	971	1740	98.6	330	9	AED07841	Aed07841 Human Igg
899	1745	98.9	468	8	ADQ66840	Adq66840 Novel hum	972	1740	98.6	330	10	AEQ04978	Aeq04978 Human Igg

973 1740 98.6 451 10 AEG05000 Anti-CD20
 974 1740 98.6 466 4 AAE03755 Chimeric
 975 1740 98.6 472 2 AAY50166 Human res
 976 1740 98.6 476 4 AAB49243 Chimeric
 977 1740 98.6 667 9 AEA38768 Humanized
 978 1740 98.6 667 9 AED53762 Amino aci
 979 1739.5 98.6 329 10 AEG04979 Human IgG
 980 1739 98.5 453 2 AAR33311 Humanised
 981 1739 98.5 453 3 AAY85199 Heavy cha
 982 1739 98.5 468 2 AAW85689 D9D10 hea
 983 1739 98.5 711 2 AAW85692 MoTAII f
 984 1738 98.5 330 3 AEA48173 Variant I
 985 1738 98.5 342 3 AAB53463 Human col
 986 1738 98.5 467 8 ADQ87978 Heavy cha
 987 1737 98.4 329 10 AEF51651 Anti-VEGF
 988 1736.5 98.4 329 8 ADS82579 Human IgG
 989 1736 98.4 447 9 AEB13695 Human ant
 990 1736 98.4 449 9 AEA48168 Mouse ant
 991 1736 98.4 539 8 ADE10009 Human pro
 992 1735 98.3 443 9 AEB43847 Human Hul
 993 1735 98.3 452 9 ADW03411 Humanized
 994 1735 98.3 452 9 AEE18948 Humanized
 995 1735 98.3 452 9 AEE18928 Humanized
 996 1735 98.3 452 10 AEE26248 2H7.v31 a
 997 1735 98.3 452 10 AEE64958 Mature 2H
 998 1735 98.3 452 10 AEE10479 Humanized
 999 1735 98.3 452 10 AEE70765 Humanized
 1000 1735 98.3 452 10 AEE70777 Humanized

ALIGNMENTS

RESULT 1
 ADQ89332
 ID ADQ89332 standard; protein; 330 AA.
 AC ADQ89332;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Human immunoglobulin protein #44.
 XX
 KW Human; immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2;
 KW CCR2; inflammatory disease; autoimmune disorder; graft rejection;
 KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;
 KW anti-HIV; virucide; antiarteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 PN US2004151721-A1.
 XX
 PD 05-AUG-2004.
 XX
 PF 10-DEC-2003; 2003US-00733563.
 XX
 PR 19-OCT-2001; 2001US-0350166P.
 PR 26-JUN-2002; 2002US-0392364P.
 PR 17-OCT-2002; 2002US-00272899.
 XX
 PA (OKEE/) O'KEEFE T.
 PA (PONA/) PONAATH P.
 XX
 PI O'keefe T, Ponath P;
 XX
 DR WPI; 2004-580175/56.
 XX
 XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,
 PT useful for diagnosing and/or treating inflammatory or autoimmune
 PT diseases, and HIV infection.
 XX
 PS Claim 1; SEQ ID NO 110; 128pp; English.
 XX

CC The invention relates to humanised immunoglobulin heavy and light chains
 CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an
 CC immunoglobulin or its antigen binding fragment comprising the chains. The
 CC humanised immunoglobulin or its antigen binding fragment preferably
 CC comprises two heavy chains and two light chains. The humanised
 CC immunoglobulin and its heavy and light chains are useful for the
 CC diagnosis, prevention and/or treatment of diseases or conditions
 CC associated with aberrant expression or activity of the CCR2 polypeptide,
 CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV
 CC infection and atherosclerosis. This sequence represents a human
 CC immunoglobulin protein of the invention.
 XX
 SQ Sequence 330 AA;

Query Match 100.0%; Score 1765; DB 8; Length 330;
 Best Local Similarity 100.0%; Pred. No. 5.1e-124;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGLCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
 DB 1 ASTKGPSVFPPLAPSSKSTSGGTAALGLCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
 QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
 DB 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
 QY 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
 DB 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
 QY 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
 DB 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFPLYSKLTVDKSRW 300
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFPLYSKLTVDKSRW 300
 QY 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330
 DB 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330

RESULT 2
 AEB09605
 ID AEB09605 standard; protein; 330 AA.
 XX
 AC AEB09605;
 XX
 DT 08-SEP-2005 (first entry)
 XX
 DE Human IgG1 constant region FcRmut SEQ ID NO 110.
 XX
 KW antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;
 KW antibody engineering; therapeutic; diagnosis; inflammation;
 KW autoimmune disease; immune disorder; graft rejection; HIV infection;
 KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;
 KW heavy chain constant region.

OS Homo sapiens.
 XX
 PN WO2005060368-A2.
 XX
 PD 07-JUL-2005.
 XX
 PF 10-DEC-2003; 2003WO-US039599.
 XX
 PR 10-DEC-2003; 2003WO-US039599.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Okeefe T, Ponath P;
 XX


```
Db 304 QQGNVFCVSVHVAEALHNHYTKLSLSPGK 333
|||||
RESULT 4
ADQ89336
ID ADQ89336 standard; protein; 333 AA.
XX
AC ADQ89336;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human immunoglobulin protein #46.
XX
KW Human; immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2;
KW CCR2; inflammatory disease; autoimmune disorder; graft rejection;
KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;
KW anti-HIV; virucide; antiarteriosclerotic.
XX
OS Homo sapiens.
XX
PN US2004151721-A1.
XX
PD 05-AUG-2004.
XX
PF 10-DEC-2003; 2003US-00733563.
XX
PR 19-OCT-2001; 2001US-0350166P.
PR 26-JUN-2002; 2002US-0392364P.
PR 17-OCT-2002; 2002US-00272899.
XX
PA (OKEE/) O'KEEFE T.
PA (PONA/) PONATH P.
XX
PI O'keefe T, Ponath P;
XX
DR WPI; 2004-580175/56.
XX
PT New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,
PT useful for diagnosing and/or treating inflammatory or autoimmune
PT diseases, and HIV infection.
XX
PS Disclosure; SEQ ID NO 114; 128pp; English.
XX
CC The invention relates to humanised immunoglobulin heavy and light chains
CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an
CC immunoglobulin or its antigen binding fragment comprising the chains. The
CC humanised immunoglobulin or its antigen binding fragment preferably
CC comprises two heavy chains and two light chains. The humanised
CC immunoglobulin and its heavy and light chains are useful for the
CC diagnosis, prevention and/or treatment of diseases or conditions
CC associated with aberrant expression or activity of the CCR2 polypeptide,
CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV
CC infection and atherosclerosis. This sequence represents a human
CC immunoglobulin protein of the invention.
XX
SQ Sequence 333 AA;
Query Match 100.0%; Score 1765; DB 8; Length 333;
Best Local Similarity 100.0%; Pred. No. 5.1e-124;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGLCKLVDFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
|||||
Db 4 ASTKGPSVFPPLAPSSKSTSGGTAALGLCKLVDFPEPVTVSWNSGALTSGVHTFPAVLQSS 63
|||||
QY 61 GLYSLSVVTVPSLSIGTQYICNVNHPKSNITKVKVEPKSCDKTHRCPPCPAPELAGA 120
|||||
Db 64 GLYSLSVVTVPSLSIGTQYICNVNHPKSNITKVKVEPKSCDKTHRCPPCPAPELAGA 123
|||||
QY 121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
|||||
Db 124 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 183
|||||
QY 181 STYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
|||||
Db 184 STYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 243
|||||
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
|||||
Db 244 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 303
|||||
QY 301 QQGNVFCVSVHVAEALHNHYTKLSLSPGK 330
|||||
Db 304 QQGNVFCVSVHVAEALHNHYTKLSLSPGK 333
|||||
RESULT 5
AEB09609
ID AEB09609 standard; protein; 333 AA.
XX
AC AEB09609;
XX
DT 08-SEP-2005 (first entry)
XX
DE Human IgG1 constant region FcRmut SEQ ID NO 114.
XX
KW antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;
KW antibody engineering; therapeutic; diagnosis; inflammation;
KW autoimmune disease; immune disorder; graft rejection; HIV infection;
KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;
KW light chain constant region.
XX
OS Homo sapiens.
XX
PN WO2005060368-A2.
XX
PD 07-JUL-2005.
XX
PF 10-DEC-2003; 2003WO-US039599.
XX
PR 10-DEC-2003; 2003WO-US039599.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Okeefe T, Ponath P;
XX
DR WPI; 2005-488561/49.
DR N-PSDB; AEB09610.
XX
PT New humanized immunoglobulin or its antigen binding portion having
PT binding specificity for CC-chemokine receptor 2 and having a heavy chain
PT and light chain, for treating inflammatory diseases, HIV, and autoimmune
PT diseases.
XX
PS Disclosure; SEQ ID NO 114; 192pp; English.
XX
CC The invention describes a humanized immunoglobulin (I) or its antigen
CC binding portion having binding specificity for CC-chemokine receptor 2
CC (CCR2) and having a heavy chain and a light chain, where the heavy chain
CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)
CC sequence, given in specification or its portion, and the light chain
CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given
CC in specification. Also described are: a humanized immunoglobulin heavy
CC chain, or its antigen binding fragment, having binding specificity for
CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the
CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized
CC immunoglobulin light chain, or its antigen binding fragment, having
CC binding specificity for CCR2 and comprising the amino acid sequence of
CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)
CC sequence, given in specification. The following are disclosed: isolated
CC nucleic acid molecules comprising nucleic acid sequence encoding (I); a
CC construct comprising nucleic acid molecule encoding (I); and host cell
CC comprising the nucleic acid molecule. (I) is useful as a therapeutic
CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus
CC reducing inflammatory response, for use in the treatment of diseases
```

CC associated with leukocyte infiltration of tissue, e.g. in the treatment
CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV
CC infection and monocytic-mediated disorders such as atherosclerosis. (I) Is
CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.
CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel
CC fluid), and for modulating binding function and/or leukocyte trafficking
CC modulated by CCR2. This is the amino acid sequence of human IgG1 constant
CC region FcRmut used in the creation of a humanized anti-CCR2-antibody.
XX
SQ Sequence 333 AA;

Query Match 100.0%; Score 1765; DB 9; Length 333;
Best Local Similarity 100.0%; Pred. No. 5.1e-124; Indels 0; Gaps 0;
Matches 330; Conservative 0; Mismatches 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
DB 4 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 63
QY 61 GLYSLSVVTVPSSSLGQTQYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGA 120
DB 64 GLYSLSVVTVPSSSLGQTQYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGA 123
QY 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 124 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 183
QY 181 STYRVSVVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 184 STYRVSVVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 243
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 300
DB 244 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 303
QY 301 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 330
DB 304 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 333

RESULT 6
ADJ95974
ID ADJ95974 standard; protein; 356 AA.
XX
AC ADJ95974;
DE 06-MAY-2004 (first entry)
XX Immunoglobulin DNA cassette polypeptide seqid 70.
XX
KW cytostatic; antibody therapy; immunoglobulin cassette construct;
KW immunoglobulin leader molecule; immunoglobulin domain;
KW immunoglobulin therapeutic molecule; monobody; cancer.
XX
OS Synthetic.
XX
XX US2004033561-A1.
XX
XX 19-FEB-2004.
XX
XX 17-OCT-2002; 2002US-00272899.
XX
XX 19-OCT-2001; 2001US-0350166P.
XX 26-JUN-2002; 2002US-0392364P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX O'keefe TL, Healey JJ, Newman W, Ponath PD, Keyt BA;
PI WPI; 2004-180050/17.
XX N-PSDB; ADJ95973.
XX
XX New isolated nucleic acid molecules having an immunoglobulin cassette

PT construct, useful for producing immunoglobulin therapeutic molecules
PT termed monobodies, used as a therapeutic group in cancer disorders.
XX
XX Disclosure; SEQ ID NO 70; 84pp; English.
XX
CC The invention describes an isolated nucleic acid molecule comprising an
CC immunoglobulin cassette construct, wherein the immunoglobulin cassette
CC comprises an immunoglobulin leader molecule operably linked to a stable
CC immunoglobulin domain region. The methods and compositions of the present
CC invention are useful for producing immunoglobulins, in particular
CC immunoglobulin therapeutic molecules termed monobodies, used as a
CC therapeutic group in cancer disorders. This is the amino acid sequence of
CC an immunoglobulin DNA cassette construct.
XX
SQ Sequence 356 AA;

Query Match 100.0%; Score 1765; DB 8; Length 356;
Best Local Similarity 100.0%; Pred. No. 5.6e-124; Indels 0; Gaps 0;
Matches 330; Conservative 0; Mismatches 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
DB 27 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 86
QY 61 GLYSLSVVTVPSSSLGQTQYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGA 120
DB 87 GLYSLSVVTVPSSSLGQTQYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGA 146
QY 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 147 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 206
QY 181 STYRVSVVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 207 STYRVSVVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 266
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 300
DB 267 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 326
QY 301 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 330
DB 327 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 356

RESULT 7
AAV32263
ID AAV32263 standard; protein; 444 AA.
XX
AC AAV32263;
XX
DT 15-FEB-2000 (first entry)
XX
DE Humanised anti-CD23 Mab C11 heavy chain.
XX
KW CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; human;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
therapy.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key
XX Location/Qualifiers
XX 1..30
XX /note= "framework region 1"
XX 31..35
XX Region

FT	Region	/note= "CDR 1"	
FT	36. .49		
FT	/note= "framework region 2"		
FT	50. .68		
FT	/note= "CDR 2"		
FT	69. .100		
FT	/note= "framework region 3"		
FT	101. .103		
FT	/note= "CDR 3"		
FT	104. .111		
FT	/note= "framework region 4"		
FT	112. .444		
FT	/note= "constant region"		
XX			
PN	WO9958679-Al.		
XX			
XX	18-NOV-1999.		
XX			
XX	07-MAY-1999; 99WO-GB001434.		
XX			
XX	09-MAY-1998; 98GB-00009839.		
XX			
XX	(GLAX) GLAXO GROUP LTD.		
XX			
XX	Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;		
XX			
DR	WPI; 2000-053101/04.		
DR	N-PSDB; AAZ34748.		
XX			
XX	Cell receptor specific antibodies useful for treating e.g. arthritis,		
XX	diabetes, multiple sclerosis and psoriasis.		
XX			
PS	Claim 9; Fig 4; 81pp; English.		
XX			
CC	This amino acid sequence represents the heavy chain of humanised anti-		
CC	CD23 (FCERII) monoclonal antibody C11, composed of a human framework		
CC	(HSGKVI) and the heavy chain complementarity determining regions (see		
CC	AAV32257-59) of murine antibody C11. The DNA was constructed by splice		
CC	or overlap PCR. The invention provides altered antibodies, such as chimeric		
CC	or humanised antibodies, which comprise sufficient of the amino acid		
CC	sequences of the C11 light and heavy chain complementarity determining		
CC	regions to render them capable of binding to the CD23 type II molecule		
CC	expressed on haematopoietic cells. The antibodies are used to block		
CC	soluble CD23 formation in human therapy, for the treatment of arthritis,		
CC	lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,		
CC	diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome,		
CC	glomerulonephritis, inflammatory bowel disease, ulcerative colitis,		
CC	Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,		
CC	intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-		
CC	versus-host disease, COPD, insulinitis, bronchitis (particularly chronic		
CC	bronchitis) or diabetes (particularly type I diabetes), and B-cell		
CC	malignancies (claimed). They are also useful for studying interactions		
CC	between CD23 and various ligands and determining the binding agents		
XX			
SQ	Sequence 444 AA;		
	Query Match 100.0%; Score 1765; DB 3; Length 444;		
	Best Local Similarity 100.0%; Pred. No. 7.3e-124;		
	Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60		
DB	115 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 174		
QY	61 GLYSSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120		
DB	175 GLYSSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 234		
QY	121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180		
DB	235 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 294		
QY	181 STYRVVSVLTVLHQDLNGKEYKCKVSNKALPAPIEKTIISKAKGQRPFPQVITLPPSRDE 240		
DB	295 STYRVVSVLTVLHQDLNGKEYKCKVSNKALPAPIEKTIISKAKGQRPFPQVITLPPSRDE 354		
QY	241 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300		
DB	355 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 414		
QY	301 QCGNVFSCSVNHEALHNHYTQKSLSLSPGK 330		
DB	415 QCGNVFSCSVNHEALHNHYTQKSLSLSPGK 444		
	RESULT 8		
	ADP88447		
ID	ADP88447 standard; protein; 448 AA.		
XX			
AC	ADP88447;		
XX			
DT	09-SEP-2004 (first entry)		
XX			
DE	Antibody TRX1 heavy chain SEQ ID NO: 24.		
XX			
KW	immunosuppressive; transplant rejection; antigen tolerance; antibody;		
TRX1.			
XX			
OS	Unidentified.		
XX			
PN	WO2004052398-Al.		
XX			
PD	24-JUN-2004.		
XX			
XX	09-DEC-2003; 2003WO-US039165.		
PF			
XX	09-DEC-2002; 2002US-0431839P.		
XX			
XX	(TOLE-) TOLERRX INC.		
XX			
PI	Windsor-Hines D, Rao P, Ringler DJ;		
XX			
XX	WPI; 2004-468712/44.		
DR			
PT	Treating a primate to induce tolerance to at least one antigen comprises		
PT	administering at least one anti-CD4 antibody or its fragment in an		
PT	initial dose of at least 40 mg/kg and at least one compound that inhibits		
PT	CD8+ T cells.		
XX			
PS	Disclosure; SEQ ID NO 24; 113pp; English.		
XX			
XX	The present invention relates to a process of treating a primate to		
CC	induce tolerance to at least one antigen, which comprises administering		
CC	to the primate at least one anti-CD4 antibody or its fragment in an		
CC	initial dose of at least 40 mg/kg and at least one compound that inhibits		
CC	CD8+ T cells, where the anti-CD4 antibody or its fragment is present in		
CC	the primate when the antigen is present in the primate. The method is		
CC	useful in treating a primate to induce tolerance to at least one foreign		
CC	antigen to prevent transplant rejection. The present sequence is an		
CC	antibody fragment used in the exemplification of the invention.		
XX			
SQ	Sequence 448 AA;		
	Query Match 100.0%; Score 1765; DB 8; Length 448;		
	Best Local Similarity 100.0%; Pred. No. 7.4e-124;		
	Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60		
DB	119 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 178		
QY	61 GLYSSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120		
DB	179 GLYSSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 238		
QY	121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180		

Db 239 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNAKTKPREEQYN 298
QY 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 299 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 358
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 359 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 418
QY 301 QGQNVFSCSVMEALHNHYTQKSLSLSPGK 330
Db 419 QGQNVFSCSVMEALHNHYTQKSLSLSPGK 448
RESULT 9
ADP88431
ID ADP88431 standard; protein; 448 AA.
XX AC ADP88431;
XX DT 09-SEP-2004 (first entry)
XX DE Antibody TRX1 heavy chain SEQ ID NO: 8.
XX KW immunosuppressive; transplant rejection; antigen tolerance; antibody;
XX KW TRX1.
XX OS Unidentified.
XX XX WO2004052398-A1.
XX PN 24-JUN-2004.
XX PD
XX PF 09-DEC-2003; 2003WO-US039165.
XX PR 09-DEC-2002; 2002US-0431839P.
XX PA (TOLE-) TOLERRX INC.
XX PI Windsor-Hines D, Rao P, Ringler DJ;
XX XX WPI; 2004-468712/44.
XX DR
XX PT Treating a primate to induce tolerance to at least one antigen comprises
XX PT administering at least one anti-CD4 antibody or its fragment in an
XX PT initial dose of at least 40 mg/kg and at least one compound that inhibits
XX PT CD8+ T cells.
XX PS Disclosure; SEQ ID NO 8; 113pp; English.
XX CC The present invention relates to a process of treating a primate to
XX CC induce tolerance to at least one antigen, which comprises administering
XX CC to the primate at least one anti-CD4 antibody or its fragment in an
XX CC initial dose of at least 40 mg/kg and at least one compound that inhibits
XX CC CD8+ T cells, where the anti-CD4 antibody or its fragment is present in
XX CC the primate when the antigen is present in the primate. The method is
XX CC useful in treating a primate to induce tolerance to at least one foreign
XX CC antigen to prevent transplant rejection. The present sequence is an
XX CC antibody fragment used in the exemplification of the invention.
XX SQ Sequence 448 AA;
Query Match 100.0%; Score 1765; DB 8; Length 448;
Best Local Similarity 100.0%; Pred. No. 7.4e-124;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPPSSKSTSGGTAALGCLVKDYFPPVTVSMNSGALTSGVHTFPAVLQSS 60
Db 119 ASTKGPSVFPLAPPSSKSTSGGTAALGCLVKDYFPPVTVSMNSGALTSGVHTFPAVLQSS 178
QY 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120

Db 179 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 238
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNAKTKPREEQYN 180
Db 239 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNAKTKPREEQYN 298
QY 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 299 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 358
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 359 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 418
QY 301 QGQNVFSCSVMEALHNHYTQKSLSLSPGK 330
Db 419 QGQNVFSCSVMEALHNHYTQKSLSLSPGK 448
RESULT 10
AEF27216
ID AEF27216 standard; protein; 448 AA.
XX AC AEF27216;
XX DT 09-MAR-2006 (first entry)
XX DE Anti-CD4 antibody TRX1 heavy chain without leader sequence SEQ ID NO:24.
XX KW antibody engineering; immunotherapy; immunosuppressive; cd4.
XX OS Synthetic.
XX XX
XX FH Key
XX FT Region
XX FT /note= "Framework region"
XX FT Region
XX FT /note= "CDR1"
XX FT Region
XX FT /note= "Framework region"
XX FT Region
XX FT /note= "CDR2"
XX FT Region
XX FT /note= "Framework region"
XX FT Region
XX FT /note= "CDR3"
XX FT Region
XX FT /note= "Framework region"
XX FT Region
XX FT /note= "Modified constant region"
XX FT Modified-site
XX FT /note= "Glycosylated"
XX XX
XX PN US2006002921-A1.
XX XX
XX PD 05-JAN-2006.
XX XX
XX PF 21-JUN-2005; 2005US-00158505.
XX XX
XX PR 22-JUN-2004; 2004US-0582181P.
XX XX
XX PA (TOLE-) TOLERRX INC.
XX XX
XX PI Windsor-Hines D, Rao P, Ringler DJ, Ponath P;
XX XX WPI; 2006-066198/07.
XX XX
XX PT Treating a primate to induce tolerance to a foreign antigen, e.g. an
XX PT allogeneic or xenogeneic transplanted antigen, comprises administering an
XX PT anti-CD4 antibody or its CD4 binding fragment.
XX PS Disclosure; SEQ ID NO 24; 116pp; English.

XX The invention relates to a novel method for treating a primate, to induce
CC tolerance to at least one foreign antigen, comprises administering to the
CC primate at least one anti-CD4 antibody or its CD4 binding fragment. The
CC method of the invention has immunosuppressive activity. The method is
CC useful in immunotherapy. The methods are useful for treating a primate to
CC induce tolerance to at least one foreign antigen, e.g., an allogeneic or
CC xenogeneic transplanted antigen. The present sequence represents an anti-
CC CD4 antibody heavy chain of the invention without leader sequence.
XX
SQ Sequence 448 AA;

Query Match 100.0%; Score 1765; DB 10; Length 448;
Best Local Similarity 100.0%; Pred. No. 7.4e-124;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 60
DB 119 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 178
QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 179 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELAGA 238
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
DB 239 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 298
QY 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 299 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 358
QY 241 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
DB 359 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 418
QY 301 QQGNVFCSCVMHEALHNHYTOKSLSPGK 330
DB 419 QQGNVFCSCVMHEALHNHYTOKSLSPGK 448

RESULT 11
AEF27200
ID AEF27200 standard; protein; 448 AA.
XX
AC AEF27200;
XX
XX
DT 09-MAR-2006 (first entry)
XX
DE Anti-CD4 antibody TRX1 heavy chain without leader sequence SEQ ID NO:8.
XX antibody engineering; immunotherapy; immunosuppressive; cd4.
KW
OS Synthetic.
XX
FH Key
FT Region 1..30 Location/Qualifiers
FT /note= "Framework region"
FT 31..35
FT /note= "CDR1"
FT 36..49
FT /note= "Framework region"
FT 50..66
FT /note= "CDR2"
FT 67..98
FT /note= "Framework region"
FT 99..107
FT /note= "CDR3"
FT 108..118
FT /note= "Framework region"
FT 119..448
FT /note= "Modified constant region"
FT Modified-site 298..300

FT /note= "Glycosylated"
XX
FN US2006002921-A1.
XX
PD 05-JAN-2006.
XX
PF 21-JUN-2005; 2005US-00158505.
XX
PR 22-JUN-2004; 2004US-0582181P.
XX
PA (TOLE-) TOLERRX INC.
XX
PI Winsor-Hines D, Rao P, Ringler DJ, Ponath P;
XX
DR WPI; 2006-066198/07.
XX
PT Treating a primate to induce tolerance to a foreign antigen, e.g. an
PT allogeneic or xenogeneic transplanted antigen, comprises administering an
PT anti-CD4 antibody or its CD4 binding fragment.
XX
PS Disclosure; SEQ ID NO 8; 116pp; English.
XX
CC The invention relates to a novel method for treating a primate, to induce
CC tolerance to at least one foreign antigen, comprises administering to the
CC primate at least one anti-CD4 antibody or its CD4 binding fragment. The
CC method of the invention has immunosuppressive activity. The method is
CC useful in immunotherapy. The methods are useful for treating a primate to
CC induce tolerance to at least one foreign antigen, e.g., an allogeneic or
CC xenogeneic transplanted antigen. The present sequence represents an anti-
CC CD4 antibody heavy chain of the invention without leader sequence.
XX
SQ Sequence 448 AA;

Query Match 100.0%; Score 1765; DB 10; Length 448;
Best Local Similarity 100.0%; Pred. No. 7.4e-124;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 60
DB 119 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 178
QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 179 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELAGA 238
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
DB 239 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 298
QY 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 299 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 358
QY 241 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
DB 359 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 418
QY 301 QQGNVFCSCVMHEALHNHYTOKSLSPGK 330
DB 419 QQGNVFCSCVMHEALHNHYTOKSLSPGK 448

RESULT 12
AED19177
ID AED19177 standard; protein; 450 AA.
XX
XX AED19177;
XX
XX 15-DEC-2005 (first entry)
XX
DE Humanized oncostatin M antibody 15E10 heavy chain, Fc mutated.
XX heavy chain; oncostatin M; therapeutic; antibody production;
KW

KW rheumatoid arthritis; osteoarthritis; psoriasis; asthma;
KW chronic obstructive pulmonary disease; pulmonary disease; dementia; pain;
KW immune disorder; inflammation; musculoskeletal disease;
KW dermatological disease; respiratory disease; neurological disease;
KW cardiovascular disease; metabolic disorder; neoplasia; atherosclerosis;
KW cancer; Antiarthritic; Antirheumatic; Antipsoriatic; Antiinflammatory;
KW Respiratory-Gen.; Antiasthmatic; Neuroprotective; Nootropic; Analgesic;
KW Antiarteriosclerotic; Cytostatic.
XX
OS Mus musculus.
OS Homo sapiens.
OS Chimeric.
XX
PN WO2005095457-A2.
XX
XX 13-OCT-2005.
XX
XX 29-MAR-2005; 2005WO-GB001147.
XX
XX 30-MAR-2004; 2004GB-00007193.
PR 30-MAR-2004; 2004GB-00007197.
XX
XX (GLAX) GLAXO GROUP LTD.
PA
XX Ellis JH, Eon-Duval A, Geraschewski V, Plumpton C, Rapson NT;
PI West MR;
XX
XX WPI; 2005-725491/74.
XX
XX New therapeutic antibody that specifically binds human Oncostatin M
PT (hOSM) and modulates the interaction between OSM and gp130, useful for
PT treating, e.g. rheumatoid arthritis, psoriasis, severe asthma, or
PT multiple sclerosis.
XX
PS Disclosure; SEQ ID NO 61; 197pp; English.
XX
XX The invention relates to a therapeutic antibody that specifically binds
CC Oncostatin M (OSM), preferably human OSM (hOSM), and modulates the
CC interaction between OSM and gp130. The therapeutic antibody or antigen
CC binding fragment is useful in the manufacture of a medicament for the
CC treatment of a disease responsive to modulation of the interaction
CC between hOSM and gp130 such as rheumatoid arthritis, osteoarthritis,
CC psoriasis, asthma, or COPD. The therapeutic antibody, which specifically
CC binds the protein backbone of glycosylated hOSM is also useful in the
CC manufacture of a medicament for the treatment of a disease or disorder
CC selected from an arthritic disease such as rheumatoid arthritis, juvenile
CC onset arthritis, psoriatic arthritis, ankylosing spondylitis, psoriasis
CC such as chronic plaque disease, inflammatory lung disease such as COPD or
CC severe asthma, multiple sclerosis, dementia such as Alzheimer's disease,
CC pain such as neuropathic or inflammatory pain, atherosclerosis, diseases
CC of cell cycle regulation such as cancer (e.g. prostate), or myeloma. The
CC therapeutic antibody or antigen-binding fragment is useful in the
CC treatment of the above diseases. The present sequence represents the
CC amino acid sequence of the humanized oncostatin M binding antibody 15E10
CC heavy chain.
XX
SQ Sequence 450 AA;
Query Match 100.0%; Score 1765; DB 9; Length 450;
Best Local Similarity 100.0%; Pred. No. 7,4e-124; Indels 0; Gaps 0;
Matches 330; Conservative 0; Mismatches 0;
QY 1 ASTKGSPVFPPLAPSSKSTGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
DB 121 ASTKGSPVFPPLAPSSKSTGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 180
QY 61 GLYSLSVVVTPSSSLGTQTYICNVNHPKSNTPKVDKVEPKSCDKTHITCPPCPAPELAGA 120
DB 181 GLYSLSVVVTPSSSLGTQTYICNVNHPKSNTPKVDKVEPKSCDKTHITCPPCPAPELAGA 240
QY 121 PSVFLFPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREQYN 180
DB 241 PSVFLFPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREQYN 300

QY 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 240
DB 301 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 360
QY 241 LTKNQVSLTCLVKGYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
DB 361 LTKNQVSLTCLVKGYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 420
QY 301 QQGNVFSCSVMEALHNHYTKLSLSPOK 330
DB 421 QQGNVFSCSVMEALHNHYTKLSLSPOK 450
RESULT 13
AEB08800
ID AEB08800 standard; protein; 462 AA.
XX
AC AEB08800;
XX
DT 08-SEP-2005 (first entry)
XX
DE Anti-NOGO-antibody heavy chain SEQ ID NO 88.
XX
KW cerebroprotective; vasotropic; neuroprotective; vulnerary; nootropic;
KW antiparkinsonian; anticonvulsant; neuroleptic; antibody engineering;
KW pharmaceutical; cerebrovascular ischemia; cardiovascular disease;
KW neurological disease; brain injury; injury; spinal cord injury;
KW Alzheimers disease; degeneration; dementia; neuropathy;
KW parkinsons disease; Huntingtons chorea; Genetic disorder;
KW multiple sclerosis; immune disorder; Creutzfeldt Jakob disease;
KW infection; schizophrenia; psychiatric disorder; motor neurone disease;
KW cns-gen.; muscular-gen.
XX
OS Synthetic.
XX
PN WO2005061544-A2.
XX
XX 07-JUL-2005.
PF 20-DEC-2004; 2004WO-GB005325.
XX
PR 22-DEC-2003; 2003GB-00029684.
PR 22-DEC-2003; 2003GB-00029711.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Ellis JH, Eon-Duval A, Grundy RI, Hussain F, Mcadam R;
PI Plumpton C, Prinjha RK, Wilson PA;
XX
DR WPI; 2005-479448/48.
DR N-PSDB; AEB08802.
XX
PT New antibody or its functional fragment that binds with and neutralizes
PT human neurite outgrowth useful for treating or prophylaxis of stroke and
PT other neurological disease e.g. traumatic brain injury, spinal cord
PT injury, Alzheimer's disease.
XX
XX Example 8; SEQ ID NO 88; 143pp; English.
XX
CC The invention describes an antibody (A1) or its functional fragment, that
CC binds with and neutralizes human neurite outgrowth (NOGO). Also described
CC are: providing a first vector encoding a heavy chain of the antibody;
CC providing a second vector encoding a light chain of the antibody; co-
CC transfecting a mammalian host cell with the first and second vectors;
CC culturing the host cell in culture media (preferably serum free) under
CC conditions permissive to the secretion of the antibody from the host cell
CC into the culture media; recovering (and optionally purifying) the
CC secreted antibody; and promoting axonal sprouting involving contacting a
CC human axon with an anti-NOGO antibody. The antibody is useful in the
CC preparation of a medicament for treating or prophylaxis of stroke and
CC other neurological disease/disorders (e.g. traumatic brain injury, spinal
CC cord injury, Alzheimer's disease, frontotemporal dementias (tauopathies),

CC peripheral neuropathy, Parkinson's disease, Huntington's disease and
CC multiple sclerosis); Creutzfeldt-jakob disease (CJD), Schizophrenia,
CC amyotrophic lateral sclerosis (ALS), inclusion body myositis. The
CC antibody inhibits neurodegeneration and/or promotes functional recovery
CC in a human patient suffering, or at risk of developing, stroke or other
CC neurological diseases/disorder. This is the amino acid sequence of an
CC anti-NOGO-antibody heavy chain created in the invention.
XX
SQ Sequence 462 AA;

Query Match 100.0%; Score 1765; DB 9; Length 462;
Best Local Similarity 100.0%; Pred. No. 7.7e-124;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 133 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 192

QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCCPPAPAPELAGA 120
DB 193 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCCPPAPAPELAGA 252

QY 121 PSVFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 253 PSVFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 312

QY 181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 313 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 372

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
DB 373 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 432

QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
DB 433 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 462

RESULT 14
ADA47334
ID ADA47334 standard; protein; 467 AA.
XX
AC ADA47334;
XX
XX
DT 20-NOV-2003 (first entry)
XX
XX TRX1 heavy chain encoding DNA #SEQ ID 7.
DE
XX
XX Antibody; TRX1; immunosuppressive; immunomodulator; vaccine; antigen;
KW graft rejection; autoimmune disease; humanised.
XX
XX Homo sapiens.
XX
XX WO2002102853-A2.
XX
XX PD 27-DEC-2002.
XX
XX PF 14-JUN-2002; 2002WO-GB002796.
XX
XX PR 14-JUN-2001; 2001GB-00014517.
XX PR 20-SEP-2001; 2001GB-00027274.
XX PR 19-OCT-2001; 2001US-0345194P.
XX PR 18-APR-2002; 2002US-0373470P.
XX PR 18-APR-2002; 2002US-0373471P.
XX
XX (ISIS-) ISIS INNOVATION LTD.
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
PA (TOLE-) TOLERRX INC.
XX
XX Frewin M, Waldmann H, Gorman S, Hale G, Rao P, Kornaga T;
PI Ringler D, Cobbold S, Winsor-Hines D;
XX

DR WPI: 2003-1755228/17.
DR N-PSDB; ADA47333.
XX
PT Treating a primate to induce tolerance to at least one antigen, useful
PT for inhibiting graft rejection or treating an autoimmune disease,
PT comprises administering a TRX1 antibody to reduce the amount of CD4+
PT CD25+ cells produced.
XX
XX Claim 26; Fig 1D; 13lpp; English.
XX
CC The invention relates to a method for treating a primate to induce
CC tolerance to at least one antigen. The method of the invention comprises
CC administering at least one compound which when in a primary mixed
CC lymphocyte reaction in vitro reduces the amount of CD4+ CD25+ cells
CC produced. The preferred compound is a humanised antibody or its fragment,
CC that does not bind to the Fc receptor, and includes CDRs that are free of
CC a glycosylation site. The method of the invention is useful for inducing
CC tolerance to at least one antigen, specifically for inhibiting,
CC ameliorating or reducing an immune response to an antigen. The antibody
CC is useful for manufacturing a medicament for inducing tolerance to an
CC antigen (possibly in the form of a vaccine), for inhibiting an immune
CC response, for inhibiting the rejection of a graft (such as an organ) in a
CC human patient, and for treating an autoimmune disease. The current
CC sequence represents the TRX1 heavy chain.
XX
SQ Sequence 467 AA;

Query Match 100.0%; Score 1765; DB 6; Length 467;
Best Local Similarity 100.0%; Pred. No. 7.8e-124;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197

QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCCPPAPAPELAGA 120
DB 198 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCCPPAPAPELAGA 257

QY 121 PSVFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 258 PSVFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 317

QY 181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 318 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
DB 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 437

QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
DB 438 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 467

RESULT 15
ADA47336
ID ADA47336 standard; protein; 467 AA.
XX
XX AC ADA47336;
XX
XX DT 20-NOV-2003 (first entry)
XX
XX DE TRX1 heavy chain #SEQ ID 9.
XX
XX KW Antibody; TRX1; immunosuppressive; immunomodulator; vaccine; antigen;
KW graft rejection; autoimmune disease; humanised.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
FT Peptide 1..19

FT	Region	/label= leader peptide	
FT		50..54	
FT	Region	/label= CDR	
FT		69..85	
FT	Region	/label= CDR	
FT		118..126	
FT	Region	/label= CDR	
XX			
PN	WO2002102853-A2.		
XX			
PD	27-DEC-2002.		
XX			
PF	14-JUN-2002; 2002WO-GB002796.		
XX			
PR	14-JUN-2001; 2001GB-00014517.		
PR	20-SEP-2001; 2001GB-00022724.		
PR	19-OCT-2001; 2001US-0345194P.		
PR	18-APR-2002; 2002US-0373470P.		
PR	18-APR-2002; 2002US-0373471P.		
XX			
PA	(ISIS-) ISIS INNOVATION LTD.		
PA	(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.		
PA	(TOLE-) TOLEREX INC.		
XX			
PI	Frewin M, Waldmann H, Gorman S, Hale G, Rao P, Kornaga T;		
PI	Ringler D, Cobbold S, Winsor-Hines D;		
XX			
DR	WPI; 2003-175228/17.		
XX			
PT	Treating a primate to induce tolerance to at least one antigen, useful		
PT	for inhibiting graft rejection or treating an autoimmune disease,		
PT	comprises administering a TRX1 antibody to reduce the amount of CD4+		
PT	CD25+ cells produced.		
XX			
PS	Claim 27; Fig 1F; 131pp; English.		
XX			
CC	The invention relates to a method for treating a primate to induce		
CC	tolerance to at least one antigen. The method of the invention comprises		
CC	administering at least one compound which when in a primary mixed		
CC	lymphocyte reaction in vitro reduces the amount of CD4+ CD25+ cells		
CC	produced. The preferred compound is a humanised antibody or its fragment,		
CC	that does not bind to the Fc receptor, and includes CDRs that are free of		
CC	a glycosylation site. The method of the invention is useful for inducing		
CC	tolerance to at least one antigen, specifically for inhibiting,		
CC	ameliorating or reducing an immune response to an antigen. The antibody		
CC	is useful for manufacturing a medicament for inducing tolerance to an		
CC	antigen (possibly in the form of a vaccine), for inhibiting an immune		
CC	response, for inhibiting the rejection of a graft (such as an organ) in a		
CC	human patient, and for treating an autoimmune disease. The current		
CC	sequence represents the TRX1 heavy chain amino acid sequence.		
XX			
SQ	Sequence 467 AA;		
	Query Match	100.0%; Score 1765; DB 6; Length 467;	
	Best Local Similarity	100.0%; Pred. No. 7.8e-124;	
	Matches 330; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60	
DB	138	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 197	
QY	61	GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120	
DB	198	GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 257	
QY	121	PSVFLFPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180	
DB	258	PSVFLFPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 317	
QY	181	STYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240	
DB	318	STYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377	
QY	241	LTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300	
DB	378	LTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 437	
QY	301	QOQNVFSCSVWHEALHNHYTOKSLSLSPGK 330	
DB	438	QOQNVFSCSVWHEALHNHYTOKSLSLSPGK 467	
XX			
RESULT 16			
ADP88446			
ID	ADP88446 standard; protein; 467 AA.		
XX			
AC	ADP88446;		
XX			
DT	09-SEP-2004 (first entry)		
XX			
DE	Antibody TRX1 heavy chain with leader sequence SEQ ID NO: 23.		
XX			
KW	immunosuppressive; transplant rejection; antigen tolerance; antibody;		
KW	TRX1.		
XX			
OS	Unidentified.		
XX			
PN	WO2004052398-Al.		
XX			
PD	24-JUN-2004.		
XX			
PF	09-DEC-2003; 2003WO-US039165.		
XX			
PR	09-DEC-2002; 2002US-0431839P.		
XX			
PA	(TOLE-) TOLEREX INC.		
XX			
PI	Windsor-Hines D, Rao P, Ringler DJ;		
XX			
DR	WPI; 2004-468712/44.		
DR	N-PSDB; ADP88444, ADP88445.		
XX			
PT	Treating a primate to induce tolerance to at least one antigen comprises		
PT	administering at least one anti-CD4 antibody or its fragment in an		
PT	initial dose of at least 40 mg/kg and at least one compound that inhibits		
PT	CD8+ T cells.		
XX			
PS	Disclosure; SEQ ID NO 23; 113pp; English.		
XX			
CC	The present invention relates to a process of treating a primate to		
CC	induce tolerance to at least one antigen, which comprises administering		
CC	to the primate at least one anti-CD4 antibody or its fragment in an		
CC	initial dose of at least 40 mg/kg and at least one compound that inhibits		
CC	CD8+ T cells, where the anti-CD4 antibody or its fragment is present in		
CC	the primate when the antigen is present in the primate. The method is		
CC	useful in treating a primate to induce tolerance to at least one foreign		
CC	antigen to prevent transplant rejection. The present sequence is an		
CC	antibody fragment used in the exemplification of the invention.		
XX			
SQ	Sequence 467 AA;		
	Query Match	100.0%; Score 1765; DB 8; Length 467;	
	Best Local Similarity	100.0%; Pred. No. 7.8e-124;	
	Matches 330; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60	
DB	138	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 197	
QY	61	GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120	
DB	198	GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 257	
QY	121	PSVFLFPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180	
DB	258	PSVFLFPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 317	
QY	181	STYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240	
DB	318	STYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377	

```
QY 161 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQRPQVYTLPPSRDE 240
DB 318 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQRPQVYTLPPSRDE 377
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
DB 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 437
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
DB 438 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 467

RESULT 17
ADP88430
ID ADP88430 standard; protein; 467 AA.
XX
AC ADP88430;
XX
DT 09-SEP-2004 (first entry)
XX
DE Antibody TRX1 heavy chain with leader sequence SEQ ID NO: 7.
XX
KW immunosuppressive; transplant rejection; antigen tolerance; antibody;
KW TRX1.
XX
OS Unidentified.
XX
PN WO2004052398-A1.
XX
PD 24-JUN-2004.
XX
PF 09-DEC-2003; 2003WO-US039165.
XX
PR 09-DEC-2002; 2002US-04318399.
XX
PA (TOLE-) TOLERRX INC.
XX
PI Windsor-Hines D, Rao P, Ringler DJ;
XX
DR N-PSDB; ADP88429, ADP88428.
XX
PT Treating a primate to induce tolerance to at least one antigen comprises
PT administering at least one anti-CD4 antibody or its fragment in an
PT initial dose of at least 40 mg/kg and at least one compound that inhibits
PT CD8+ T cells.
XX
PS Disclosure; SEQ ID NO 7; 113pp; English.
XX
CC The present invention relates to a process of treating a primate to
CC induce tolerance to at least one antigen, which comprises administering
CC to the primate at least one anti-CD4 antibody or its fragment in an
CC initial dose of at least 40 mg/kg and at least one compound that inhibits
CC CD8+ T cells, where the anti-CD4 antibody or its fragment is present in
CC the primate when the antigen is present in the primate. The method is
CC useful in treating a primate to induce tolerance to at least one foreign
CC antigen to prevent transplant rejection. The present sequence is an
CC antibody fragment used in the exemplification of the invention.
XX
SQ Sequence 467 AA;

Query Match 100.0%; Score 1765; DB 8; Length 467;
Best Local Similarity 100.0%; Pred. No. 7.8e-124;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWGALTSQVHTFPAVLQSS 60
DB 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWGALTSQVHTFPAVLQSS 197
QY 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHCTCPCPAPELAGA 120
|||||
```

```
DB 198 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHCTCPCPAPELAGA 257
QY 121 PSVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
|||||
DB 258 PSVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 317
|||||
QY 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQRPQVYTLPPSRDE 240
|||||
DB 318 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQRPQVYTLPPSRDE 377
|||||
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
DB 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 437
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
DB 438 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 467

RESULT 18
ADQ87966
ID ADQ87966 standard; protein; 467 AA.
XX
AC ADQ87966;
XX
DT 04-NOV-2004 (first entry)
XX
DE Heavy chain of a humanised TRX1 antibody #1.
XX
KW Primate; tolerance; antigen; mixed lymphocyte reaction; MLR; CD4+; CD25+;
KW IL-2; IL-4; IL-12; immune response; graft rejection; immunosuppressive;
KW antirheumatic; antiarthritic; antidiabetic; neuroprotective;
KW antiinflammatory; antiallergic; antiasthmatic; cytostatic; antimicrobial;
KW transplant; graft-versus-host disease; autoimmune disease; inflammation;
KW allergy; asthma; cancer; infection; humanised; TRX1; heavy.
XX
OS Unidentified.
XX
FH Key
FT Peptide 1..19 Location/Qualifiers
FT Region 20..49 /label= Leader peptide
FT Region 50..54 /label= Framework region 1
FT Region 55..68 /label= Complementarity determining region 1
FT Region 69..85 /label= Framework region 2
FT Region 86..117 /label= Complementarity determining region 2
FT Region 118..126 /label= Framework region 3
FT Region 127..137 /label= Complementarity determining region 3
FT Region 138..467 /label= Framework region 4
FT Region /label= Constant region
XX WO2004067554-A2.
XX 12-AUG-2004.
XX
XX 28-JAN-2004; 2004WO-US002643.
XX
XX 29-JAN-2003; 2003US-00353708.
XX
PA (TOLE-) TOLERRX INC.
PA (ISIS-) ISIS INNOVATION LTD.
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
PI Frewin M, Waldmann H, Gorman S, Hale G, Rao P, Kornaga T;
PI Ringler D, Cobbold S, Winsor-Hines D;
XX
```

DR WPI; 2004-580970/56.
 DR N-PSDB; ADQ87965.
 XX Inducing tolerance to an antigen comprises administering a CD4 antibody
 PT alone or in combination with other compounds that induce tolerance
 PT against one or more antigens.
 XX Claim 11; Fig 1D; 85pp; English.
 XX The invention relates to a novel method for treating a primate to induce
 CC tolerance to at least one antigen. The method comprises administering a
 CC compound, or a combination of compounds, that induces tolerance against
 CC one or more antigens. The compound or the combination being in a primary
 CC mixed lymphocyte reaction (MLR) in vitro, which reduces the amount of
 CC CD4+ CD25+ cells produced in the mixed lymphocyte reaction and that
 CC generates in the primary mixed lymphocyte reaction a cell population that
 CC reduces at least one of the amount of CD4+ CD25+ cells produced in vitro
 CC in at least one of a primary and secondary mixed lymphocyte reactions,
 CC and the amount of at least one of IL-2, IL-4 and IL-12 in a secondary
 CC mixed lymphocyte reaction. The compound or the combination being
 CC administered in an amount and for a time so as to induce tolerance
 CC against the antigen, the compound or the combination being present in the
 CC primate when the antigen is present in the primate. The invention further
 CC comprises: an antibody that binds to the same epitope as the humanised
 CC antibody given in the specification; a composition comprising the
 CC antibody and a pharmaceutical carrier; inducing tolerance to an antigen
 CC in a patient; inhibiting an immune response in a patient or for
 CC inhibiting the rejection of a graft in a human patient; and screening for
 CC a compound, or a combination of at least two compounds for use in
 CC inducing tolerance. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic,
 CC antidiabetic, neuroprotective, antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic, and antimicrobial. The composition and methods
 CC are useful for inhibiting, preventing or ameliorating an immune response
 CC against an antigen, such as in the inhibition or treatment of transplant
 CC rejection, graft-versus-host disease, autoimmune diseases (e.g.
 CC rheumatoid arthritis, diabetes or multiple sclerosis), inflammation,
 CC allergy, asthma, cancer or infections. These may also be used for
 CC identifying compounds or agents useful for inducing tolerance against
 CC antigens. This sequence represents the protein of a humanised TRX1
 CC antibody region of the invention.
 XX Sequence 467 AA;
 SQ
 Query Match 100.0%; Score 1765; DB 8; Length 467;
 Best Local Similarity 100.0%; Pred. No. 7.8e-124;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWGALTSVHTFPVAVLQSS 60
 Db |||||
 QY 138 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWGALTSVHTFPVAVLQSS 197
 Db |||||
 QY 61 GLYSLSVVTPSSLSIGTQYICNVNHPKSNTPKDKVEPKSCDKTHTCPCPAPELAGA 120
 Db |||||
 QY 198 GLYSLSVVTPSSLSIGTQYICNVNHPKSNTPKDKVEPKSCDKTHTCPCPAPELAGA 257
 Db |||||
 QY 121 PSVFLFPKPKDITLMISRTPEVTCVVDVSHDEPKENWYVDGVEVHNATKPREQYN 180
 Db |||||
 QY 258 PSVFLFPKPKDITLMISRTPEVTCVVDVSHDEPKENWYVDGVEVHNATKPREQYN 317
 Db |||||
 QY 181 STYRVSVLTVLHQDLNKGKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
 Db |||||
 QY 318 STYRVSVLTVLHQDLNKGKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377
 Db |||||
 QY 241 LTKNOVSLTCLVKGPSPDIKAVESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
 Db |||||
 QY 378 LTKNOVSLTCLVKGPSPDIKAVESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 437
 Db |||||
 QY 301 OQGNVFCSVMEALHNHYTKSLSPGK 330
 Db |||||
 QY 438 OQGNVFCSVMEALHNHYTKSLSPGK 467
 Db |||||

RESULT 19
 ADQ87974
 ID ADQ87974 standard; protein; 467 AA.
 XX
 AC ADQ87974;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Heavy chain of a humanised TRX1 antibody #3.
 XX
 KW Primate; tolerance; antigen; mixed lymphocyte reaction; MLR; CD4+; CD25+;
 IL-2; IL-4; IL-12; immune response; graft rejection; immunosuppressive;
 KW antirheumatic; antidiabetic; antidiabetic; neuroprotective;
 KW antiinflammatory; antiallergic; antiasthmatic; cytostatic; antimicrobial;
 KW transplant; graft-versus-host disease; autoimmune disease; inflammation;
 KW allergy; asthma; cancer; infection; humanised; TRX1; heavy.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= Leader peptide
 FT Region 20..49
 FT /label= Framework region 1
 FT Region 50..54
 FT /label= Complementarity determining region 1
 FT Region 55..68
 FT /label= Framework region 2
 FT Region 69..85
 FT /label= Complementarity determining region 2
 FT Region 86..117
 FT /label= Framework region 3
 FT Region 118..126
 FT /label= Complementarity determining region 3
 FT Region 127..137
 FT /label= Framework region 4
 FT Region 138..147
 FT /label= Constant region
 XX WO2004067554-A2.
 XX
 PD 12-AUG-2004.
 XX
 PF 28-JAN-2004; 2004WO-US002643.
 XX
 PR 29-JAN-2003; 2003US-00353708.
 XX
 XX (TOLE-) TOLERRX INC.
 PA (ISIS-) ISIS INNOVATION LTD.
 PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
 XX
 PI Frewin M, Waldmann H, Gorman S, Hale G, Rao P, Kornaga T;
 PI Ringler D, Cobbold S, Winsor-Hines D;
 XX
 WPI; 2004-580970/56.
 DR N-PSDB; ADQ87973.
 XX
 PT Inducing tolerance to an antigen comprises administering a CD4 antibody
 PT alone or in combination with other compounds that induce tolerance
 PT against one or more antigens.
 XX
 PS Claim 11; Fig 3D; 85pp; English.
 XX
 CC The invention relates to a novel method for treating a primate to induce
 CC tolerance to at least one antigen. The method comprises administering a
 CC compound, or a combination of compounds, that induces tolerance against
 CC one or more antigens. The compound or the combination being in a primary
 CC mixed lymphocyte reaction (MLR) in vitro, which reduces the amount of
 CC CD4+ CD25+ cells produced in the mixed lymphocyte reaction and that
 CC generates in the primary mixed lymphocyte reaction a cell population that
 CC reduces at least one of the amount of CD4+ CD25+ cells produced in vitro
 CC in at least one of a primary and secondary mixed lymphocyte reactions,
 CC and the amount of at least one of IL-2, IL-4 and IL-12 in a secondary

CC mixed lymphocyte reaction. The compound or the combination being
CC administered in an amount and for a time so as to induce tolerance
CC against the antigen, the compound or the combination being present in the
CC primate when the antigen is present in the primate. The invention further
CC comprises: an antibody that binds to the same epitope as the humanised
CC antibody given in the specification; a composition comprising the
CC antibody and a pharmaceutical carrier; inducing tolerance to an antigen
CC in a patient; inhibiting an immune response in a patient or for
CC inhibiting the rejection of a graft in a human patient; and screening for
CC a compound, or a combination of at least two compounds for use in
CC inducing tolerance. The compositions of the invention have the following
CC activities: immunosuppressive, antirheumatic, antiarthritic,
CC antidiabetic, neuroprotective, antiinflammatory, antiallergic,
CC antiasthmatic, cyostatic, and antimicrobial; the composition and methods
CC are useful for inhibiting, preventing or ameliorating an immune response
CC against an antigen, such as in the inhibition or treatment of transplant
CC rejection, graft-versus-host disease, autoimmune diseases (e.g.
CC rheumatoid arthritis, diabetes or multiple sclerosis), inflammation,
CC allergy, asthma, cancer or infections. These may also be used for
CC identifying compounds or agents useful for inducing tolerance against
CC antigens. This sequence represents the protein of a humanised TRX1
XX antibody region of the invention.
SQ Sequence 467 AA;

Query Match 100.0%; Score 1765; DB 8; Length 467;
Best Local Similarity 100.0%; Pred. No. 7.8e-124; Indels 0; Gaps 0;
Matches 330; Conservative 0; Mismatches 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
DB 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 197
QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 198 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELAGA 257
QY 121 PSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 258 PSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 317
QY 181 STYRVSVSLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
DB 318 STYRVSVSLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 377
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
DB 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 437
QY 301 QQGNVFCVSMHEALHNHYTQKSLSLSPGK 330
DB 438 QQGNVFCVSMHEALHNHYTQKSLSLSPGK 467

RESULT 20
AEF27213
ID AEF27213 standard; protein; 467 AA.
XX AC AEF27213;
XX DT 09-MAR-2006 (first entry)
XX DE Anti-CD4 antibody TRX1 heavy chain SEQ ID NO:21.
XX KW antibody engineering; immunotherapy; immunosuppressive; cd4.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Peptide 1..19
FT FT /label= Leader sequence
FT FT 20..49
FT FT Region
FT FT /note= "Framework region"

FT Region 50..54
FT /note= "CDR1"
FT Region 55..68
FT /note= "Framework region"
FT Region 69..85
FT /note= "CDR2"
FT Region 86..117
FT /note= "Framework region"
FT Region 118..126
FT /note= "CDR3"
FT Region 127..137
FT /note= "Framework region"
FT Region 138..467
FT /note= "Modified constant region"
FT Modified-site 317..319
FT /note= "Glycosylated"
PN US2006002921-A1.
PD 05-JAN-2006.
PF 21-JUN-2005; 2005US-00158505.
PR 22-JUN-2004; 2004US-0582181P.
XX (TOLE-) TOLERX INC.
XX Winsor-Hines D, Rao P, Ringler DJ, Ponath P;
DR WPI; 2006-066198/07.
XX N-PSDB; AEF27214.
PT Treating a primate to induce tolerance to a foreign antigen, e.g. an
PT allogeneic or xenogeneic transplanted antigen, comprises administering an
PT anti-CD4 antibody or its CD4 binding fragment.
XX Example 1; SEQ ID NO 21; 116pp; English.
XX The invention relates to a novel method for treating a primate, to induce
XX tolerance to at least one foreign antigen, comprises administering to the
XX primate at least one anti-CD4 antibody or its CD4 binding fragment. The
XX method of the invention has immunosuppressive activity. The method is
XX useful in immunotherapy. The methods are useful for treating a primate to
XX induce tolerance to at least one foreign antigen, e.g., an allogeneic or
XX xenogeneic transplanted antigen. The present sequence represents an anti-
XX CD4 antibody heavy chain of the invention.
SQ Sequence 467 AA;

Query Match 100.0%; Score 1765; DB 10; Length 467;
Best Local Similarity 100.0%; Pred. No. 7.8e-124; Indels 0; Gaps 0;
Matches 330; Conservative 0; Mismatches 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
DB 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 197
QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 198 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELAGA 257
QY 121 PSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 258 PSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 317
QY 181 STYRVSVSLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
DB 318 STYRVSVSLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 377
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
DB 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 437

QY 301 QQGNVFCSCVMHEALHNHYTKSLSPGK 330
 ID AEF27197
 Db 438 QQGNVFCSCVMHEALHNHYTKSLSPGK 467

RESULT 21

AEF27197
 ID AEF27197 standard; protein; 467 AA.

XX AC AEF27197;

XX DT 09-MAR-2006 (first entry)

XX DE Anti-CD4 antibody TRX1 heavy chain SEQ ID NO:5.

XX KW antibody engineering; immunotherapy; immunosuppressive; cd4.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Region /label= Leader sequence
 FT Region 20..49
 FT Region /note= "Framework region"
 FT Region 50..54
 FT Region /note= "CDR1"
 FT Region 55..68
 FT Region /note= "Framework region"
 FT Region 69..85
 FT Region /note= "CDR2"
 FT Region 86..117
 FT Region /note= "Framework region"
 FT Region 118..126
 FT Region /note= "CDR3"
 FT Region 127..137
 FT Region /note= "Framework region"
 FT Region 138..467
 FT Modified-site /note= "Modified constant region"
 FT 317..319
 FT /note= "Glycosylated"

XX PN US2006002921-A1.

XX PD 05-JAN-2006.

XX PF 21-JUN-2005; 2005US-00158505.

XX PR 22-JUN-2004; 2004US-0582181P.

XX PA (TOLE-) TOLEREX INC.

XX PI Winsor-Hines D, Rao P, Ringler DJ, Ponath P;

XX DR WPI; 2006-066198/07.

XX DR N-PSDB; AEF27198.

XX XX Treating a primate to induce tolerance to a foreign antigen, e.g. an allogeneic or xenogeneic transplanted antigen, comprises administering an anti-CD4 antibody or its CD4 binding fragment.

XX PS Example 1; SEQ ID NO 5; 116pp; English.

XX CC The invention relates to a novel method for treating a primate, to induce tolerance to at least one foreign antigen, comprises administering to the primate at least one anti-CD4 antibody or its CD4 binding fragment. The method of the invention has immunosuppressive activity. The method is useful in immunotherapy. The methods are useful for treating a primate to induce tolerance to at least one foreign antigen, e.g., an allogeneic or xenogeneic transplanted antigen. The present sequence represents an anti-CD4 antibody heavy chain of the invention.

XX SQ Sequence 467 AA;

Query Match 100.0%; Score 1765; DB 10; Length 467;
 Best Local Similarity 100.0%; Pred. No. 7.8e-124;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPPETVTVSNWGALTSGVHTTTPAVLQSS 60
 |||||
 Db 138 ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPPETVTVSNWGALTSGVHTTTPAVLQSS 197
 |||||

QY 61 GLYSLSVVTVPSLSLGTOTYICNVNHKPSNTKVDKKVPEKSCDKTHTCPPCPAPELAGA 120
 |||||
 Db 198 GLYSLSVVTVPSLSLGTOTYICNVNHKPSNTKVDKKVPEKSCDKTHTCPPCPAPELAGA 257
 |||||

QY 121 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
 |||||
 Db 258 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 317
 |||||

QY 181 STYRVSVLTIVLHODWLNQKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYVLTLPSSRDE 240
 |||||
 Db 318 STYRVSVLTIVLHODWLNQKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYVLTLPSSRDE 377
 |||||

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
 |||||
 Db 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 437
 |||||

QY 301 QQGNVFCSCVMHEALHNHYTKSLSPGK 330
 |||||
 Db 438 QQGNVFCSCVMHEALHNHYTKSLSPGK 467
 |||||

RESULT 22

AEF27215

ID AEF27215 standard; protein; 467 AA.

XX AC AEF27215;

XX DT 09-MAR-2006 (first entry)

XX DE Anti-CD4 antibody TRX1 heavy chain with leader sequence SEQ ID NO:23.

XX KW antibody engineering; immunotherapy; immunosuppressive; cd4.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Region /label= Leader sequence
 FT Region 20..49
 FT Region /note= "Framework region"
 FT Region 50..54
 FT Region /note= "CDR1"
 FT Region 55..68
 FT Region /note= "Framework region"
 FT Region 69..85
 FT Region /note= "CDR2"
 FT Region 86..117
 FT Region /note= "Framework region"
 FT Region 118..126
 FT Region /note= "CDR3"
 FT Region 127..137
 FT Region /note= "Framework region"
 FT Region 138..467
 FT Modified-site /note= "Modified constant region"
 FT 317..319
 FT /note= "Glycosylated"

XX PN US2006002921-A1.

XX PD 05-JAN-2006.

XX PF 21-JUN-2005; 2005US-00158505.

XX PR 22-JUN-2004; 2004US-0582181P.

XX XX

PA (TOLE-) TOLERRX INC.
XX Winsor-Hines D, Rao P, Ringler DJ, Ponath P;
XX WPI; 2006-066198/07.
DR N-PSDB; AEF27214.
XX
XX Treating a primate to induce tolerance to a foreign antigen, e.g. an
FT allogeneic or xenogeneic transplanted antigen, comprises administering an
FT anti-CD4 antibody or its CD4 binding fragment.
XX
XX Disclosure; SEQ ID NO 23; 116pp; English.
PS
XX The invention relates to a novel method for treating a primate, to induce
CC tolerance to at least one foreign antigen, comprises administering to the
CC primate at least one anti-CD4 antibody or its CD4 binding fragment. The
CC method of the invention has immunosuppressive activity. The method is
CC useful in immunotherapy. The methods are useful for treating a primate to
CC induce tolerance to at least one foreign antigen, e.g., an allogeneic or
CC xenogeneic transplanted antigen. The present sequence represents an anti-
CC CD4 antibody heavy chain of the invention with leader sequence.
XX
XX Sequence 467 AA;
Query Match 100.0%; Score 1765; DB 10; Length 467;
Best Local Similarity 100.0%; Pred. No. 7.8e-124; Indels 0; Gaps 0;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197
QY 61 GLYSLSSVTVVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 198 GLYSLSSVTVVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 257
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 258 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 317
QY 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 318 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
DB 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 437
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
DB 438 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 467
RESULT 23
ID AEF27199
XX AEF27199 standard; protein; 467 AA.
XX AC AEF27199;
XX DT 09-MAR-2006 (first entry)
XX DE Anti-CD4 antibody TRX1 heavy chain with leader sequence SEQ ID NO:7.
XX antibody engineering; immunotherapy; immunosuppressive; cd4.
XX Synthetic.
XX Key Location/Qualifiers
FT Peptide 1..19
FT Region 20..49
FT /note= "Framework region"
FT 50..54

FT Region /note= "CDR1"
FT 55..68
FT /note= "Framework region"
FT 69..85
FT /note= "CDR2"
FT 86..117
FT /note= "Framework region"
FT 118..126
FT /note= "CDR3"
FT 127..137
FT /note= "Framework region"
FT 138..146
FT /note= "Modified constant region"
FT Modified-site 317..319
FT /note= "Glycosylated"
XX US2006002921-A1.
XX 05-JAN-2006.
XX 21-JUN-2005; 2005US-00158505.
XX 22-JUN-2004; 2004US-0582181P.
XX (TOLE-) TOLERRX INC.
XX Winsor-Hines D, Rao P, Ringler DJ, Ponath P;
XX WPI; 2006-066198/07.
XX N-PSDB; AEF27198.
XX Treating a primate to induce tolerance to a foreign antigen, e.g. an
FT allogeneic or xenogeneic transplanted antigen, comprises administering an
FT anti-CD4 antibody or its CD4 binding fragment.
XX
XX Disclosure; SEQ ID NO 7; 116pp; English.
XX
XX The invention relates to a novel method for treating a primate, to induce
CC tolerance to at least one foreign antigen, comprises administering to the
CC primate at least one anti-CD4 antibody or its CD4 binding fragment. The
CC method of the invention has immunosuppressive activity. The method is
CC useful in immunotherapy. The methods are useful for treating a primate to
CC induce tolerance to at least one foreign antigen, e.g., an allogeneic or
CC xenogeneic transplanted antigen. The present sequence represents an anti-
CC CD4 antibody heavy chain of the invention with leader sequence.
XX
XX Sequence 467 AA;
Query Match 100.0%; Score 1765; DB 10; Length 467;
Best Local Similarity 100.0%; Pred. No. 7.8e-124; Indels 0; Gaps 0;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197
QY 61 GLYSLSSVTVVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 198 GLYSLSSVTVVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 257
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 258 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 317
QY 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 318 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
DB 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 437
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330


```
Query Match      100.0%; Score 1765; DB 8; Length 475;
Best Local Similarity 100.0%; Pred. No. 8e-124;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
    |||||
Db 146 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 205

Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNITKVDKVEPKSCDKTHTCPPCPAPELAGA 120
    |||||
Db 206 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNITKVDKVEPKSCDKTHTCPPCPAPELAGA 265

Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
    |||||
Db 266 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 325

Qy 181 STYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
    |||||
Db 326 STYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 385

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
    |||||
Db 386 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 445

Qy 301 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 330
    |||||
Db 446 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 475

RESULT 26
ADL23054
ID ADL23054 standard; protein; 475 AA.
XX
AC ADL23054;
XX
XX 20-MAY-2004 (first entry)
XX
DE Humanised anti-MAG antibody #1.
XX
KW antibody; MAG; myelin associated glycoprotein; stroke;
KW neurodegenerative disorder; gene therapy; vaccine; human.
XX
OS Homo sapiens.
OS Chimeric.
OS Unidentified.
XX
PN WO2004014953-A2.
XX
XX 19-FEB-2004.
XX
XX 05-AUG-2003; 2003WO-EP008749.
XX
PR 06-AUG-2002; 2002GB-00018229.
PR 06-AUG-2002; 2002GB-00018230.
PR 06-AUG-2002; 2002GB-00018232.
PR 06-AUG-2002; 2002GB-00018234.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Ellis JH, Germaschewski V;
XX
XX WPI; 2004-180641/17.
XX
XX New altered antibody that binds to and neutralizes myelin associated
XX glycoprotein (MAG), useful for preparing a composition for treating or
XX preventing stroke or other neurodegenerative disorders e.g., Alzheimer's
XX disease.
XX
XX Example 4; Fig 5; 67pp; English.
XX
XX The present invention relates to a new altered antibody or its functional
XX fragment, which binds to and neutralizes myelin associated glycoprotein
XX
```

```
CC (MAG) and comprises a light chain variable domain (VL) comprising
CC complementary determining region light 1 (CDRL1), CDRL2 or CDRL3 and/or a
CC heavy chain variable domain (VH) comprising CDRH1, CDRH2 or CDRH3. The
CC antibody is useful for preparing a composition for treating or preventing
CC stroke or other neurodegenerative disorders in a human, e.g., traumatic
CC brain injury, Alzheimer's disease, dementias, peripheral neuropathy,
CC Parkinson's disease, Huntington's disease and multiple sclerosis. The
CC present sequence is a humanised anti-MAG antibody.
XX
SQ Sequence 475 AA;
    Query Match      100.0%; Score 1765; DB 8; Length 475;
    Best Local Similarity 100.0%; Pred. No. 8e-124;
    Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
    |||||
Db 146 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 205

Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNITKVDKVEPKSCDKTHTCPPCPAPELAGA 120
    |||||
Db 206 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNITKVDKVEPKSCDKTHTCPPCPAPELAGA 265

Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
    |||||
Db 266 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 325

Qy 181 STYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
    |||||
Db 326 STYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 385

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
    |||||
Db 386 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 445

Qy 301 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 330
    |||||
Db 446 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 475

RESULT 27
ADS88803
ID ADS88803 standard; protein; 475 AA.
XX
AC ADS88803;
XX
XX 16-DEC-2004 (first entry)
XX
DE Humanised anti-MAG antibody heavy chain.
XX
XX oligodendrocyte; stroke; neurological disease;
KW myelin-associated glycoprotein; MAG; anti-MAG antibody;
KW Alzheimer's disease; multiple sclerosis.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO2004083363-A2.
XX
XX 30-SEP-2004.
XX
XX 02-FEB-2004; 2004WO-EP001016.
XX
XX 19-MAR-2003; 2003GB-00006309.
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Vinson M, Irving EA;
XX
XX WPI; 2004-691029/67.
XX
XX Promoting oligodendrocyte survival in humans with neurological diseases,
XX such as Alzheimer's disease, multiple sclerosis and/or stroke, using an
XX
```

PT anti-myelin-associated glycoprotein (MAG) antibody.
XX Claim 17; SEQ ID NO 18; 45pp; English.
XX
XX The specification describes a method for promoting oligodendrocyte
CC survival in a human suffering or at risk of developing stroke or another
CC neurological diseases. The method comprises administering to the human an
CC anti-myelin-associated glycoprotein (MAG) antibody or its functional
CC fragment. The anti-MAG antibody or its functional fragment is useful in
CC the manufacture of a medicament for the promotion of oligodendrocyte
CC survival in a human suffering from or at risk of developing stroke or
CC another neurological disease. They can also be used in treating
CC neurological diseases, such as Alzheimer's disease, multiple sclerosis
CC and/or stroke, by promoting oligodendrocyte survival. The present
CC sequence represents a humanised immunoglobulin heavy chain in which the
CC humanised anti-MAG heavy chain variable region is associated with a
CC functional immunoglobulin secretion signal sequence, and with an altered
CC form of the human IgG1 constant region in which Kabat residues 248 and
CC 250 have been mutated to alanine in order to disable the effector
CC functions of binding to Fc gammaRI and complement protein C1q. Antibodies
CC used in the method of the invention may comprise the present heavy chain.
XX
SQ Sequence 475 AA;

Query Match 100.0%; Score 1765; DB 8; Length 475;
Best Local Similarity 100.0%; Pred. No. 8e-124;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db |||||
Qy 146 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 205
Db |||||
Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db |||||
Qy 206 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 265
Db |||||
Qy 121 PSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db |||||
Qy 266 PSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 325
Db |||||
Qy 181 STYRVSVVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db |||||
Qy 326 STYRVSVVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 385
Db |||||
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db |||||
Qy 386 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 445
Db |||||
Qy 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330
Db |||||
Qy 446 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 475
Db |||||

RESULT 28
AD588792
ID ADS88792 standard; protein; 475 AA.
XX
XX AD588792;
XX
XX
DT 16-DEC-2004 (first entry)
XX
XX A mouse/human chimeric anti-MAG antibody heavy chain.
XX
XX oligodendrocyte; stroke; neurological disease;
KW myelin-associated glycoprotein; MAG; anti-MAG antibody;
KW Alzheimer's disease; multiple sclerosis;
KW chain complementarity determining region; CDR; chimera.
XX
XX Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
XX WO2004083363-A2.
FN

XX 30-SEP-2004.
PD
XX
XX 02-FEB-2004; 2004WO-EP001016.
PF
XX
XX 19-MAR-2003; 2003GB-00006309.
PR
XX
XX (GLAX) GLAXO GROUP LTD.
PA
XX
XX Vinson M, Irving EA;
PI
XX
XX WPI; 2004-691029/67.
DR
XX
XX Promoting oligodendrocyte survival in humans with neurological diseases,
PT such as Alzheimer's disease, multiple sclerosis and/or stroke, using an
PT anti-myelin-associated glycoprotein (MAG) antibody.
XX
XX Claim 9; SEQ ID NO 7; 45pp; English.
PS
XX
XX The specification describes a method for promoting oligodendrocyte
CC survival in a human suffering or at risk of developing stroke or another
CC neurological diseases. The method comprises administering to the human an
CC anti-myelin-associated glycoprotein (MAG) antibody or its functional
CC fragment. The anti-MAG antibody or its functional fragment is useful in
CC the manufacture of a medicament for the promotion of oligodendrocyte
CC survival in a human suffering from or at risk of developing stroke or
CC another neurological disease. They can also be used in treating
CC neurological diseases, such as Alzheimer's disease, multiple sclerosis
CC and/or stroke, by promoting oligodendrocyte survival. The present
CC sequence represents a mouse/human chimeric anti-MAG antibody heavy chain
CC in which the murine anti-MAG heavy chain variable region is associated
CC with a functional immunoglobulin secretion signal sequence, and with an
CC altered form of the human IgG1 constant region, and in which Kabat
CC residues 248 and 250 have been mutated to alanine in order to disable the
CC effector functions of binding to Fc gammaRI and complement protein C1q.
CC Antibodies used in the method of the invention may comprise the present
CC heavy chain.
XX
SQ Sequence 475 AA;

Query Match 100.0%; Score 1765; DB 8; Length 475;
Best Local Similarity 100.0%; Pred. No. 8e-124;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db |||||
Qy 146 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 205
Db |||||
Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db |||||
Qy 206 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 265
Db |||||
Qy 121 PSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db |||||
Qy 266 PSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 325
Db |||||
Qy 181 STYRVSVVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db |||||
Qy 326 STYRVSVVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 385
Db |||||
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db |||||
Qy 386 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 445
Db |||||
Qy 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330
Db |||||
Qy 446 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 475
Db |||||

RESULT 29
ADL23199
ID ADL23199 standard; protein; 469 AA.
XX

AC ADL23199;
XX 20-MAY-2004 (first entry)
XX Human anti-CD18 antibody heavy chain.
DE Human; bactericidal/permeability-increasing protein; BPI; Ep-CAM; CAB2.1;
KW recombinant polypeptide production; ING-1; antibody; anti-CD18 antibody;
KW cosmetic product.
XX Homo sapiens.
OS US2003203447-A1.
XX 30-OCT-2003.
XX 31-MAR-2003; 2003US-00404724.
XX 29-MAR-2002; 2002US-0368530P.
XX (HORW/) HORWITZ A H.
XX Horwitz AH;
PI WPI; 2003-875646/81.
XX N-PSDB; ADL23198.
XX Producing recombinant polypeptide, useful for treating or diagnosing
PT comprises culturing cells transformed or transfected with a vector
PT comprising multiple copies of a transcription unit separated by a
PT selective marker gene.
XX Example 13; SEQ ID NO 72; 133pp; English.
XX The invention relates to producing a recombinant polypeptide comprising
CC culturing cells, which have been transformed or transfected with a
CC vector, or its segment comprising multiple copies of a transcription unit
CC separated by at least one selective marker gene, where the transcription unit
CC unit encodes a polypeptide under selective conditions. Also included are
CC a vector or segment comprising multiple copies of a transcription unit
CC separated by at least one selective marker gene where the transcription
CC unit encodes a polypeptide, a host cell comprising an expression vector
CC or segment and a stable cell line comprising an expression vector or
CC segment. Each transcription unit is under the control of its own promoter
CC and 3' untranslated region, where the promoter is an SV40, HSV, bovine
CC growth hormone, thymidine kinase, MPSV, mouse beta globin, human BFI, MSV
CC -LTR, RSV, MMTV-LTR, CMV, MLV, Chinese hamster elongation factor or mouse
CC Abelson LTR promoter. The expression vector further comprises multiple
CC enhancers. The transcription unit also encodes two different subunits of
CC a multimeric protein, an immunoglobulin light and heavy chain
CC polypeptides or at least the variable regions of the immunoglobulin light
CC and heavy chain polypeptides. It further encodes a BPI protein
CC (bactericidal/permeability-increasing protein) product. The protein
CC product BPI protein fragment, BPI analogue, BPI variant or BPI-derived
CC peptide. The transcription unit encodes an rBPI21 and is under the
CC control of an hCMV promoter and mouse light chain 3' untranslated region,
CC where the vector further comprises 0, 1 or 2 copies of a human heavy
CC chain enhancer and either a gpt or neo gene. Other genes suitable for
CC expression using the method of the invention are Ep-CAM and CAB2.1 (both
CC not defined). The immunoglobulin may be the ING-1 chimaeric mouse/human
CC antibody (or humanised versions or proline substitution mutants) or an
CC anti-CD18 antibody. The method is useful for producing recombinant
CC polypeptide. Recombinant polypeptide compositions are useful in
CC therapies, in diagnostic procedures or as tools in preventive medicine.
CC Recombinant polypeptides are also found in a wide array of both health
CC and cosmetic products, used to increase the quality of life. Complex
CC polypeptide products are also routinely used in research laboratories
CC both as end products of analyses and as agents in assays for the study or
CC preparation of other molecules. Advantages of the present invention
CC includes increased recombinant polypeptide production, increased
CC production efficiency, greater control and/or regulation over the
CC qualities of the polypeptide expressed, increased stability of cell
CC lines, and/or decreased costs for materials, reagents and/or other

CC resources. The present sequence represents a light or heavy chain from a
CC antibody gene suitable for inclusion in the transcription unit of the
CC invention.
XX SQ Sequence 469 AA;
Query Match 99.6%; Score 1758; DB 7; Length 469;
Best Local Similarity 99.7%; Pred. No. 2.6e-123;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
DB 140 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 199
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 200 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 259
QY 121 PSVFLFPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
DB 260 PSVFLFPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 319
QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 240
DB 320 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 379
QY 241 LTKQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
DB 380 LTKQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 439
QY 301 QQGNVFSCVMHEALHNHYTOKSLSLSPGK 330
DB 440 QQGNVFSCVMHEALHNHYTOKSLSLSPGK 469
RESULT 30
AAB04071
ID AAB04071 standard; protein; 330 AA.
XX AC AAB04071;
XX 11-APR-2001 (first entry)
XX Zcytor 10::IGG gamma fusion peptide.
XX zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand;
KW binding; detection; modulation; recombinant cell; haematopoietic cell;
KW lymphoid cell; myeloid cell; lymph; immune system; blood; bone;
KW inflammatory response; inflammation; spleen; human.
XX Synthetic.
OS Homo sapiens.
XX WO200068381-A1.
XX 16-NOV-2000.
XX 11-MAY-2000; 2000WO-US012924.
XX 11-MAY-1999; 99US-00309861.
XX (ZYMO) ZYMOGENETICS INC.
XX Presnell SR, Foster DC, Hammond AK, Lok S;
XX WPI; 2001-016096/02.
XX N-PSDB; AAA54473.
XX New cytokine receptor mouse zcytor 10, useful for detecting ligands that
PT stimulate proliferation or development of hematopoietic, lymphoid and
PT myeloid cells.
XX Example 17; Page 120-121; 134pp; English.

XX Isolating a nucleotide which encodes the zcytor 10 cytokine receptor
 CC enables the production of recombinant cells expressing the receptor.
 CC Those cells can then be used to detect the presence of a modulator of
 CC zcytor10 protein by culturing the cells in the presence of a test ligand
 CC and comparing levels of activity of mouse zcytor10 in the presence and
 CC absence of the test sample. Similarly, detection of zcytor10 receptor
 CC ligand within a test sample can be achieved. The method comprising
 CC contacting a test sample containing an amino acid sequence from Cys15 or
 CC Gly25 to Pro230 of the zcytor 10 cytokine receptor and detecting the
 CC binding of the polypeptide to a ligand in the sample. Specified peptide
 CC fragments of the zcytor 10 cytokine receptor and the methods described
 CC are used to identify ligands that stimulate the proliferation and/or
 CC development of haematopoietic, lymphoid and myeloid cells. Peptide
 CC fragments of the cytokine receptor are useful for treating lymphoid,
 CC immune, inflammatory, splenic, blood or bone disorders and for generating
 CC antibodies directed against the receptor. A vector expressing a secreted
 CC human zcytor 10 heterodimer is constructed. In this construct the
 CC extracellular cytokine binding domain of zcytor 10 is fused to the heavy
 CC chain of IgG gamma and the extracellular portion of the heteromeric
 CC cytokine receptor subunit (an interleukin receptor subunit) is fused to
 CC human kappa light chain (see GENESEQ record AAA54474). The two sequences
 CC are fused together using two primers (AAA54475, AAA54476)
 CC
 XX Sequence 330 AA;

Query Match 99.5%; Score 1756; DB 4; Length 330;
 Best Local Similarity 99.4%; Pred. No. 2.4e-123;
 Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
 DB 1 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
 QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTCPPCPAPELAGA 120
 DB 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTCPPCPAPELGG 120
 QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 180
 DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 180
 QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
 DB 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
 QY 301 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 330
 DB 301 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 330

RESULT 31
 AAM47856
 ID AAM47856 standard; protein; 330 AA.
 XX
 AC AAM47856;
 XX
 XX 22-FEB-2002 (first entry)
 DT
 DE Human Ig-gamma heavy chain constant region amino acid sequence.
 XX
 XX Human; immunoadhesin; intercellular adhesion molecule; ICAM-1;
 KW human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;
 KW transgenic plant.
 XX
 OS Homo sapiens.
 XX
 FN WO200183529-A2.
 XX

PD 08-NOV-2001.
 XX
 PF 28-APR-2001; 2001WO-US013932.
 XX
 PR 28-APR-2000; 2000US-0200298P.
 XX
 PA (PLAN-) PLANET BIOTECHNOLOGY INC.
 XX
 PI Larrick JW, Wycoff KL;
 XX
 WI: 2002-041481/05.
 DR N-PSDB; ABA05265.
 XX
 PT Immunoadhesin for treating human rhinovirus infection comprises chimeric
 CC intercellular adhesion molecule-1, and optionally a J chain and secretory
 CC component in association.
 XX
 PS Disclosure; Fig 7; 138pp; English.
 XX
 CC The invention relates to an immunoadhesin comprising: (a) a chimeric
 CC intercellular adhesion molecule (ICAM)-1 comprising a rhinovirus receptor
 CC protein linked to at least a portion of an immunoglobulin heavy chain;
 CC and (b) optionally a J chain and secretory component associated with the
 CC chimeric ICAM-1 molecule. The immunoadhesin has plant-specific
 CC glycosylation and virucide activity. The immunoadhesin is useful for
 CC reducing infection by human rhinovirus (HRV) and hence the initiation or
 CC spread of the common cold by HRV. The immunoadhesin binds to HRV and
 CC reduces its infectivity, competing with cell surface ICAM-1 for binding
 CC sites, interfering with virus entry or coating and directing premature
 CC release of viral RNA and formation of empty capsids. Expression of the
 CC immunoadhesin in plants would be tetrameric, rather than dimeric.
 CC Immunoadhesin having multiple binding sites have a higher effective
 CC affinity for the virus, thereby increasing the effectiveness of the
 CC immunoadhesin. Association of secretory component and immunoglobulin J
 CC chain increases the stability of the immunoadhesin in the mucosal
 CC environment. Production is significantly less expensive in plants than in
 CC animal cell culture and production in plants is safer for human use,
 CC since plants are not known to harbor any animal viruses. The present
 CC sequence is that of a human immunoglobulin protein sequence, useful to
 CC the invention
 XX
 SQ Sequence 330 AA;

Query Match 99.5%; Score 1756; DB 5; Length 330;
 Best Local Similarity 99.4%; Pred. No. 2.4e-123;
 Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
 DB 1 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
 QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTCPPCPAPELAGA 120
 DB 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTCPPCPAPELGG 120
 QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 180
 DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 180
 QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
 DB 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
 QY 301 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 330
 DB 301 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 330

RESULT 32

AAE21960
ID AAE21960 standard; protein; 330 AA.
XX
AC AAE21960;
XX
DT 25-JUL-2002 (first entry)
XX
DE Human death domain containing receptor (DR6) protein-related protein.
XX
KW Human; therapy; death domain containing receptor; DR6; receptor; anaemia;
KW apoptosis; rheumatoid arthritis; eczema; asthma; psoriasis; pancreatitis;
KW diabetes; cancer; multiple sclerosis; Graves disease; glomerulonephritis;
KW transplant rejection; systemic lupus erythematosus; hepatitis; cirrhosis;
KW autoimmune; gastritis; dermatosis; cardiopathy; infertility; haemostatic;
KW H. pylori-associated ulceration; antiinflammatory; vasodilator; virucide;
KW acquired immunodeficiency syndrome; AIDS; human immunodeficiency virus;
KW HIV; haemolytic uraemic syndrome; HUS; immunodeficiency; neuroprotective;
KW adult respiratory distress syndrome; ARDS; cytostatic; thyromimetic;
KW dermatological; hepatotropic; antibacterial.
XX
OS Homo sapiens.
XX
FN WO200185209-A2.
XX
PD 15-NOV-2001.
XX
PF 30-APR-2001; 2001WO-US011735.
XX
PR 10-MAY-2000; 2000US-0203015P.
XX
PA (ELIT) LILLY & CO ELI.
XX
PI Heuer JG, Liu J, Na S, Song HY, Yang D;
XX
DR WPI; 2002-351283/38.
XX
PT Treating or preventing T cell or Th2 cell mediated condition e.g., asthma
PT or multiple sclerosis in mammal, comprises administering composition
PT comprising death domain containing receptor, DR6 agonist or antagonist.
XX
PS Disclosure; Page 132-133; 133pp; English.
XX
CC The invention relates to a method for treating or preventing a T cell
CC mediated condition or a Th2 cell mediated condition in a mammal. The
CC method comprising administering to the mammal a pharmaceutical
CC composition comprising a death domain containing receptor (DR6) agonist
CC or antagonist. The method is useful for treating or preventing a T cell
CC mediated condition or a Th2 cell mediated condition in a mammal. A DR6
CC agonist is useful in the manufacture of a medicament for treating or
CC preventing at least one symptom associated with aberrant apoptosis, graft
CC -versus-host disease (GVHD), rheumatoid arthritis, eczema, asthma, atopy,
CC inflammatory bowel disease, vasculitis, psoriasis, pancreatitis, insulin-
CC dependent diabetes mellitus, cancer, multiple sclerosis, Hashimoto's
CC thyroiditis, Graves disease, transplant rejection, systemic lupus
CC erythematosus, autoimmune dermatosis, autoimmune cardiopathy, autoimmune
CC infertility, Behcet's disease, autoimmune gastritis, fibrosing lung
CC disease, organ rejection after transplantation, thrombotic
CC thrombocytopenic purpura (TTP), chronic glomerulonephritis, haemolytic
CC uraemic syndrome (HUS), aplastic anaemia, myelodysplasia, multiple organ
CC dysfunction syndrome (MODS), adult respiratory distress syndrome (ARDS)
CC or a condition or symptom related to the above mentioned diseases in a
CC mammal. An DR6 antagonist is useful in the manufacture of a medicament
CC for treating or preventing at least one symptom associated with
CC immunodeficiency, aberrant apoptosis, bacterial, viral or microbial
CC infection, complications of infection, human immunodeficiency virus
CC (HIV), HIV-induced lymphoma, HIV-induced acquired immunodeficiency
CC syndrome (AIDS), fulminant viral hepatitis B, fulminant viral hepatitis
CC C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis, H. pylori
CC associated ulceration, cytoprotection during cancer treatment,
CC recuperation from chemotherapy, recuperation from irradiation therapy, or
CC a condition or symptom related to the above mentioned diseases in a
CC mammal. The present sequence is human DR6 protein-related protein
XX

SQ Sequence 330 AA;
Query Match 99.5%; Score 1756; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLIVKDYFPEPVTVSNNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLIVKDYFPEPVTVSNNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVVPSSSLGTQTVICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 61 GLYSLSSVTVVPSSSLGTQTVICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPELIGG 120
QY 121 PSVFLFPPKPDLMISRTPEVTCVVDVSHEDPEVKFNWVVDGVEVHNATKPREEOYN 180
DB 121 PSVFLFPPKPDLMISRTPEVTCVVDVSHEDPEVKFNWVVDGVEVHNATKPREEOYN 180
QY 181 STYRVSVLVTLVHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 181 STYRVSVLVTLVHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
QY 301 QQGNVFSCSVNMEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFSCSVNMEALHNHYTQKSLSLSPGK 330
RESULT 33
ABB81641
ID ABB81641 standard; protein; 330 AA.
XX
AC ABB81641;
XX
DT 25-SEP-2002 (first entry)
XX
DE Human IgG gamma 1 heavy chain SEQ ID NO:15.
XX
KW Human; zcytor19; cytokine receptor; immunosuppressive; cytostatic;
KW antithematic; antiarthritic; neuroprotective; antiinflammatory;
KW antididiabetic; nephrotropic; dermatological; anti-HIV; haemostatic;
KW vaccine; immune system; T-cell specific leukaemia; lymphoma; lupus;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; HIV;
KW diabetes mellitus; inflammatory bowel disease; Crohn's disease; aschma;
KW immunologic renal disease; glomerulonephritis; vasculitis; polyarteritis;
KW mesangioproliferative disease; chronic lymphocytic leukaemia; bronchitis;
KW secondary glomerulonephritis; scleroderma; amyloidosis; multiple myeloma;
KW haemolytic uraemic syndrome; renal neoplasm; urological neoplasm;
KW emphysema; chronic airway disease.
XX
OS Homo sapiens.
FN WO200244209-A2.
XX
PD 06-JUN-2002.
XX
PF 28-NOV-2001; 2001WO-US044808.
XX
PR 28-NOV-2000; 2000US-0253561P.
PR 07-FEB-2001; 2001US-0267211P.
XX
PI (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Xu W, Novak JE, Whitmore TE, Grant FJ;
XX
DR WPI; 2002-527700/56.
DR N-PSDB; ABQ73076.
XX
PT Novel Zycotor19 polypeptides and polynucleotides useful for stimulating
PT immune responses in animals for producing antibodies, and for treating

PT	autoimmune diseases, leukemia and asthma.	OS	Homo sapiens.
XX		XX	
PS	Example 7; Page 171-172; 200pp; English.	PN	WO200200721-A2.
XX		XX	
XX	The present invention describes an isolated human zcytor19 protein (I),	PD	03-JAN-2002.
CC	and truncated zcytor19 proteins. (I) has immunosuppressive, cytostatic,	XX	26-JUN-2001; 2001WO-US020484.
CC	antirheumatic, antiarthritic, neuroprotective, antiinflammatory,	PF	26-JUN-2000; 2000US-0214282P.
CC	antidiabetic, nephrotropic, dermatological, anti-HIV and haemostatic	XX	29-JUN-2000; 2000US-0214955P.
CC	activities, and can be used in vaccines. (I) or an antibody binding (I)	PR	08-FEB-2001; 2001US-0267963P.
CC	can be used for suppressing the immune system for reducing rejection of	PR	
CC	tissue or organ transplants and grafts and for treating T-cell specific	XX	(ZYMO) ZYMOGENETICS INC.
CC	leukaemias or lymphomas and autoimmune diseases including rheumatoid	PA	
CC	arthritis, multiple sclerosis, diabetes mellitus, inflammatory bowel	XX	Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL;
CC	disease and Crohn's disease. The antibodies can also be used for treating	PI	Maurer MF;
CC	immunologic renal diseases, glomerulonephritis, mesangiolipofiferative	PI	WPI; 2002-090519/12.
CC	disease, chronic lymphocytic leukaemia, secondary glomerulonephritis or	DR	N-PSDB; ABA93797.
CC	vasculitis associated with lupus, polyarteritis, scleroderma, HIV-related	XX	
CC	diseases, amyloidosis and haemolytic uraemic syndrome. (I) and the	XX	Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
CC	antibodies can also be used for renal or urological neoplasms and	PT	useful for treating and diagnosing lymphoid, immune, inflammatory,
CC	multiple myelomas, asthma, bronchitis, emphysema and other chronic airway	PT	splenic, blood or bone disorders.
CC	diseases. Human zcytor19 is located to chromosome 1, more specifically to	XX	
CC	chromosome 1p36.11. The present sequence represents a human IgG gamma 1	XX	Example 17; Page 187-188; 235pp; English.
CC	heavy chain protein, which is used in an example from the present	XX	
CC	invention	XX	The present invention describes a cytokine receptor designated zcytor17.
XX		XX	Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
SQ	Sequence 330 AA;	CC	antirheumatic, antiarthritic and muscular activities. The zcytor17
		CC	proteins are useful for treating and diagnosing lymphoid, immune,
		CC	inflammatory, splenic, blood or bone disorders. Agonists or anti-
		CC	zcytor17 antibodies are useful in stimulating cell-mediated immunity and
		CC	for stimulating lymphocyte proliferation, such as in the treatment of
		CC	infections involving immunosuppression, including certain viral
		CC	infections. They are also useful for inducing cytotoxicity and for
		CC	treating leukopenias. Antagonist of zcytor17 polypeptides are useful for
		CC	treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
		CC	sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
		CC	pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
		CC	chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
		CC	ABA93843 and ABB05730 to ABB05745 represent sequences used in the
		CC	exemplification of the present invention
		XX	
		SQ	Sequence 330 AA;
			Query Match 99.5%; Score 1756; DB 5; Length 330;
			Best Local Similarity 99.4%; Pred. No. 2.4e-123;
			Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60	QY	1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
Db	1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60	Db	1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
QY	61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTCPCPAPELAGA 120	QY	61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTCPCPAPELAGA 120
Db	61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTCPCPAPELGG 120	Db	61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTCPCPAPELGG 120
QY	121 PSVFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREQYN 180	QY	121 PSVFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREQYN 180
Db	121 PSVFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 180	Db	121 PSVFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 180
QY	181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 240	QY	181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 240
Db	181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 240	Db	181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 240
QY	241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKGRW 300	QY	241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKGRW 300
Db	241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKGRW 300	Db	241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKGRW 300
QY	301 OQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330	QY	301 OQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db	301 OQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330	Db	301 OQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
			RESULT 34
			ABB05736
			ID ABB05736 standard; protein; 330 AA.
XX			
XX			ABB05736;
XX			
DT			01-MAY-2002 (first entry)
XX			
DE			Human immunoglobulin G gamma 1 protein sequence SEQ ID NO:38.
XX			
KW	Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;		
KW	antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;		
KW	muscular; lymphoid; immune; inflammatory; splenic; blood; bone;		
KW	infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;		
KW	autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;		
XX	inflammatory disease; pancreatitis; inflammatory bowel disease.		

CC rheumatoid arthritis, asthma, eczema, inflammatory bowel disease, cancer,
 CC vasculitis, psoriasis, insulin-dependent diabetes mellitus, pancreatitis,
 CC psoriasis, multiple sclerosis, Hashimoto's thyroiditis, Graves' disease,
 CC transplant rejection, systemic lupus erythematosus, Behcet's disease,
 CC autoimmune nephropathy, autoimmune haematopathy, idiopathic interstitial
 CC pneumonia, hypersensitivity pneumonitis, autoimmune dermatosis,
 CC autoimmune cardiopathy, autoimmune infertility, autoimmune gastritis,
 CC fibrosing lung disease, fulminant viral hepatitis B, fulminant viral
 CC hepatitis C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis,
 CC Helicobacter pylori-associated ulceration, organ rejection after
 CC transplantation, chronic glomerulonephritis, thrombotic thrombocytopenic
 CC purpura (TTP) and haemolytic uraemic syndrome (HUS), aplastic anaemia,
 CC myelodysplasia, multiple organ dysfunction syndrome (MDS), adult
 CC respiratory distress syndrome (ARDS), and at least one condition or
 CC symptom related to the conditions, in a mammal; and (3) use of DR6
 CC antagonist in the manufacture of a medicament for treating or preventing
 CC at least one symptom associated with conditions (C2) such as aberrant
 CC apoptosis, immunodeficiency, bacterial infection, viral infection,
 CC microbial infection, complications of infection, HIV, HIV-induced
 CC lymphoma, HIV-induced AIDS, fulminant viral hepatitis B, fulminant viral
 CC hepatitis C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis,
 CC H. pylori-associated ulceration, cytoprotection during cancer treatment,
 CC recuperation from chemotherapy, recuperation from irradiation therapy,
 CC and at least one condition or symptom related to the conditions, in a
 CC mammal. DR6 has immunosuppressive, antirheumatic, antiarthritic,
 CC antiasthmatic, dermatological, antiinflammatory, antipsoriatic,
 CC antidibetic, cyostatic, neuroprotective, thymimetic, antithyroid,
 CC nephrotropic, antiinfertility, vasotropic, virucide, hepatotropic,
 CC antibacterial, anticancer, haemostatic, antianemic, antimicrobial and
 CC anti-HIV activities. (M1) is useful for treating or preventing at least
 CC one symptom associated with (C1) in a mammal, preferably human, by
 CC administering DR6 agonist, and for treating or preventing at least one
 CC symptom associated with (C2) by administering DR6 antagonist. The present
 CC sequence represents a human DR6 related amino acid sequence, which is
 CC given in the exemplification of the present invention
 XX
 SQ Sequence 330 AA;

Query Match 99.5%; Score 1756; DB 6; Length 330;
 Best Local Similarity 99.4%; Pred. No. 2.4e-123;
 Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWNSGALTSGVHTFPAVLQSS 60
 DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWNSGALTSGVHTFPAVLQSS 60
 QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNPKVDKVEPKSCDKTHTCPPCPAPELAGA 120
 DB 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNPKVDKVEPKSCDKTHTCPPCPAPELAGG 120
 QY 121 PSVFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
 DB 121 PSVFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
 QY 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
 DB 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
 QY 301 QGQNVFSCSVMHAEALHNHYTKSLSPGK 330
 DB 301 QGQNVFSCSVMHAEALHNHYTKSLSPGK 330

RESULT 39
 AAO31102
 ID AAO31102 standard; protein; 330 AA.
 XX
 AC AAO31102;
 XX

DT 06-OCT-2003 (first entry)
 XX Human A2-G8 SCF antibody heavy chain constant region.
 DE Human; antibody; stem cell factor; mast cell growth factor; asthma; SCF;
 XX steel factor; c-kit ligand; gene therapy; heavy chain.
 KW Homo sapiens.
 XX WO2003051311-A2.
 XX 26-JUN-2003.
 XX 16-DEC-2002; 2002WO-US040227.
 XX 17-DEC-2001; 2001US-0342174P.
 XX (FARB) BAYER CORP.
 XX Takeuchi T, Tomkinson A, Neben S;
 XX WPI; 2003-523500/49.
 XX N-PSDB; AAL62618.
 XX New purified human antibody that binds to stem cell factor protein,
 XX useful for preparing a composition for treating asthma.
 XX Example 10; Page 47-48; 94pp; English.
 XX The invention provides human antibodies that bind to stem cell factor
 XX (SCF) protein. SCF is also known as mast cell growth factor, steel factor
 XX or c-kit ligand. Antibodies of the invention are useful for preparing
 XX compositions for treating asthma. They are also used in gene therapy. The
 XX present sequence is human SCF antibody heavy chain constant region
 XX
 SQ Sequence 330 AA;

Query Match 99.5%; Score 1756; DB 6; Length 330;
 Best Local Similarity 99.4%; Pred. No. 2.4e-123;
 Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWNSGALTSGVHTFPAVLQSS 60
 DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWNSGALTSGVHTFPAVLQSS 60
 QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNPKVDKVEPKSCDKTHTCPPCPAPELAGA 120
 DB 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNPKVDKVEPKSCDKTHTCPPCPAPELAGG 120
 QY 121 PSVFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
 DB 121 PSVFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
 QY 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
 DB 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
 QY 301 QGQNVFSCSVMHAEALHNHYTKSLSPGK 330
 DB 301 QGQNVFSCSVMHAEALHNHYTKSLSPGK 330

RESULT 40
 ABR55836
 ID ABR55836 standard; protein; 330 AA.
 XX
 AC ABR55836;
 XX
 DT 02-SEP-2003 (first entry)

XX DE Anti-Ang-2 antibody IgG1 constant region.
XX KW Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;
KW gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
XX angio genesis; antibody; human.
XX OS Homo sapiens.
XX PN WO2003030833-A2.
XX PD 17-APR-2003.
XX KW 11-OCT-2002; 2002WO-US0332613.
XX PR 11-OCT-2001; 2001US-0328604P.
XX PR 10-OCT-2002; 2002US-00269805.
XX KW (AMGE-) AMGEN INC.
XX PA Oliner JD;
XX PI WPI; 2003-504963/47.
XX DR New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful
XX PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,
XX PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
XX KW Example 4; Page 96; 161pp; English.
XX PS The invention relates to a specific binding agent, which comprises at
XX CC least one peptide selected from any of 62 peptides (ABR55769-830) or its
XX CC fragment. The binding agents are antibodies that recognize and bind to
XX CC angiotensin-2 (Ang-2). The specific binding agent, particularly the
XX CC antibody, is useful for inhibiting undesired angiogenesis, treating
XX CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-
XX CC 2 activity, modulating vascular permeability or plasma leakage, or
XX CC treating a disease (e.g. ocular neovascular disease, obesity,
XX CC haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,
XX CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic
XX CC disease, bone-related disease, or psoriasis) in a mammal. The present
XX CC sequence represents a human IgG1 constant region of an anti-Ang-2
XX CC antibody
XX SQ Sequence 330 AA;
Query Match 99.5%; Score 1756; DB 6; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVVTVSPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKTHHTCCPCAPAPELAGA 120
Db 61 GLYSLSSVVTVSPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKTHHTCCPCAPAPELGG 120
QY 121 PSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQYN 180
Db 121 PSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQYN 180
QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
QY 301 QGQNVFCSVMHEALHNHYTQKSLSLSPGK 330
Db 301 QGQNVFCSVMHEALHNHYTQKSLSLSPGK 330

RESULT 41
AAO30893
ID AAO30893 standard; protein; 330 AA.
XX AC AAO30893;
XX DT 22-SEP-2003 (first entry)
XX DE Human immunoglobulin gamma (IgG) 1 constant region.
XX KW Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;
KW gene therapy; immunoglobulin; Ig; human.
XX OS Homo sapiens.
XX PN WO2003048334-A2.
XX PD 12-JUN-2003.
XX PF 04-DEC-2002; 2002WO-US038780.
XX PR 04-DEC-2001; 2001US-0337113P.
XX PR 12-APR-2002; 2002US-0371966P.
XX PA (EMDL-) EMD LEXIGEN RES CENT CORP.
XX PI Gillies SD;
XX DR WPI; 2003-513757/48.
XX PT New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2
XX PT moiety, useful for preparing a composition for treating cancer, viral
XX PT infections or immune disorders.
XX PS Example 1; Page 51-53; 71pp; English.
XX CC The invention relates to cytokine fusion proteins with increased
XX CC therapeutic index and methods for increasing the therapeutic index of
XX CC such fusion proteins. The fusion protein comprises a non-interleukin-2
XX CC (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a
XX CC composition for treating cancer, viral infections or immune disorders.
XX CC The fusion protein is also used in gene therapy. The present sequence is
XX CC human immunoglobulin gamma (IgG) constant region. This sequence is used
XX CC to illustrate the method of the invention
XX SQ Sequence 330 AA;
Query Match 99.5%; Score 1756; DB 6; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVVTVSPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKTHHTCCPCAPAPELAGA 120
Db 61 GLYSLSSVVTVSPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKTHHTCCPCAPAPELGG 120
QY 121 PSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQYN 180
Db 121 PSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQYN 180
QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300

```
QY 301 OQGNVFCSCVMHEALHNHYTKSLSPGK 330
DB 301 OQGNVFCSCVMHEALHNHYTKSLSPGK 330

RESULT 42
ADFL1389
ID ADFL1389 standard; protein; 330 AA.
XX
AC ADFL1389;
XX
DT 12-FEB-2004 (first entry)
XX
DE Anti-OPGL antibody heavy chain constant region SEQ ID NO:2.
XX
KW human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.
XX
OS Homo sapiens.
XX
PN WO2003086289-A2.
XX
PD 23-OCT-2003.
XX
PF 07-APR-2003; 2003WO-US010749.
XX
PR 05-APR-2002; 2002US-0370407P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;
XX
DR N-PSDB; ADFL1388.
XX
WPI; 2003-845253/78.
XX
PT New isolated antibody that specifically binds osteoprotegerin ligand,
PT useful for diagnosing or treating bone disorders, such as osteoporosis,
PT bone loss from arthritis, Paget's disease or osteopenia.
XX
XX
Example 3; SEQ ID NO 2; 156pp; English.
XX
PS The present invention describes an isolated human antibody (I) that
CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
CC pharmaceutical composition comprising a pharmaceutical carrier and a
CC therapeutic amount of (I); (2) methods of treating an osteopenic disorder
CC in a patient, comprising administering to a patient the pharmaceutical
CC composition of (I) or a pharmaceutical amount of (I); and (3) a method
CC for detecting OPGL in a biological sample, comprising contacting the
CC sample with (I) under conditions that allow for binding of the antibody
CC to OPGL, and measuring the level of bound antibody in the sample. (I) has
CC osteopathic, antiarthritic and cytostatic activities, and can be used in
CC gene therapy. The composition and methods are useful in diagnosing or
CC treating bone disorders, such as osteoporosis, bone loss from arthritis,
CC Paget's disease or osteopenia. The antibody (I) may also be used for
CC detecting OPGL in biological samples and in identifying cells or tissues
CC that produce the protein. The present sequence represents a sequence
CC which is used in the exemplification of the present invention.
XX
XX
Sequence 330 AA;

Query Match 99.5%; Score 1756; DB 7; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTPKVDKVPKSCDKTHTCPCPAPPELLAG 120
DB 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTPKVDKVPKSCDKTHTCPCPAPPELLGG 120

QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVFNAKTKPREEQYN 180
DB 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVFNAKTKPREEQYN 180
QY 181 STYRVSVLTVLHODWLNKKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYVTLPPSRDE 240
DB 181 STYRVSVLTVLHODWLNKKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYVTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
QY 301 OQGNVFCSCVMHEALHNHYTKSLSPGK 330
DB 301 OQGNVFCSCVMHEALHNHYTKSLSPGK 330

RESULT 43
ADE97351
ID ADE97351 standard; protein; 330 AA.
XX
AC ADE97351;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human IgG1 heavy chain constant region protein - SEQ ID 20.
XX
KW immunoadhesin; immunoglobulin heavy chain; J chain; joining; toxin;
KW virucide; antibacterial; anthrax; rhinovirus infection; common cold;
KW intercellular adhesion molecule; ICAM-1; human; constant region; IgG.
XX
OS Homo sapiens.
XX
PN WO2003064992-A2.
XX
PD 07-AUG-2003.
XX
PF 25-OCT-2002; 2002WO-US034197.
XX
PR 26-OCT-2001; 2001US-00047542.
XX
PA (PLAN-) PLANET BIOTECHNOLOGY INC.
PA (LARR/) LARRICK J W.
XX (WYCO/) WYCOFF K L.
XX Larrick JW, Wycoff KL;
XX WPI; 2003-636816/60.
XX N-PSDB; ADE97350, ADE97376.
XX
PT New immunoadhesin, useful for treating anthrax and rhinovirus, comprises
PT chimeric toxin receptor protein linked to immunoglobulin heavy chain, and
PT J chain and secretory component associated with the chimeric toxin
PT receptor protein.
XX
PS Disclosure; SEQ ID NO 20; 288pp; English.
XX
CC The invention relates to a novel immunoadhesin comprising a chimeric
CC toxin receptor protein consisting of a toxin receptor protein linked to
CC at least a portion of an immunoglobulin heavy chain with a J (joining)
CC chain and secretory component (SC) associated with the chimeric toxin
CC receptor protein. The immunoadhesin comprises a chimeric bacterial or
CC viral toxin receptor protein and the immunoadhesin has plant-specific
CC glycosylation. The immunoadhesin of the invention demonstrates virucide
CC and antibacterial activities and may be useful for reducing the binding
CC of a viral or bacterial antigen to a host cell and thus for treating or
CC preventing anthrax, as well as human rhinovirus infection which results
CC in the common cold. The current sequence is that of the human
CC immunoadhesin-related protein of the invention.
XX
SQ Sequence 330 AA;

Query Match 99.5%; Score 1756; DB 7; Length 330;
```

Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSVTVTPSSSLGTQYIICNVNHNKPSNTKVDKKVPEKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSVTVTPSSSLGTQYIICNVNHNKPSNTKVDKKVPEKSCDKTHTCPPCPAPELAGG 120
Qy 121 PSVFLPPKPKDGLMIKSRTEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 121 PSVFLPPKPKDGLMIKSRTEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 44
ADF83605
ID ADF83605 standard; protein; 330 AA.
XX AC ADF83605;
XX DE 26-FEB-2004 (first entry)
XX DT Cytokine receptor related human Zcytor19 protein, SEQ ID NO 15.
XX KW soluble cytokine receptor; virucide; cytostatic; immunosuppressive;
XX KW antirheumatic; antiarthritic; neuroprotective; antidiabetic;
XX KW nephrotropic; antiinflammatory; viral infection; cancer;
XX KW autoimmune disease; ligand blocking; human.
XX OS Homo sapiens.
XX PN WO2003089603-A2.
XX XX 30-OCT-2003.
XX 18-APR-2003; 2003WO-US012030.
XX PF 19-APR-2002; 2002US-0373813P.
XX PR (ZYMO) ZYMOGENETICS INC.
XX FA Presnell SR, Xu W, Novak JF, Whitmore TE, Grant FJ;
XX PI Kindsvogel WR, Klucher KM;
XX DR WPI; 2003-854110/79.
XX N-PSDB; ADF83604.
XX XX
XX New Zcytor19 receptor polypeptides and polynucleotides, useful for
XX PT detecting and treating viral infections, cancer or autoimmune diseases
XX PT (e.g. rheumatoid arthritis, multiple sclerosis, diabetes or
XX PT glomerulonephritis).
XX XX
XX Example 7; SEQ ID NO 15; 186pp; English.
XX PS
XX CC The invention relates to a novel isolated polynucleotide that encodes a
XX CC soluble cytokine receptor polypeptide. The encoded polypeptide comprises:
XX CC a sequence of 211 amino acids fully defined in the specification, or a
XX CC region from amino acid residues 21-163, 1-163, 21-211 or 1-211; or a
XX CC sequence at least 90% identical to the 211 amino acids. The cytokine
XX CC sequence at least 90% identical to the 211 amino acids. The cytokine

CC polynucleotides and polypeptides have the following activities: virucide
CC cytostatic, immunosuppressive, antirheumatic, antiarthritic,
CC neuroprotective, antidiabetic, nephrotropic, and antiinflammatory. The
CC composition and methods are useful in detecting and treating viral
CC infections, cancer or autoimmune diseases (e.g. rheumatoid arthritis,
CC multiple sclerosis, diabetes, glomerulonephritis or inflammatory bowel
CC diseases) in vitro and in vivo. The ligand-binding receptor polypeptides
CC may also be used in blocking ligand activity in vitro and in vivo. This
CC sequence represents a cytokine receptor related human protein of the
XX invention.
XX SQ Sequence 330 AA;
Query Match 99.5%; Score 1756; DB 7; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0
Qy 1 ASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSVTVTPSSSLGTQYIICNVNHNKPSNTKVDKKVPEKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSVTVTPSSSLGTQYIICNVNHNKPSNTKVDKKVPEKSCDKTHTCPPCPAPELAGG 120
Qy 121 PSVFLPPKPKDGLMIKSRTEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 121 PSVFLPPKPKDGLMIKSRTEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 45
ADF75001
ID ADF75001 standard; protein; 330 AA.
XX AC ADF75001;
XX DT 26-FEB-2004 (first entry)
XX DE Human Ig gamma-1 heavy chain constant region.
XX KW Human; fusion protein; epitope; major histocompatibility complex;
XX KW MHC type II; T-cell receptor; immunogenicity; glycosylation; cytokine;
XX KW hormone.
XX OS Homo sapiens.
XX PN US2003166877-A1.
XX PD 04-SEP-2003.
XX PF 29-MAR-2002; 2002US-00112582.
XX PR 30-MAR-2001; 2001US-0280625P.
XX PA (LEXI-) LEXIGEN PHARM CORP.
XX PI Gillies SD, Way J, Hamilton AA;
XX DR WPI; 2003-898110/82.
XX PT Reducing the immunogenicity of a fusion protein by identifying a

PT candidate T-cell epitope within a junction region spanning a fusion
PI protein and changing an amino acid within the junction region.
XX
PS Disclosure: SEQ ID NO 1; 34pp; English.
XX
XX The invention relates to reducing the immunogenicity of a fusion protein
CC comprising: identifying a candidate T-cell epitope (binding to MHC class
CC II (major histocompatibility complex)) within a junction region spanning
CC a fusion protein and changing an amino acid within the junction region to
CC reduce the ability of the candidate T-cell epitope to interact with a T-
CC cell receptor. Also included are a method for reducing the immunogenicity
CC of a fusion protein, a fusion protein with reduced immunogenicity and a
CC nucleic acid encoding the fusion protein with reduced immunogenicity. The
CC method also comprises introducing a glycosylation site within 5 or 2
CC amino acids of the fusion junction. The first protein of the fusion
CC protein comprises IgG1 or IgG2, having a C-terminal that is linked to the
CC N-terminus of the second protein. The second protein comprises cytokine
CC or hormone activity. The junction region comprises a spacer or linker. It
CC comprises an Asn-X-Ser/Thr-Gly-amino acid sequence, where X is any amino
CC acid. It comprises an IgG sequence having an ARAI amino acid sequence
CC instead of an LSUS amino acid sequence. The method is useful for reducing
CC the immunogenicity of a fusion protein. The present sequence is a human
CC IgG protein suitable for inclusion in a fusion protein.
XX
SQ Sequence 330 AA;

Query Match 99.5%; Score 1756; DB 7; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPPSSSLGTQTICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
DB 61 GLYSLSVVTVPPSSSLGTQTICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGG 120
QY 121 PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
DB 121 PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
QY 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEVESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEVESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRW 300
QY 301 QGQNVFSCSVNHEALHNHYTQKSLSLSPGK 330
DB 301 QGQNVFSCSVNHEALHNHYTQKSLSLSPGK 330

RESULT 46
ADM41537
ID ADM41537 standard; protein; 330 AA.
XX
AC ADM41537;
XX
XX 03-JUN-2004 (first entry)
DT
DE Anti-interleukin-1 receptor type 1 antibody heavy chain constant region.
XX Human; monoclonal antibody; antibody; interleukin-1; receptor;
KW antiaesthetic; antiinflammatory; dermatological; antiallergic;
KW protozoacide; antirheumatic; antiarthritic; osteopathic; vasotropic;
KW analgesic; antidiabetic; nephrotropic; antianemic; nootropic;
KW anticonvulsant; dermatological; antitigout; antiparkinsonian; antidiabetic;
XX cycostatic.
XX
OS Homo sapiens.

XX WO2004022718-A2.
PN 18-MAR-2004.
XX
XX 05-SEP-2003; 2003WO-US027978.
PF
XX 06-SEP-2002; 2002US-0408719P.
PR
XX (AMGE-) AMGEN INC.
PA
XX Varnum B, Vezina C, Witte A, Qian X, Martin F, Huang H;
PI Elliott G;
XX WPI; 2004-248462/23.
DR N-PSDB; ADM41536.
XX
XX Isolated human antibody that specifically binds interleukin-1 receptor
CC type 1 (IL-1R1) useful for treating IL-1 mediated diseases such as
CC rheumatoid arthritis, osteoarthritis and inflammatory conditions.
PT
XX Disclosure: SEQ ID NO 2; 179pp; English.
XX
XX The present sequence is that of a human anti-interleukin-1 receptor type
CC 1 (IL-1R1) monoclonal antibody (Mab) heavy chain IgG1 constant region.
CC Human Mabs to IL-1R1 were prepared using the HCo7 strain of transgenic
CC mice, which expresses human antibody genes. These mice were immunised
CC with purified recombinant IL-1R1, and splenocytes from immunised mice
CC were fused to a mouse myeloma cell line to generate hybridomas.
CC Hybridomas which secreted a Mab that bound with high avidity to IL-1R1
CC were selected. The Mabs inhibit IL-1 signalling by competing with IL-
CC lbeta and IL-1alpha binding to IL-1R. These Mabs, as well as single chain
CC antibodies single chain Fv antibodies, Fab antibodies, Fab' antibodies
CC and (Fab')2 antibodies derived from them, are used in methods of treating
CC IL-1 mediated diseases or for detecting the amount of IL-1R1 in a sample.
CC IL-1 mediated diseases include acute pancreatitis, amyotrophic lateral
CC sclerosis, Alzheimer's disease, cachexia, anorexia, asthma,
CC atherosclerosis, autoimmune vasculitis, chronic fatigue syndrome,
CC Clostridium associated illnesses, coronary conditions, cancer including
CC leukaemia and tumour metastasis, diabetes, endometriosis, fever,
CC fibromyalgia, glomerulonephritis, graft versus host disease,
CC osteoarthritis, rheumatoid arthritis, inflammatory eye disease,
CC ischaemia, Kawasaki's disease, learning impairment, lung disease,
CC multiple sclerosis, myopathy, osteoporosis, pain, Parkinson's disease,
CC periodontal disease, pre-term labour, psoriasis, reperfusion injury,
CC septic shock, side effects of radiation therapy, temporal mandibular
CC joint disease, sleep disturbance, uveitis, or an inflammatory condition
CC resulting from strain, sprain, cartilage damage, trauma, orthopaedic
CC surgery, infection or other disease processes.
XX
SQ Sequence 330 AA;
Query Match 99.5%; Score 1756; DB 8; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPPSSSLGTQTICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
DB 61 GLYSLSVVTVPPSSSLGTQTICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGG 120
QY 121 PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
DB 121 PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
QY 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEVESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRW 300

Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
301 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 330
301 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 47
ADM68911
ID ADM68911 standard; protein; 330 AA.
XX
AC ADM68911;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human IgG1 heavy chain.
XX
KW Human; batch reformatting vector; ligand screening; phagemid;
KW phage display vector; pBRV; pRRV; internal ribosome entry site; IRSS;
KW rapid reformatting vector; IgG1; immunoglobulin; heavy chain.
XX
OS Homo sapiens.
XX
PN US2003224408-A1.
XX
PD 04-DEC-2003.
XX
PF 07-MAR-2003; 2003US-00383902.
XX
PR 07-MAR-2002; 2002US-0362403P.
XX
PA (DYAX-) DYAX CORP.
XX
PI Hoogenboom HRJM, Mullberg J, Ladner RC;
XX
DR WPI: 2004-119700/12.
DR N-PSDB; ADM68909.
XX
PT Screening ligands, by providing initial nucleic acid cassettes, modifying
PT cassette in single reaction mixture, introducing modified cassette into
PT mammalian cell, expressing modified cassette in transfected cells.
XX
PS Disclosure; SEQ ID NO 6; 63pp; English.
XX
CC The invention relates to screening ligands, by providing several initial
CC nucleic acid cassettes, modifying each nucleic acid cassette in single
CC reaction mixture so that it is functional in a second expression system,
CC introducing each modified nucleic acid cassette into a mammalian cell to
CC produce a mixture of transfected cells, and expressing each modified
CC nucleic acid cassette in transfected cells. Also included are screening
CC nucleic acids (involving providing a number of first different nucleic
CC acids, each encoding a hetero oligomeric candidate ligand, selecting a
CC subset of a number of first different nucleic acids by contacting
CC candidate ligands encoded by the members of a number of first different
CC nucleic acids to a target, reformatting each nucleic acid of the subset
CC for mammalian cell expression, such that each nucleic acid encodes a
CC hetero-oligomeric protein that includes a first functional domain of one
CC subunit of the candidate ligand, a second functional domain of another
CC subunit of the candidate ligand and an effector domain not encoded by the
CC nucleic acids of a number of first different nucleic acids, introducing
CC members of the subset into a mammalian cell to form several expression
CC cells that can produce the protein that includes the functional domain
CC and the effector domain, and screening the expression cells to identify
CC cells that produce at least a threshold amount of a ligand-effector
CC domain fusion protein) and evaluating display library members (involving
CC providing several display library members, determining an assessment for
CC each library member with respect to a property, storing information about
CC the assessments of the library members in a computer database, filtering
CC the information to identify a subset of the library members, and
CC reformatting each member of the subset for expression in a mammalian cell
CC by a method that comprises disposing nucleic acid for each member of the
CC selected subset into a single container). The method is useful for

CC screening ligands. Bacterial and mammalian expression vectors
CC (reformatting vectors) were prepared that support the transfer
CC individually or en masse of Fab heavy and light chain genes from a
CC bacterial expression vector to a mammalian expression vector. Typically,
CC the display vector was a phagemid or phage display vector, which mediate
CC the expression of the Fab on the surface of the bacteriophage M13 or fd.
CC The Fab-encoding segment was transferred from the bacterial display
CC vector to the eukaryotic vector, e.g., pBRV or pRRV by restricting the
CC sites of pBRV (batch reformatting vector) or pRRV (rapid reformatting
CC vector) with ApaLI and BstE2. This fragment was subcloned into ApaLI/BstE2
CC vector). This vector contained a CMV eukaryotic promoter in place of the
CC first bacterial leader sequence. The VH-CH1 sequence encoding an
CC to gene III but was fused in-frame to a sequence encoding an
CC immunoglobulin FC region, e.g., including Hinge-CH2-CH3. Two intervening
CC segments which were inserted between heavy and light chain coding
CC sequences were I-ES between the EcoRI and XbaI site for internal ribosome
CC entry and translation of the second coding region. The present sequence
CC represents the human IgG1 heavy chain for use in the constructs of the
CC method of the invention.
XX
SQ Sequence 330 AA;
Query Match 99.5%; Score 1756; DB 8; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHCTCPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHCTCPCPAPELGG 120
QY 121 PSVFLFPPKPKDGLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 180
Db 121 PSVFLFPPKPKDGLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 180
QY 181 STYRVSVSLTVLHQQDLNKGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVSLTVLHQQDLNKGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 330
RESULT 48
ADR43460
ID ADR43460 standard; protein; 330 AA.
XX
AC ADR43460;
XX
DT 04-NOV-2004 (first entry)
XX
DE Heavy chain constant region of clone Mab 136.
XX
KW antibody; variable light chain; variable heavy chain; Antiallergic;
KW Dermatological; Immunosuppressive; IgE; asthma; allergic rhinitis;
KW eczema; urticaria; atopic dermatitis; food allergy; CDR.
XX
OS Unidentified.
XX
PN WO2004070011-A2.
XX
PD 19-AUG-2004.
XX
PF 02-FEB-2004; 2004WO-US002894.
XX

```
PR 01-FEB-2003; 2003US-0444229P.
XX (TANO-) TANOX INC.
XX Singh S, Foster C, Wu H;
XX WPI; 2004-604433/58.
XX New high affinity human monoclonal antibodies, particularly those
PT directed against isotypic determinants of immunoglobulin E, useful for
PT asthma, allergic rhinitis, eczema, urticaria, atopic dermatitis, or a
PT food allergy.
XX Claim 15; SEQ ID NO 60; 101pp; English.
XX The present invention relates to an antibody comprising a variable light
CC chain region or a variable heavy chain region. The antibody and methods
CC are useful for treating a disorder associated with an abnormally high IgE
CC level, e.g. asthma, allergic rhinitis, eczema, urticaria, atopic
CC dermatitis, or a food allergy. The present sequence represents an
CC antibody region of clone Mab 136.
XX Sequence 330 AA;
SQ
    Query Match          99.5%; Score 1756; DB 8; Length 330;
    Best Local Similarity 99.4%; Pred. No. 2.4e-123;
    Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGG 120
QY 121 PSVFLFPPKPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
DB 121 PSVFLFPPKPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
QY 181 STYRVSVSLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
DB 181 STYRVSVSLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
QY 241 LTKQVSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
DB 241 LTKQVSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
QY 301 QQGNVFSCVMHEALHNHYTOKSLSPGK 330
DB 301 QQGNVFSCVMHEALHNHYTOKSLSPGK 330
RESULT 49
ADR31605
ID ADR31605 standard; protein; 330 AA.
XX AC ADR31605;
XX DT 04-NOV-2004 (first entry)
XX DE Human IgG1 CH1-3 protein.
XX KW Antibody; diagnostic; prophylaxis; therapy; heavy chain constant region;
XX CH; human; IgG1.
XX OS Homo sapiens.
XX PN WO2004070010-A2.
XX PD 19-AUG-2004.
XX PF 02-FEB-2004; 2004WO-US002892.
```

```
XX 01-FEB-2003; 2003US-0444229P.
XX (TANO-) TANOX INC.
XX Singh S, Foster C, Wu H;
XX WPI; 2004-604432/58.
XX Generating a humanized, high affinity antibody from an antibody of
PT interest comprises selecting a suitable human template as the framework
PT for the H and L chain variable domains of the high affinity antibody to
PT be made.
XX Example 11; SEQ ID NO 60; 100pp; English.
XX The invention relates to a method for generating a humanised high
CC affinity antibody from an antibody of interest. The method involves
CC selecting a suitable human template as the framework for the H (heavy)
CC and L (light) chain variable (V) domains of the high affinity antibody to
CC be made. The method is useful for generating high affinity antibodies
CC useful in diagnostics, prophylaxis and treatment of diseases. The present
CC sequence is human IgG1 CH (heavy chain constant region) protein.
XX Sequence 330 AA;
SQ
    Query Match          99.5%; Score 1756; DB 8; Length 330;
    Best Local Similarity 99.4%; Pred. No. 2.4e-123;
    Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGG 120
QY 121 PSVFLFPPKPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
DB 121 PSVFLFPPKPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
QY 181 STYRVSVSLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
DB 181 STYRVSVSLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
QY 241 LTKQVSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
DB 241 LTKQVSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
QY 301 QQGNVFSCVMHEALHNHYTOKSLSPGK 330
DB 301 QQGNVFSCVMHEALHNHYTOKSLSPGK 330
RESULT 50
ADS87909
ID ADS87909 standard; protein; 330 AA.
XX AC ADS87909;
XX DT 18-NOV-2004 (first entry)
XX DE Anti-IFN-gamma antibody heavy chain constant region SEQ ID NO:2.
XX KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
XX anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
XX antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
XX gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
XX multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
XX myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
XX systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
XX vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
```


KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX Homo sapiens.
XX WO2004034988-A2.
XX PD 29-APR-2004.
XX PF 14-OCT-2003; 2003WO-US032678.
XX PR 16-OCT-2002; 2002US-0419057P.
XX PR 17-JUN-2003; 2003US-0479241P.
XX PA (AMGE-) AMGEN INC.
XX PI Welcher A, Chute H, Li L, Huang H;
XX WPI; 2004-348323/32.
XX DR N-PSDB; ADS87908.
XX New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX Example 4; SEQ ID NO 2; 115pp; English.
PS The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC (ADS87943) in the same order and spacing, or an isolated polynucleotide
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianemic, antiarteriosclerotic, hepatotropic, antipruritic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain constant region, which is used in
CC the exemplification of the present invention.
XX SQ Sequence 330 AA;
Query Match 99.5%; Score 1756; DB 8; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELAGG 120
QY 121 PSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
DB 121 PSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
QY 181 STYRVSVLTVLHODWLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 181 STYRVSVLTVLHODWLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
DB |||||
301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
RESULT 51
ADN33230
ID ADN33230 standard; protein; 330 AA.
XX AC ADN33230;
XX DT 18-NOV-2004 (first entry)
XX IG1-CH heavy chain constant region.
XX IG1-CH; antibody; IgG; heavy chain constant region;
KW FcRn binding affinity; asthma; autoimmune disease; cancer;
KW viral infection; antiasthmatic; immunosuppressive; cytostatic; virucide.
XX Unidentified.
XX PN WO2004035752-A2.
XX PD 29-APR-2004.
XX PF 15-OCT-2003; 2003WO-US033037.
XX PR 15-OCT-2002; 2002US-0418972P.
XX PR 10-APR-2003; 2003US-0462014P.
XX PR 03-JUN-2003; 2003US-0475762P.
XX PR 29-AUG-2003; 2003US-0499048P.
XX PA (PROT-) PROTEIN DESIGN LABS INC.
XX PI Hinton PR, Tsurushita N, Tso YJ, Vasquez M;
XX WPI; 2004-348446/32.
XX New modified antibody of class IgG having an altered FcRn binding
PT affinity and/or serum half-life, useful in immunology and protein
PT engineering, and for diagnosing or treating asthma, autoimmune diseases,
PT cancer and viral infections.
XX Disclosure; SEQ ID NO 3; 140pp; English.
XX The invention relates to a modified antibody of class IgG where at least
CC one amino acid residue from the heavy chain constant region is different
CC from that present in an unmodified class IgG antibody, and where the FcRn
CC binding affinity and/or serum half-life of the modified antibody is
CC altered relative to that of the unmodified antibody. The methods and
CC compositions of the present invention are useful in the fields of
CC immunology and protein engineering, in particular for using modified
CC class IgG antibodies for diagnosing and treating asthma, autoimmune
CC diseases, cancer and viral infections. This sequence represents the
CC antibody IgG1-CH heavy chain constant region of the invention.
XX SQ Sequence 330 AA;
Query Match 99.5%; Score 1756; DB 8; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELAGG 120
QY 121 PSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
DB 121 PSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180

QY 181 STYRVSVSLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVSLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
RESULT 52
AD594906
ID AD594906 standard; protein; 330 AA.
AC AD594906;
XX
XX 02-DEC-2004 (first entry)
DT
DE Anti-IFN-gamma antibody heavy chain constant region SEQ ID NO:2.
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
XX WO2004035747-A2.
PN
XX 29-APR-2004.
PD
XX 16-OCT-2003; 2003WO-US032871.
PF
XX 16-OCT-2002; 2002US-0419057P.
PR
XX 17-JUN-2003; 2003US-0479241P.
PR
XX (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
XX Welcher AA, Chute HT, Li Y, Huang H;
PI
XX WPI; 2004-348443/32.
DR N-PSDB; AD594905.
XX
XX New human anti-interferon-gamma neutralizing antibodies for treating
XX interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
XX Example 4; SEQ ID NO 2; 115pp; English.
PS
XX The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (AD594940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (AD594941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's

CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain constant region, which is used in
CC the exemplification of the present invention.
XX
XX Sequence 330 AA;
Query Match 99.5%; Score 1756; DB 8; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTVICNVNHKPSNTKVDKKVEPKSCDKTHTCTCPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTVICNVNHKPSNTKVDKKVEPKSCDKTHTCTCPCPAPELGG 120
QY 121 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 121 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
QY 181 STYRVSVSLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVSLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
RESULT 53
AD533009
ID AD533009 standard; protein; 330 AA.
XX
AC AD533009;
XX
DT 30-DEC-2004 (first entry)
DE
XX Human IgG1 chain C polypeptide.
XX
XX Human; IgG1 chain C; constant heavy immunoglobulin domain;
KW membrane-anchored receptor; growth factor; cytokine; TRAIL; TNF; VEGF;
KW IL-15; apoptosis; autoimmune disorder; AIDS; heart disorder;
KW myocardial infarction; graft-versus-host disorder; transplant rejection;
KW spinal cord injury; paraplegia; sepsis; hepatitis; inflammation;
KW ischaemic reperfusion injury; renal disorder.
XX
OS Homo sapiens.
XX
XX WO2004085478-A2.
PN
XX 07-OCT-2004.
PD
XX 26-MAR-2004; 2004WO-EP003239.
PF
XX 26-MAR-2003; 2003EP-00006949.
PR
XX (APOG-) APOGENIX BIOTECHNOLOGY AG.
PA
XX Walczak H;
PI
XX WPI; 2004-700134/68.
DR
XX New fusion protein comprising at least one first domain comprising a
PT biologically active polypeptide fused to a heterologous second domain,
PT

useful for the prophylaxis and/or treatment of disorders associated with apoptosis.

Disclosure: Fig 2: 44pp: English.

The invention relates to a fusion protein comprising at least one first domain comprising a biologically active polypeptide fused to a heterologous second domain comprising at least a portion of a constant immunoglobulin domain where there is at least one amino acid overlap between the first domain and the second domain in the fusion region. The invention also relates to a nucleic acid molecule encoding the fusion protein or its precursor, a cell transformed or transfected with the nucleic acid molecule, a non-human organism transformed or transfected with the nucleic acid molecule, a pharmaceutical composition comprising as an active agent the fusion protein or the nucleic acid molecule, and manufacturing a fusion protein comprising at least one first domain comprising a biologically active polypeptide fused to a second domain comprising at least a portion of a constant immunoglobulin domain with reduced immunogenic potential, where the first domain is fused to the second domain with at least one amino acid overlap. The fusion protein comprises a first domain selected from a ligand-binding domain of a receptor and a receptor-binding domain of a ligand. The first domain is a ligand-binding receptor domain comprising an extracellular domain of a membrane-anchored receptor or its ligand-binding fragment. The receptor is selected from death receptors, growth factor receptors and cytokine receptors. The receptor is selected from CD95, a TRAIL receptor, a TNF receptor and a VEGF receptor. The first domain is a receptor-binding ligand domain. The ligand is selected from death ligands, growth factors and cytokines. The ligand is selected from CD95 ligand, TRAIL, TNF, VEGF and IL-15. The first domain is derived from a human protein. The second domain comprises at least a portion of a constant heavy immunoglobulin domain. The second domain is an Fc fragment of a constant heavy immunoglobulin domain comprising the CH2 and CH3 domain and optionally at least a part of the hinge region. The second domain comprises at least a portion of a constant IgG1, IgG2, IgG3 or IgG4 immunoglobulin domain or its variant. The second domain is derived from a human immunoglobulin. The fusion proteins are useful for the prophylaxis and/or treatment of disorders associated with apoptosis such as autoimmune disorders, AIDS, heart disorders such as myocardial infarction, graft-versus-host-disorders such as transplant rejection, spinal cord injuries such as paraplegia, sepsis, hepatitis, disorders associated with inflammation, ischemic reperfusion injury and renal disorders. This sequence represents a human IgG1 chain C polypeptide used in the scope of the invention.

Sequence 330 AA;

```
Query Match      99.5%; Score 1756; DB 8; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328: Conservative 0; Mismatches 2; Indels
```

Qy	1	ASTKGPSPVFLPAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS	60
Db	1	ASTKGPSPVFLPAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS	60
Qy	61	GLYSLSSTVTVPPSSSLGTQTIVICNNHKKPSNTKVDKVKPEKSCDKHTHCCPCPAPELAGA	120
Db	61	GLYSLSSTVTVPPSSSLGTQTIVICNNHKKPSNTKVDKVKPEKSCDKHTHCCPCPAPELGG	120
Qy	121	PSVFLPPPKPKDITLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	180
Db	121	PSVFLPPPKPKDITLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	180
Qy	181	STRVRSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISAKGQPREPQVYTLPPSRDE	240
Db	181	STRVRSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISAKGQPREPQVYTLPPSRDE	240
Qy	241	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW	300
Db	241	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW	300
Qy	301	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	330

db 301 OCGNVFSCVMHEALHNHYTOKSLSPGK 330

RESULT 54
ADT88869

ADT88869
ID ADT88869 standard: protein: 330 AA.

AC · ADT88869;

DT 30-DEC-2004 (first entry)

Human IgG1 antibody constant domain SEQ ID NO:8.

KW antibody; IGF-IR; Insulin-like growth factor I receptor; cytostatic;
KW antibody therapy: tumor: cancer: IgG1.

XX Homo sapiens.

PN WO2004087756-A2.

PD 14-OCT-2004.

PF 01-APR-2004; 2004WO-EP003442.

PR 02-APR-2003; 2003US-0459837P.

[illegible]

XX
XX
OFF / HOFFMAN

PI Graus I, Kopetzki E, Kuemker R, Mundt S, Fahren F, Rebels F;
PI Schumacher R, Van De Winkel J, Van Vugt M;

DR WPI; 2004-737667/72.

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

PT and inhibiting the binding of IGF-I and IGF-II to IGF-IR, useful for treating cancers of the colon, breast, prostate and lung.

PS Disclosure; SEQ ID NO 8; 81pp; English.

The invention relates to a novel antibody binding to insulin-like growth factor I receptor (IGF-IR) and inhibiting the binding of IGF-I and IGF-II to IGF-IR. An antibody binding to insulin-like growth factor I receptor (IGF-IR) and inhibiting the binding of IGF-I and IGF-II to IGF-IR, where the antibody is of IgG1 isotype and shows a ratio of inhibition of the binding of IGF-I to IGF-IR to the inhibition of binding of IGF-II to IGF-IR of 1:3 to 3:1 and induces cell death of 20% or more cells of a preparation of IGF-IR expressing cells after 24 hours at a concentration of the antibody of 100 nM by ADCC, is new. An antibody of the invention has cytostatic activity, and may have a use in antibody therapy. The methods and compositions of the present invention are useful for the treatment of tumors and cancers of the colon, breast, prostate and lung using antibodies against human insulin-like growth factor I receptor (IGF-IR). The present sequence represents the constant domain of a human IgG1 type antibody.

Sequence 330 AA:

Query Match 99.5%; Score 1756; DB 8; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels

[illegible]

Db 121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
QY 181 STYRVSVLTVLHODWLNKEYCKVSNKALPAPIEKTISKAKGQRPQPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHODWLNKEYCKVSNKALPAPIEKTISKAKGQRPQPQVYTLPPSRDE 240
QY 241 LTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 55

ADT51577

ID ADT51577 standard; protein; 330 AA.

XX AC ADT51577;

XX DT 13-JAN-2005 (first entry)

XX DE Heavy chain constant region of human OST577-IgG1.

XX KW Human; antibody; immunoglobulin G; IgG; heavy chain constant region; CH;
XX KW FcRn binding affinity; serum half-life; dactilizumab; fontolizumab;
XX KW visilizumab; M200; cancer; inflammatory disorder; asthma;
XX KW autoimmune disease; viral infection; cytostatic; antiinflammatory;
XX KW antiasthmatic; immunosuppressive; virucide.

XX OS Homo sapiens.

XX PN WO2004092219-A2.

XX PD 28-OCT-2004.

XX PF 09-APR-2004; 2004WO-US011213.

XX PR 10-APR-2003; 2003US-0462014P.

XX PR 03-JUN-2003; 2003US-0475762P.

XX PR 29-AUG-2003; 2003US-0499048P.

XX PR 15-OCT-2003; 2003US-00687118.

XX PA (PROT-) PROTEIN DESIGN LABS INC.

XX PI Hinton PR, Tsurushita N, Tso JY, Vasquez M;

XX DR WPI; 2004-758341/74.

XX PT New modified antibodies of class IgG that have altered binding affinities
XX PT for FcRn or altered serum half-lives, useful for diagnosing or treating
XX PT for e.g. cancer, inflammation, autoimmune diseases or viral infections.

XX PS Disclosure; SEQ ID NO 3; 157pp; English.

XX CC The present invention relates to a modified human antibody of class
XX CC immunoglobulin G (IgG) where at least one amino acid residue from the
XX CC heavy chain constant (CH) region selected from amino acid residues 250,
XX CC 314 and 428 is different from that present in an unmodified class IgG
XX CC antibody, and where the FcRn binding affinity and/or serum half-life of
XX CC the modified antibody is altered relative to that of the unmodified
XX CC antibody. The numbering of the residues in the heavy chain is that of the
XX CC EU index. Also disclosed are methods of modifying an antibody of class
XX CC IgG and producing the modified antibody cited, and a pharmaceutical
XX CC composition comprising the above modified immunoglobulins, proteins and
XX CC other bioactive molecules having altered half-lives. The unmodified or
XX CC naturally occurring class IgG antibody is selected from dactilizumab,
XX CC fontolizumab, visilizumab and M200. The amino acid residue 250 from the
XX CC heavy chain constant region is glutamic acid or glutamine, or the amino
XX CC acid residue 428 from the heavy chain constant region is phenylalanine or
XX CC leucine. Alternatively, the amino acid residue 250 from the heavy chain
XX CC constant region is glutamic acid and the amino acid residue 428 from the

CC heavy chain constant region is phenylalanine, or the amino acid residue
CC 250 from the heavy chain constant region is glutamine and the amino acid
CC residue 428 from the heavy chain constant region is phenylalanine, or the
CC amino acid residue 250 from the heavy chain constant region is glutamine
CC and the amino acid residue 428 from the heavy chain constant region is
CC leucine. The modified therapeutic antibody of class IgG has an in vivo
CC elimination half-life of at least 1.3-fold longer than that of the
CC corresponding unmodified class IgG antibody. The composition and methods
CC of the invention are useful for various diagnostic and therapeutic
CC purposes, especially in the treatment of cancer, inflammatory disorders
CC (e.g. asthma), autoimmune diseases or viral infections. The present
CC sequence represents a CH region of a human IgG antibody.

SQ Sequence 330 AA;

Query Match 99.5%; Score 1756; DB 8; Length 330;

Best Local Similarity 99.4%; Pred. No. 2.4e-123;

Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLGG 60

Db 1 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLGG 60

QY 61 GLYSLSVSVTVFVPSVSLGTTQYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELAGA 120

Db 61 GLYSLSVSVTVFVPSVSLGTTQYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELGG 120

QY 121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Db 121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

QY 181 STYRVSVLTVLHODWLNKEYCKVSNKALPAPIEKTISKAKGQRPQPQVYTLPPSRDE 240

Db 181 STYRVSVLTVLHODWLNKEYCKVSNKALPAPIEKTISKAKGQRPQPQVYTLPPSRDE 240

QY 241 LTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300

Db 241 LTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300

QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 56

ADT51581

ID ADT51581 standard; protein; 330 AA.

XX AC ADT51581;

XX DT 13-JAN-2005 (first entry)

XX DE Heavy chain constant region of human Huld10-IgG1.

XX KW Human; antibody; immunoglobulin G; IgG; heavy chain constant region; CH;
XX KW FcRn binding affinity; serum half-life; dactilizumab; fontolizumab;
XX KW visilizumab; M200; cancer; inflammatory disorder; asthma;
XX KW autoimmune disease; viral infection; cytostatic; antiinflammatory;
XX KW antiasthmatic; immunosuppressive; virucide.

XX OS Homo sapiens.

XX PN WO2004092219-A2.

XX PD 28-OCT-2004.

XX PF 09-APR-2004; 2004WO-US011213.

XX PR 10-APR-2003; 2003US-0462014P.

XX PR 03-JUN-2003; 2003US-0475762P.

XX PR 29-AUG-2003; 2003US-0499048P.

XX PR 15-OCT-2003; 2003US-00687118.

XX XX

CC	PSMA antibody. Also included are a method of treating prostate cancer in a subject, a method of monitoring a patient receiving an anti-PSMA antibody to treat prostate cancer and a method of selecting a patient for treatment with an anti-PSMA antibody. Also disclosed are anti-PSMA antibodies. The antibody or antigen-binding fragment is a human antibody (or antigen-binding fragment) a modified antibody (or an antigen-binding fragment). The modified antibody is selected from CDR-grafted antibodies, humanized antibody, delaminized antibody, or antigen binding fragments. The modified antibody or antigen-binding fragment has one or more CDRs (complementarity determining region) from a mouse monoclonal antibody selected from J591, J415, J533, or E99. The anti-PSMA antibody or antigen-binding fragment is useful for treating prostate cancer, monitoring a patient receiving an anti-PSMA antibody to treat prostate cancer, or selecting a patient for treatment with an anti-PSMA antibody. The present sequence is a functional region from a delaminized heavy chain variable and constant region from one of the mouse monoclonal antibodies listed above.	CC
XX	Sequence 330 AA;	SQ
Query Match 99.5%; Score 1756; DB 8; Length 330; Best Local Similarity 99.4%; Pred. No. 2.4e-123; Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
Qy	1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60	
Db	1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60	
Qy	61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGA 120	
Db	61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGG 120	
Qy	121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKPREEQYN 180	
Db	121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKPREEQYN 180	
Qy	181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 240	
Db	181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 240	
Qy	241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFPLYSKLTVDKSRW 300	
Db	241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFPLYSKLTVDKSRW 300	
Qy	301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330	
Db	301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330	
RESULT 59		
ADW08868	ADW08868 standard; protein; 330 AA.	
XX	ADW08868;	
XX	07-APR-2005 (first entry)	
XX	IGF-IR antibody 18 constant region domain, SEQ ID 6.	
DE	Cytostatic; Antibody; antibody therapy; antibody production;	
KW	insulin-like growth factor I receptor; IGF-IR; constant region.	
KW	Homo sapiens.	
OS	US2005008642-A1.	
XX	13-JAN-2005.	
XX	08-JUL-2004; 2004US-00886838.	
XX	10-JUL-2003; 2003EP-00015526.	
XX	(GRAU/) GRAUS Y.	

PA (KOE/) KOPETZKI E.
PA (KUN/) KUNKELE K.
PA (MUN/) MUNDIGL O.
PA (PAR/) PARREN P.
PA (REBE/) REBERS F.
PA (SCHU/) SCHUMACHER R.
PA (VWIN/) VAN DE WINKEL J.
PA (VUGT/) VUGT M V.
PI Graus Y, Kopetzki E, Kuenkele K, Mundigl O, Parren P, Rebers F;
PI Schumacher R, Van De Winkel J, Vugt MV;
XX WPI; 2005-099927/11.
DR N-PSDB; ADW08667.
XX
XX Novel antibody capable of inhibiting binding of insulin like growth
PT factor I (IGF-I) and IGF-II to IGF-I receptor, useful for treating
PT cancer.
XX
XX Disclosure; SEQ ID NO 6; 38pp; English.
XX
XX The present invention relates to antibodies 18 and 22. (A1) which bind to
CC insulin like growth factor I receptor (IGF-IR). The antibody is capable
CC of inhibiting the binding of IGF-I and IGF-II to IGF-IR, and is of the
CC IGF1 isotype. The antibodies induce cell death of 20% or more cells of a
CC preparation of IGF-IR expressing cells by antibody dependent cellular
CC toxicity (ADCC). (A1) are useful for making a pharmaceutical composition
CC which inhibits the binding of IGF-I and IGF-II to IGF-IR, which involves
CC combining (A1) with a carrier. (A1) is also useful for treating a patient
CC in need of an antitumor therapy, which involves administering (A1) alone
CC or in combination with a cytotoxic agent, its prodrug or cytotoxic
CC radiotherapy to the patient. The present sequence is the constant region
CC of antibody 18.
XX
XX SQ Sequence 330 AA;
Query Match 99.5%; Score 1756; DB 9; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 60
Db 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 60
Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGG 120
Qy 121 PSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREQYN 180
Db 121 PSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREQYN 180
Qy 181 STYRVSVLTVLHODWLNKGEYKCKVSKNALPAPIEKTISKAKGPREPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHODWLNKGEYKCKVSKNALPAPIEKTISKAKGPREPQVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Qy 301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
RESULT 60
ADW86657
ID ADW86657 standard; protein; 330 AA.
XX
XX AC ADW86657;
XX
XX DT 21-APR-2005 (first entry)
XX

DE Human immunoglobulin gamma-1 chain constant region IgG1 protein.
XX
XX crystallography; tumor necrosis factor receptor 2; antirheumatic;
KW antiarthritic; antipsoriatic; cardiovascular-Gen.; antibacterial;
KW virucide; protozoacide; antilipemic; neuroprotective; analgesic;
KW antipyretic; cytostatic; antianemic; respiratory-Gen.; dermatological;
KW endocrine-Gen.; uropathic; auditory; osteopathic; anorectic;
KW gynecological; immunosuppressive; nootropic; etanercept; TNF-alpha;
KW tumor necrosis factor alpha; rheumatoid arthritis; psoriatic arthritis;
KW psoriasis; ankylosing spondylitis; cardiovascular disease;
KW bacterial infection; viral infection; protozoal infection;
KW hyperlipidemia; neurological disease; pain; fever; anemia; tumor;
KW pulmonary disease; obesity.
XX
XX Homo sapiens.
OS
XX WO2005012353-A1.
PN
XX 10-FEB-2005.
PD
XX 29-JUL-2004; 2004WO-US024738.
PF
XX 01-AUG-2003; 2003US-0491827P.
PR
XX (AMGE-) AMGEN INC.
PA
XX Osslund TD, Clogston CL, Crampton SL, Bass RB;
DR WPI; 2005-142876/15.
XX
XX Crystal of therapeutic etanercept polypeptide (tumor necrosis factor
PT receptor 2 polypeptide) useful for treating conditions such as rheumatoid
PT arthritis, psoriatic arthritis, psoriasis and ankylosing spondylitis.
XX
XX Disclosure; SEQ ID NO 2; 76pp; English.
XX
XX This invention relates to a novel crystal of etanercept (tumor necrosis
CC factor receptor 2 polypeptide). The invention may be useful for the
CC development of compounds with an antirheumatic, antiarthritic,
CC antipsoriatic, cardiovascular-Gen., antibacterial, virucide,
CC protozoacide, antilipemic, neuroprotective, analgesic, antipyretic,
CC cytostatic, antianemic, respiratory-Gen., dermatological,
CC uropathic, auditory, osteopathic, anorectic, gynecological,
CC immunosuppressive or nootropic activity. A composition developed by
CC reconstituting crystalline etanercept is useful for preparing a
CC medicament for treating a condition characterized by excessive TNF-alpha
CC (tumor necrosis factor alpha) levels. The medicament reduces levels of
CC TNF-alpha in the serum or tissues of the subject. The condition is
CC rheumatoid arthritis, psoriatic arthritis, psoriasis, or ankylosing
CC spondylitis. The compound may be useful for treating a disease chosen
CC from cardiovascular disorders, bacterial, viral or protozoal infections,
CC familial combined hyperlipidemia (FCH), neurological disorders, pain,
CC fever, oncologic and hematologic disorders, anemia, solid tumors,
CC pulmonary disorders, rheumatic and skin disorders, disorders of endocrine
CC system, disorders of genitourinary system, disorders that involves
CC hearing loss, non-arthritis medical conditions of the bones and joints,
CC obesity, disorders that affect female reproductive system, autoimmune
CC disorders, autism spectrum disorder and other pervasive developmental
CC disorders. The present sequence is that of the human immunoglobulin gamma
CC -1 chain constant region IgG1 protein which is related to the invention.
XX
XX SQ Sequence 330 AA;
Query Match 99.5%; Score 1756; DB 9; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 60
Db 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 60
Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120

Db 61 GLYSLSSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 120
Qy 121 PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
Db 121 PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
Qy 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 61

ADX97894
ID ADX97894 standard; protein; 330 AA.

XX AC ADX97894;

XX DT 05-MAY-2005 (first entry)

XX DE Human Ig gamma-1 chain.

XX KW immunoglobulin gamma-1 chain; Ig gamma-1 chain; cytokine; pharmaceutical;
XX KW allergy; asthma; fibrosis; immune deficiency; cancer; antiallergic;
XX KW antiasthmatic; antiinflammatory; immunostimulant; cytostatic.

XX OS Homo sapiens.

XX PN WO2005014646-A1.

XX PD 17-FEB-2005.

XX PF 14-JUN-2004; 2004WO-US018753.

XX PR 11-JUN-2003; 2003US-0477548P.

XX PA (AMHP) WYETH.

XX PI Wood CR, Murtha-Riel P, Lee GW, Leonard M;

XX DR WPI; 2005-152547/16.

XX DR N-PSDB; ADX97893.

XX PT Producing an interleukin (IL)-13 antagonist polypeptide to treat
XX PT disorders associated with IL-13 activity (e.g. allergy), comprises co-
XX PT expressing an IL-13 antagonist polypeptide with a nucleic acid encoding a
XX PT complexing polypeptide.

XX PS Disclosure; SEQ ID NO 8; 77pp; English.

XX The invention relates to a method of producing an interleukin-13 (IL-13)
XX antagonist polypeptide. The method comprises co-expressing an IL-13
XX antagonist polypeptide with a nucleic acid encoding a complexing
XX polypeptide for the IL-13 antagonist polypeptide. Also described are
XX methods of reducing the level of IL-13 or a cytokine in a patient, a
XX pharmaceutical composition comprising the IL-13 antagonist polypeptide
XX produced by the above method or the IL-13 Ralpa2Fc polypeptide, and a
XX pharmaceutical carrier, and a purified preparation of a soluble IL-13
XX antagonist polypeptide, where at least 40% of the soluble IL-13
XX antagonist polypeptide is present in monomer or dimer form following
XX incubation for at least one week at 4 degrees centigrade. The complexing
XX polypeptide comprises the amino acid sequence of human IL-13 polypeptide
XX as fully defined in the specification (SEQ ID NO: 17) or comprises a
XX variant amino acid sequence of SEQ ID NO: 17, where the arginine at amino
XX acid 126 is replaced with aspartic acid, glutamic acid or proline. The
XX composition and methods of the invention are useful for treating

CC conditions associated with aberrant IL-13 activity or expression, such as
CC allergies, asthma, fibrosis, immune deficiencies, or cancer. This
CC sequence represents human immunoglobulin gamma-1 (Ig gamma-1) chain.
XX
SQ Sequence 330 AA;

Query Match 99.5%; Score 1756; DB 9; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
Db 61 GLYSLSSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPCPAPELGG 120

Qy 121 PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
Db 121 PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180

Qy 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300

Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 62

ADX98273
ID ADX98273 standard; protein; 330 AA.

XX AC ADX98273;

XX DT 05-MAY-2005 (first entry)

XX DE Human anti-HGF antibody IgG1 heavy chain constant region protein -SEQ 45.

XX KW antibody; cytostatic; cancer; neoplasm; solid tumor;
XX KW hepatocyte growth factor; HGF; heavy chain constant region;
XX KW immunoglobulin G1.

XX OS Homo sapiens.

XX PN WO2005017107-A2.

XX PD 24-FEB-2005.

XX PF 16-JUL-2004; 2004WO-US018936.

XX PR 18-JUL-2003; 2003US-0488681P.

XX PA (AMGE-) AMGEN INC.

XX PA (ABGE-) ABGENIX INC.

XX PI Burgess TL, Coxon A, Green LL, Zhang K;

XX DR WPI; 2005-182350/19.

XX DR N-PSDB; ADX98250.

XX PT New polypeptide comprising a complementarity determining region (CDR)
XX PT consisting of CDR1a, CDR2a, CDR3a, CDR1b, CDR2b or CDR3b and capable of
XX PT binding hepatocyte growth factor, useful in preparing a composition for
XX PT treating cancer.

XX PS Example 3; SEQ ID NO 45; 301pp; English.

XX The invention relates to a novel isolated polypeptide comprising at least
 CC one complementarity-determining region (CDR) consisting of CDR1a, CDR2a
 CC or CDR3a, or CDR1b, CDR2b or CDR3b. The polypeptide, in association with
 CC an antibody heavy or light chain, is capable of binding hepatocyte growth
 CC factor (HGF). HGF, also known as scatter factor (SF), has been identified
 CC as a potent mitogen for hepatocytes and also as a secretory protein of
 CC fibroblasts and smooth muscles that acts to induce motility of epithelial
 CC cells. The polypeptide demonstrates cytostatic activity and may be useful
 CC in preparing a composition for treating cancer or a solid tumor. The
 CC current sequence is that of the human anti-HGF antibody IgG1 heavy chain
 CC constant region protein -SEQ 45 of the invention.

XX Sequence 330 AA;

Query Match 99.5%; Score 1756; DB 9; Length 330;
 Best Local Similarity 99.4%; Pred. No. 2.4e-123;
 Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSS 60
 DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSSVVTVSPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
 DB 61 GLYSLSSVVTVSPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELGG 120

QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
 DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

QY 181 STYRVSVLTVLHQDLNGKEYCKVKSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
 DB 181 STYRVSVLTVLHQDLNGKEYCKVKSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300

QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
 DB 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 63

ADY51253
 ID ADY51253 standard; protein; 330 AA.

XX AC ADY51253;

XX DT 19-MAY-2005 (first entry)

XX DE Human IgG1 SEQ ID NO:22.

XX Immunoglobulin G1; hematopoiesis; hyperproliferation; cytostatic;
 KW antianemic; antiinflammatory; antipsoriatic; gastrointestinal-gen.;
 KW dermatological; coagulant; immunostimulant; cerebroprotective;
 KW vasotropic; antiulcer.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 97 /note= "Optionally replaced by R"

FT FT Misc-difference 239 /note= "Optionally replaced by E"

FT FT Misc-difference 241 /note= "Optionally replaced by M"

XX US2005049194-A1.

XX PD 03-MAR-2005.

XX

PF 31-OCT-2003; 2003US-00698907.

XX 09-NOV-2001; 2001US-0345206P.

PR 02-JUL-2002; 2002US-0393272P.

PR 08-NOV-2002; 2002US-00291290.

PR 03-APR-2003; 2003US-0460488P.

XX (FRIS/) FRISEN J.

PA (HOLM/) HOLMBERG J.

XX Frisen J, Holmberg J;

XX WPI; 2005-195317/20.

XX Use of ephrin and its molecules for alleviating a symptom or a disorder

PT with reduced levels of hematopoiesis, increased levels of cellular

PT proliferation in an intestinal tract, or abnormal level of cellular

PT proliferation in a tissue.

XX Disclosure; SEQ ID NO 22; 68pp; English.

CC The invention relates to a novel use of ephrin, ephrin inhibitors, and

CC ephrin receptors for alleviating a symptom of a disorder having reduced

CC levels of hematopoiesis, having increased levels of cellular

CC proliferation in an intestinal tract, or having an abnormal level of

CC cellular proliferation in a tissue. A composition of the invention has

CC cytostatic, antianemic, antiinflammatory, antipsoriatic, gastrointestinal

CC -gen., dermatological, coagulant, immunostimulant, cerebroprotective,

CC vasotropic, and antiulcer activity. The present sequence represents human

CC Immunoglobulin G1 (IgG1).

XX Sequence 330 AA;

Query Match 99.5%; Score 1756; DB 9; Length 330;

Best Local Similarity 99.4%; Pred. No. 2.4e-123;

Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSS 60

DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSSVVTVSPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELAGA 120

DB 61 GLYSLSSVVTVSPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELGG 120

QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

QY 181 STYRVSVLTVLHQDLNGKEYCKVKSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

DB 181 STYRVSVLTVLHQDLNGKEYCKVKSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300

DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300

QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

DB 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 64

ADY58147

ID ADY58147 standard; protein; 330 AA.

XX AC ADY58147;

XX DT 19-MAY-2005 (first entry)

XX Human IgG gamma 1 constant region.

XX cytostatic; virucide; immunomodulator; cancer; viral infection;

XX

KW	immune disorder; IgG; immunoglobulin; neoplasm; infection.	KW	neurological disease; NGF; nerve growth factor; heavy chain.
XX		XX	
OS	Homo sapiens.	OS	Homo sapiens.
XX		XX	
PN	WO2005021592-A2.	PN	WO2005019266-A2.
XX		XX	
PD	10-MAR-2005.	PD	03-MAR-2005.
XX		XX	
PF	30-AUG-2004; 2004WO-EP009642.	PF	15-JUL-2004; 2004WO-US022876.
XX		XX	
PR	28-AUG-2003; 2003US-0498618P.	PR	15-JUL-2003; 2003US-0487431P.
XX		XX	
PA	(MERE) MERCK PATENT GMBH.	PA	(AMGE-) AMGEN INC.
XX		XX	
PI	Gillies S, Lauder S, Way J;	PI	Wild KD, Treanor JUS, Huang H, Inoue H, Zhang TJ, Martin F;
XX		XX	
DR	WPI; 2005-214544/22.	DR	WPI; 2005-202606/21.
XX		XX	N-PSDB; ADY26686.
PT	New protein comprising an interleukin-2 protein, where Lys8 and Lys9 of the interleukin-2 protein are replaced with non-lysine amino acids, useful for treating cancer, viral infection, and an immune disorder.	PT	New human anti-nerve growth factor (NGF) neutralizing antibodies useful for manufacturing a medicament for treating painful disorders (e.g. acute pain) or conditions associated with increased expression or sensitivity to NGF.
XX		PT	
PS	Disclosure; SEQ ID NO 7; 39pp; English.	PT	
XX		XX	
CC	The invention relates to a protein comprising an interleukin-2 protein, where Lys 8 and Lys 9 of the interleukin-2 protein are replaced with non-lysine amino acids. The protein, nucleic acid, and pharmaceutical composition are useful for the manufacture of a medicament for treating cancer, viral infection, and an immune disorder. The present sequence represents the amino acid sequence of human IgG gamma 4 constant region.	PS	Disclosure; SEQ ID NO 2; 190pp; English.
XX		XX	
CC		CC	The invention describes an isolated human antibody that interacts with or binds specifically to human nerve growth factor (NGF) and neutralize the function of NGF. Also described are: methods of treating a condition caused by increased expression of NGF or increased sensitivity to NGF in a patient; methods for detecting NGF in a biological sample; an NGF specific binding agent comprising any of the 59 amino acid sequences comprising, for e.g. 123, 107 or 14 amino acids, as mentioned in the specification, and where the binding agent can bind to NGF; a pharmaceutical composition comprising a pharmaceutical carrier and a therapeutic amount of the antibody or binding agent cited above; or a medicament for treating a painful disorder or condition associated with increased expression of NGF or increased sensitivity to NGF; the medicament comprising a pharmaceutical amount of a monoclonal antibody or its immunologically functional immunoglobulin fragment, or pharmaceutical salts of the monoclonal antibody or the fragment, where the monoclonal antibody is at least one of the monoclonal antibody cited above, and a pharmaceutical carrier, diluent or excipient; a nucleic acid molecule or polynucleotide that encodes the above antibody or binding agent; an isolated cell line that produces the above antibody or binding agent; an expression vector comprising the above polynucleotide; and a host cell comprising the nucleic acid or expression vector. The composition (including the antibody) and methods are useful for manufacturing a medicament for treating a painful disorder (e.g. acute pain, dental pain, or pain from trauma or cancer), or a condition associated with increased expression of NGF or increased sensitivity to NGF. This is the amino acid sequence of a human NGF antibody heavy chain.
XX		CC	
XX		XX	
Seq	Sequence 330 AA;	Seq	Sequence 330 AA;
Query Match	99.5%; Score 1756; DB 9; Length 330;	Query Match	99.5%; Score 1756; DB 9; Length 330;
Best Local Similarity	99.4%; Pred. No. 2.4e-123;	Best Local Similarity	99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	Matches 328; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSVHTFPAVLQSS 60	QY	1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSVHTFPAVLQSS 60
Db	1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSVHTFPAVLQSS 60	Db	1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSVHTFPAVLQSS 60
QY	61 GLYSLSSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 120	QY	61 GLYSLSSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 120
Db	61 GLYSLSSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPCPAPELAGG 120	Db	61 GLYSLSSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPCPAPELLGG 120
QY	121 PSVFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180	QY	121 PSVFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db	121 PSVFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180	Db	121 PSVFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
QY	181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240	QY	181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db	181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240	Db	181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY	241 LTKQVSLTCLVKGFPYSDIAVEESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300	QY	241 LTKQVSLTCLVKGFPYSDIAVEESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
Db	241 LTKQVSLTCLVKGFPYSDIAVEESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300	Db	241 LTKQVSLTCLVKGFPYSDIAVEESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
QY	301 QQGNVFSQVMHEALHNNHYTQKLSLSLSPGK 330	QY	301 QQGNVFSQVMHEALHNNHYTQKLSLSLSPGK 330
Db	301 QQGNVFSQVMHEALHNNHYTQKLSLSLSPGK 330	Db	301 QQGNVFSQVMHEALHNNHYTQKLSLSLSPGK 330
RESULT 65			
ADY26687			
ID	ADY26687 standard; protein; 330 AA.		
XX			
XX			
AC	ADY26687;		
XX			
DT	19-MAY-2005 (first entry)		
XX			
DE	Human anti-NGF-antibody heavy chain SEQ ID NO 2.		
XX			
KW	analgesic; gene therapy; antibody engineering; pharmaceutical; pain;		

Db 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQRPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 66
AEA12531
ID AEA12531 standard; protein; 330 AA.
XX AC AEA12531;
XX DT 14-JUL-2005 (first entry)
XX DE Human IgG1 constant region.
XX KW CD52; antibody; cytostatic; antiinflammatory; antirheumatic;
KW antiarthritic; neuroprotective; immunosuppressive; gastrointestinal-Gen.;
KW dermatological; vasotropic; lymphoid leukemia; lymphoma;
KW autoimmune disease; multiple sclerosis; rheumatoid arthritis; vasculitis;
KW uveitis; inflammatory bowel disease; scleroderma; transplantation.
XX OS Homo sapiens.
XX PN WO2005042581-A2.
XX PD 12-MAY-2005.
XX PF 29-OCT-2004; 2004WO-IB003879.
XX PR 01-NOV-2003; 2003US-0516210P.
XX PA (BIOV-) BIOVATION LTD.
XX PI Carr FJ, Hamilton AA;
XX WPI; 2005-346857/35.
XX DR N-PSDB; AEA12644.

Anti-CD52 antibody, useful for treating lymphoid malignancies or autoimmune conditions, is modified to reduce the number of potential T-cell epitopes to reduce undesirable immune responses to the antibody.

Example 2; SEQ ID NO 139; 171pp; English.

The invention relates to a novel anti-CD52 antibody. The novel antibody consists of a heavy chain comprising a V-region heavy chain with a substituted variant of SEQ ID NO. 1 (AEA12193) and a light chain comprising a V-region light chain with a substituted variant of SEQ ID NO. 2 (AEA12394). The invention further comprises: a pharmaceutical composition comprising the antibody and a carrier; a method for treating a lymphoid malignancy or autoimmune condition in a patient; immunosuppressing a patient prior to or subsequent to transplantation of an organ; an expression vector comprising a nucleic acid sequence coding for a V-region heavy chain comprising a substituted variant of the 121-amino acid sequence (SEQ ID NO. 1) or light chain comprising a substituted variant of the 107-amino acid sequence (SEQ ID NO. 2), operably linked to an expression control sequence; and a cultured cell comprising or transfected with the vector. The novel anti-CD52 antibody and the composition it used in have the following activities: cytostatic, antiinflammatory, antirheumatic, antiarthritic, neuroprotective, immunosuppressive, gastrointestinal-Gen., dermatological and vasotropic. The anti-CD52 antibody is useful in preparing a composition for treating lymphoid malignancies, e.g., leukemia or lymphoma, or autoimmune conditions, e.g., multiple sclerosis, rheumatoid arthritis, systemic vasculitis, uveitis, inflammatory bowel disease or scleroderma. The antibody is also useful for immunosuppressing a patient prior or subsequent to transplantation of an organ. This sequence represents a

CC human IgG1 constant region of the invention.
XX SQ Sequence 330 AA;
Query Match 99.5%; Score 1756; DB 9; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKDKVEPKSCDKTHTCPPCPAPDELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKDKVEPKSCDKTHTCPPCPAPDELGG 120
QY 121 PSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQVN 180
Db 121 PSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQVN 180
QY 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQRPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQRPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 67
AEA25942
ID AEA25942 standard; protein; 330 AA.
XX AC AEA25942;
XX DT 28-JUL-2005 (first entry)
XX DE Human immunoglobulin constant region, SEQ ID No:25.
XX KW antibody; antibody production; immunoglobulin; transformation;
XX KW expression; heavy chain constant region; light chain constant region.
XX OS Homo sapiens.
XX PN WO2005047335-A1.
XX PD 26-MAY-2005.
XX PF 13-NOV-2004; 2004WO-KR002943.
XX PR 13-NOV-2003; 2003KR-00080299.
XX PA (HANM-) HANMI PHARM CO LTD.
XX PI Jung SY, Kim JS, Park YJ, Choi K, Kwon SC, Lee GS;
XX WPI; 2005-372351/38.

Producing an immunoglobulin constant region by transforming a prokaryotic cell with a vector encoding an E. coli-derived signal sequence and an immunoglobulin constant region.

Claim 9; SEQ ID NO 25; 92pp; English.

The invention relates to a method of producing an immunoglobulin constant region on a large scale. The method comprises transforming a prokaryotic cell with a recombinant expression vector including a nucleotide sequence encoding an E. coli-derived signal sequence and a nucleotide sequence encoding an immunoglobulin constant region, culturing a resulting

antimicrobial; infection; antiinflammatory; gastrointestinal-gen.;
 gastrointestinal disease; immune disorder; inflammation; antiarthritic;
 antirheumatic; musculoskeletal disease; kidney transplant;
 Crohn's disease; rheumatoid arthritis; breast tumor; endocrine disease;
 gynecology and obstetrics; colon tumor; gastrointestinal disease; IgG1;
 z allotype.

OS Homo sapiens.
 XX WO2005070963-A1.
 PN
 XX
 XX
 PD 04-AUG-2005.
 XX
 XX 10-JAN-2005; 2005WO-US000013.
 XX
 XX 12-JAN-2004; 2004US-0535764P.
 XX
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
 XX
 XX Allan BW, Marquis DM, Tang Y, Watkins JD;
 XX WPI; 2005-542271/55.
 DR
 XX
 XX Novel anti-CD20 antibody comprising variant of parent human Fc region,
 PT useful in immunotherapy of diseases such as lymphoma, infectious disease,
 PT Crohn's disease, rheumatoid arthritis, breast and colon cancer.
 XX
 XX Disclosure; SEQ ID NO 12; 160pp; English.

The specification describes an antibody which specifically binds human
 CD20, comprising a variant of a parent human Fc region which has at least
 one amino acid substitution compared to the parent Fc region, and the
 amino acid substitution is at a position corresponding to a position of
 the human Fc sequence chosen from 247, 251, 256, 268, 280, 330, 332, 339,
 378 and 440. Antibodies of the invention mediate antibody-dependent cell-
 mediated cytotoxicity (ADCC) in the presence of effector cells or
 mediate complement-dependent cytotoxicity (CDC) more effectively than
 the antibody comprising the parent Fc region. Antibodies of the invention
 are useful in the immunotherapy of lymphoma, infectious disease, kidney
 transplant, Crohn's disease, rheumatoid arthritis, breast and colon
 cancer. They are useful as an affinity purification reagent, and in
 diagnostic assays for detecting expression of an antigen of interest in
 specific cells, tissues, or serum, and also useful in vivo diagnostic
 assays. The present sequence represents a z allotype of human IgG1,
 CC including the CH1, hinge, CH2 and CH3 regions.

XX
 SQ Sequence 330 AA;
 Query Match 99.5%; Score 1756; DB 9; Length 330;
 Best Local Similarity 99.4%; Pred. No. 2.4e-123;
 Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
 |||||
 DB 1 ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
 |||||
 QY 61 GLYSLSVVTVPSLSLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTCPPCPAPELAGA 120
 |||||
 DB 61 GLYSLSVVTVPSLSLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTCPPCPAPELGG 120
 |||||
 QY 121 PSVFLFPKPKDITLMISRTPEVTVVVDVSHEDPEVKFNWYVDGEVHNNAKTKPREQVN 180
 |||||
 DB 121 PSVFLFPKPKDITLMISRTPEVTVVVDVSHEDPEVKFNWYVDGEVHNNAKTKPREQVN 180
 |||||
 QY 181 STYRVVSVLTVLHQLWLNCKEYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 240
 |||||
 DB 181 STYRVVSVLTVLHQLWLNCKEYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 240
 |||||
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKGRW 300
 |||||
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKGRW 300
 |||||
 QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
 |||||

Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
 |||||
 RESULT 70
 AEC08181
 ID AEC08181 standard; protein; 330 AA.
 XX
 AC AEC08181;
 XX
 XX 20-OCT-2005 (first entry)
 XX
 DE Heavy chain constant region used to create anti-IgE monoclonal antibody.
 XX
 KW epitope mapping; immunoglobulin; antibody; antibody production;
 KW monoclonal antibody; heavy chain constant region; IgG1;
 KW immune stimulation; allergy; asthma; atopic dermatitis; urticaria;
 KW eczema; antiallergic; antiasthmatic; dermatological; antiinflammatory;
 KW vaccine.
 XX
 OS Homo sapiens.
 XX
 XX WO2005075504-A1.
 XX
 PD 18-AUG-2005.
 XX
 XX 29-JUL-2004; 2004WO-US024360.
 XX
 XX 02-FEB-2004; 2004WO-US002892.
 PR
 PR 02-FEB-2004; 2004WO-US002894.
 XX
 XX (TANO-) TANOX INC.
 PA
 PI Singh S, Huang D, Fung SCM;
 XX WPI; 2005-564560/57.
 DR
 XX New isolated peptides useful for inducing an immunological response in
 PT mammals or for treating or preventing allergic conditions, such as
 PT asthma, atopic dermatitis, urticaria or eczema.
 XX
 XX Example 11; SEQ ID NO 60; 110pp; English.

The invention relates to the isolation of novel peptide epitopes derived
 from the CH3 domain of immunoglobulin E (IgE) which are recognized by
 high affinity antibodies that bind specifically to IgE. The novel IgE
 epitopes are useful for active or passive immunization of a mammal. The
 isolated IgE peptide epitope preferably comprises an amino acid sequence
 selected from a fully defined sequence given as SEQ ID Nos 72-77 in the
 specification. Also described are: (1) methods for preparing or making a
 polyclonal or monoclonal antibodies; (2) a polyclonal or monoclonal
 polyclonal or monoclonal antibodies; (3) an isolated antibody
 antibody (mAb) produced by the above method; (4) a composition
 that specifically binds to the above peptide; (5) a composition
 comprising the above peptide or (polyclonal or monoclonal) antibody, and
 a physiological carrier, diluent, stabilizer or excipient; (6) a kit
 comprising the antibody cited above; (7) a method of inducing an
 immunological response to IgE in a mammal; (8) an isolated nucleic acid
 encoding the above peptide; and (9) vectors and host cells comprising the
 nucleic acid cited above. The composition and methods of the invention
 are useful for inducing an immunological response in mammals, or for
 treating or preventing allergic conditions (e.g. asthma, atopic
 dermatitis, urticaria or eczema). This sequence represents a heavy chain
 constant region from human IgG1 that is used to create an anti-IgE
 monoclonal antibody in the examples of the present invention.

XX
 SQ Sequence 330 AA;
 Query Match 99.5%; Score 1756; DB 9; Length 330;
 Best Local Similarity 99.4%; Pred. No. 2.4e-123;
 Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
 |||||

Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCCPPCAPPELAGA 120
Db 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCCPPCAPPELLGG 120
QY 121 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 121 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
QY 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYVTLPPSRDE 240
Db 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYVTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGYFSPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKGRW 300
Db 241 LTKNQVSLTCLVKGYFSPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKGRW 300
QY 301 QQGNVFSCVMEALHNHYTQKSLSLSPCK 330
Db 301 QQGNVFSCVMEALHNHYTQKSLSLSPCK 330

RESULT 71
AEC81727
ID AEC81727 standard; protein; 330 AA.
XX AC AEC81727;
XX DT 01-DEC-2005 (first entry)
XX DE Human immunoglobulin gamma 1 heavy chain.
XX KW Fusion protein; protein production; immunoglobulin; IgG; antibody;
XX KW heavy chain.
XX OS Homo sapiens.

XX FH Key Location/Qualifiers
FT Domain 1..98
FT /label = CH1
FT Region 99..113
FT /label = Hinge
FT Misc-difference 103
FT /note = "Cys residue involved in disulfide bonding to the
FT light chain constant region"
FT Misc-difference 109
FT /note = "Cys residue involved in disulfide bonding to the
FT heavy chain constant region"
FT Misc-difference 112
FT /note = "Cys residue involved in disulfide bonding to the
FT heavy chain constant region"
FT Domain 114..223
FT /label = CH2
FT Domain 224..330
FT /label = CH3

XX WO2005087810-A2.
XX 22-SEP-2005.
XX 08-MAR-2005; 2005WO-US007590.
XX 08-MAR-2004; 2004US-0551174P.
XX (ZYMO) ZYMOGENETICS INC.
XX Moore MD, Fox BA;
XX WPI; 2005-630945/64.
XX New dimeric protein comprising a first polypeptide fusion disulfide
PT bonded to a second polypeptide fusion, useful as cytokine antagonist for

PT treating cancers, or as growth factor agonist for promoting tissue
PT growth.
XX Example 1; SEQ ID NO 1; 85pp; English.
XX
CC The present invention relates to dimeric fusion proteins and methods of
CC making them. A claimed dimeric protein comprises a first polypeptide
CC fusion disulfide bonded to a second polypeptide fusion. The first
CC polypeptide fusion has the formula P1-L1-D1-(P2)n, where: P1 is a first
CC non-immunoglobulin polypeptide; L1 is a first polypeptide linker of 18-32
CC amino acid residues where x of these residues are Cys residues; D1 is a
CC first dimerizing domain selected from an immunoglobulin CH1 domain, a T-
CC cell receptor C alpha domain, a T-cell receptor C beta domain, a major
CC histocompatibility complex (MHC) class I alpha 3 domain, beta2-
CC microglobulin, a MHC class II alpha 2 domain, and a MHC class II beta 2
CC domain; P2 is a linking polypeptide of 1-29 amino acid residues where at
CC least one residue is Cys; and n is 0 or 1. The second polypeptide fusion
CC has the formula P3-L2-D2, where: P3 is a second non-immunoglobulin
CC polypeptide; L2 is a second polypeptide linker of 18-32 amino acid
CC residues, where y of these residues are Cys residues; and D2 is a second
CC dimerizing domain selected from an immunoglobulin light chain constant
CC domain, a T-cell receptor C alpha domain, a T-cell receptor C beta
CC domain, a MHC class I alpha 3 domain, beta2-microglobulin, a MHC class II
CC alpha 2 domain and a MHC class II beta 2 domain. In the dimeric protein,
CC each of x and y is an integer of 1-8, and x=y. Also claimed are dimeric
CC proteins in which: P1 and P3 are different; n=1; x=2 and y=2; each of P1
CC and P3 is an extracellular domain of a cell surface receptor, including a
CC human cell surface receptor; each of P1 and P3 is not a member of the
CC immunoglobulin superfamily; and each of P1 and P3 is individually
CC selected from interleukin-17 receptor, interleukin-20 receptor A or B,
CC interleukin-21 receptor, interleukin-28 receptor A, interleukin-31
CC receptor A, CRF2-4 or gammaC. In a further claimed polypeptide fusion, D1
CC is an immunoglobulin CH1 domain, and D2 is an immunoglobulin kappa light
CC chain constant domain or immunoglobulin lambda light chain constant
CC domain. In a further claimed dimeric protein: (a) one of P1 and P3 is a
CC zcytor7 extracellular domain and the other of P1 and P3 is a DIRS1
CC extracellular domain; (b) one of P1 and P3 is a zcytor11 extracellular
CC domain and the other of P1 and P3 is a DIRS1 extracellular domain; (c)
CC one of P1 and P3 is a zalphall extracellular domain and the other of P1
CC and P3 is an interleukin-2 receptor gamma common extracellular domain; or
CC (d) one P1 and P3 is a PDGF alpha receptor extracellular domain and the
CC other of P1 and P3 is a PDGF beta receptor extracellular domain. Also
CC claimed are polypeptide fusions of formula P1-L-D1-(P2)n and P3-L-D2,
CC polynucleotides encoding each polypeptide fusion, expression vectors,
CC cultured cells, and a method of making the dimeric proteins of the
CC invention by culturing cells comprising first and second expression units
CC such that the encoded polypeptide fusions are produced as a dimeric
CC protein. A dimeric protein consisting of 2 polypeptide chains joined via
CC at least one disulfide bond, where each polypeptide chain is a
CC polypeptide fusion of formula P3-L-D2, and a method of making this
CC dimeric protein, are also claimed. The dimeric proteins of the invention
CC can be used for diagnosis, therapy, or research to provide one or more
CC activities associated with the first and second non-immunoglobulin
CC polypeptides. Such activities include receptor binding, receptor
CC activation and ligand binding. Therapeutic uses include use as cytokine
CC antagonists for treatment of cancers or immunological disorders, growth
CC factor agonists to promote tissue growth or healing or to promote
CC development of vasculature or other tissue. Diagnostic uses include use
CC as targeting agents for radioisotopes or other labels. The present
CC sequence is that of the human immunoglobulin gamma 1 heavy chain, which
CC includes a CH1 domain and hinge region that can be used in polypeptide
CC fusions of the invention.
XX SQ Sequence 330 AA;

Query Match 99.5%; Score 1756; DB 9; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

CC antibody is administered in combination with a second agent consisting of
CC a neuroprotective, neuroreparative, neurotrophic, neurorestorative,
CC neurogenerative or neuroconstructive agent. the present sequence
CC represents a human immunoglobulin G1 heavy chain constant domain amino
CC acid sequence, which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 330 AA;

Query Match 99.5%; Score 1756; DB 9; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLSS 60

QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
DB 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPELAGG 120

QY 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
DB 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180

QY 181 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240
DB 181 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300

QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 74
AED41916
ID AED41916 standard; protein; 330 AA.
XX
AC AED41916;
XX
DT 15-DEC-2005 (first entry)
XX
DE Deimmunized PSMA J591 heavy chain constant region.
XX
KW prostate tumor; cytostatic; andrology; genitourinary disease; neoplasm;
KW antibody; prostate specific membrane antigen; PSMA;
KW heavy chain constant region.
XX
OS Mus musculus.
XX
PN WO2005094882-A1.
XX
PD 13-OCT-2005.
XX
PF 03-MAR-2004; 2004WO-US006543.
XX
PR 03-MAR-2004; 2004WO-US006543.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Horvath CJ, Webb IJ;
XX
DR WPI; 2005-703269/72.
XX
DR N-PSDB; AED41915.
XX
PT Treating prostate cancer in a subject by administering to the subject 2-
PT 24 doses of an antibody or its antigen binding fragment that binds to the
PT extracellular domain of prostate specific membrane antigen (PSMA), and is
PT coupled to DM1.

XX Disclosure; SEQ ID NO 136; 291pp; English.
XX
CC The invention relates to a method of treating prostate cancer, in a
CC subject which comprises administering to the subject two to twenty-four
CC doses of an antibody or its antigen binding fragment, which binds to the
CC extracellular domain of prostate specific membrane antigen (PSMA) and
CC which is coupled to DM1, where each dose comprises 175-500 mg/m2 of the
CC antibody or its antigen binding fragment, to thus treat the subject. The
CC method is useful for treating prostate cancer. The present sequence
CC represents the amino acid sequence of a mouse prostate specific membrane
CC antigen (PSMA) antibody heavy chain.
XX
SQ Sequence 330 AA;

Query Match 99.5%; Score 1756; DB 9; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLSS 60

QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
DB 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPELAGG 120

QY 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
DB 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180

QY 181 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240
DB 181 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300

QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 75
AED28069
ID AED28069 standard; protein; 330 AA.
XX
AC AED28069;
XX
DT 15-DEC-2005 (first entry)
XX
DE Human gamma1 heavy chain constant region (CH) L234A/L235A (IgG1v2).
XX
KW Gene therapy; antibody therapy; inflammation; antiinflammatory;
KW thrombosis; anticoagulant; thrombolytic; cardiovascular disease;
KW hematological disease; peripheral arterial occlusive disease; vasotropic;
KW ischemia; antibody; heavy chain constant region; IgG; immunoglobulin;
KW mutein.
XX
OS Homo sapiens.
XX
PN US2005226876-A1.
XX
PD 13-OCT-2005.
XX
PF 08-APR-2005; 2005US-00102403.
XX
PR 13-APR-2004; 2004EP-00008722.
XX
PA (GRAU/) GRAUS Y.
PA (HIMB/) HIMBER J.
PA (JANS/) JANSEN-MOLENAAR M.

PA (KLIN/) KLING D.
PA (KOPE/) KOPETZKI E.
PA (PARR/) PARREN P.
PA (REBE/) REBERS F.
PA (STEI/) STEINER B.
PA (STER/) STERN A.
PA (STRE/) STREIN P.
PA (STUB/) STUBENRAUCH K.
PA (VWIN/) VAN DE WINKEL J.
PA (VVUG/) VAN VUGT M.
XX
PI Graus Y, Himber J, Jansen-Molenaar M, Kling D, Kopetzki E;
PI Parren P, Rebers F, Steiner B, Stern A, Strein P, Stubenrauch K;
PI Van De Winkel J, Van Vugt M;
XX
DR WPI; 2005-723886/74.
XX
XX New antibody containing a Fc part from human origin, binding to P-
PT selectin and non-binding to complement factor C1q, for preparing a
PT medicament for treating e.g., peripheral arterial occlusive disease.
XX
XX Example; SEQ ID NO 26; 50pp; English.
XX
XX The invention relates to an antibody containing a Fc part from human
CC origin, binding to P-selectin (CD62P, GMP-140, PADGEM or LECAM-3) and non
CC -binding to complement factor C1q. The anti-P-selectin antibody is useful
CC in preparing a medicament for treating inflammatory or thrombotic
CC disorders, preferably peripheral arterial occlusive disease (PAOD) or
CC critical limb ischemia (CLI). It is also useful in gene therapy and in
CC antibody therapy. The present sequence is the human Ig gammal heavy chain
CC constant region L234A/L235A (IgG1v1). This sequence is used in the
CC construction of expression plasmids for an anti-P-selectin IgG1 HuMab.
XX
SQ Sequence 330 AA;

Query Match 99.5%; Score 1756; DB 9; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNNTKVDKVEPKSCDKTHTCPPCPAPEAAGG 120
QY 121 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 181 STYRVSVVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFYLKSLYTDKGRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFYLKSLYTDKGRW 300
QY 301 QGQNVFSCSVMEALHNHYTQKSLSLSPCK 330
DB 301 QGQNVFSCSVMEALHNHYTQKSLSLSPCK 330

RESULT 76
AED28067
ID AED28067 standard; protein; 330 AA.
XX
AC AED28067;
XX
DT 15-DEC-2005 (first entry)
XX
DE Human Iggamma1 heavy chain constant region (CH).

XX
KW Gene therapy; antibody therapy; inflammation; antiinflammatory;
KW thrombosis; anticoagulant; thrombolytic; cardiovascular disease;
KW hematological disease; peripheral arterial occlusive disease; vasotropic;
KW ischemia; antibody; heavy chain constant region; IgG; immunoglobulin.
XX
OS Homo sapiens.
XX
PN US2005226876-A1.
XX
XX 13-OCT-2005.
XX
PF 08-APR-2005; 2005US-00102403.
XX
PR 13-APR-2004; 2004EP-00008722.
XX
PA (GRAU/) GRAUS Y.
PA (HIMB/) HIMBER J.
PA (JANS/) JANSSEN-MOLENAAR M.
PA (KLIN/) KLING D.
PA (KOPE/) KOPETZKI E.
PA (PARR/) PARREN P.
PA (REBE/) REBERS F.
PA (STEI/) STEINER B.
PA (STER/) STERN A.
PA (STRE/) STREIN P.
PA (STUB/) STUBENRAUCH K.
PA (VWIN/) VAN DE WINKEL J.
PA (VVUG/) VAN VUGT M.
XX
PI Graus Y, Himber J, Jansen-Molenaar M, Kling D, Kopetzki E;
PI Parren P, Rebers F, Steiner B, Stern A, Strein P, Stubenrauch K;
PI Van De Winkel J, Van Vugt M;
XX
DR WPI; 2005-723886/74.
XX
XX New antibody containing a Fc part from human origin, binding to P-
PT selectin and non-binding to complement factor C1q, for preparing a
PT medicament for treating e.g., peripheral arterial occlusive disease.
XX
XX Disclosure; SEQ ID NO 24; 50pp; English.
XX
XX The invention relates to an antibody containing a Fc part from human
CC origin, binding to P-selectin (CD62P, GMP-140, PADGEM or LECAM-3) and non
CC -binding to complement factor C1q. The anti-P-selectin antibody is useful
CC in preparing a medicament for treating inflammatory or thrombotic
CC disorders, preferably peripheral arterial occlusive disease (PAOD) or
CC critical limb ischemia (CLI). It is also useful in gene therapy and in
CC antibody therapy. The present sequence is the human Ig gammal heavy chain
CC constant region. This sequence is used in the construction of expression
CC plasmids for an anti-P-selectin IgG1 HuMab.
XX
SQ Sequence 330 AA;

Query Match 99.5%; Score 1756; DB 9; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNNTKVDKVEPKSCDKTHTCPPCPAPELGG 120
QY 121 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 181 STYRVSVVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

QY 241 LTKQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
 DB 241 LTKQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
 QY 301 QQGNVFCSCVMHEALHNHYTKLSLSPGK 330
 DB 301 QQGNVFCSCVMHEALHNHYTKLSLSPGK 330

RESULT 77
 AEF11770
 ID AEF11770 standard; protein; 330 AA.
 XX AEF11770;
 AC AEF11770;
 DT 09-MAR-2006 (first entry)
 DE Human SCF-binding Ab A2-G8 heavy chain constant region.
 XX antibody therapy; antibody engineering; asthma; inflammation;
 KW antiasthmatic; stem cell factor; SCF; heavy chain constant region.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO2006002064-A2.
 FN 05-JAN-2006.
 PD 14-JUN-2005; 2005WO-US021043.
 PF 14-JUN-2004; 2004US-00867506.
 PR 14-JUN-2004; 2004US-0579462P.
 XX (ABRO-) AEROVANCE INC.
 XX Neben S, Takeuchi T, Tomkinson A, Delaria K, Yan K, Wong T;
 PI Longphre M;
 XX WPI; 2006-079812/08.
 DR N-PSDB; AEF11769.
 XX
 PT New purified human antibody, which binds to stem cell factor protein,
 PT useful for treating asthma or a human disorder in which stem cell factor
 PT protein is expressed in certain cells.
 XX
 PS Example 10; SEQ ID NO 81; 108pp; English.
 XX
 CC The invention relates to: a purified human antibody (IgG) or fragment
 CC thereof which binds to stem cell factor protein; a preparation comprising
 CC the antibody, and/or a carrier; isolated polynucleotide(s) encoding the
 CC antibody; an expression vector comprising the polynucleotide(s); a host
 CC cell comprising the expression vector; a method of producing a human
 CC antibody; a method of treating asthma or a human disorder in which stem
 CC cell factor protein is expressed in certain cells; and a method for
 CC identifying a disorder in which stem cell factor protein level is
 CC elevated. The purified human antibody comprises the heavy chain variable
 CC region human VH3 consensus framework residues, the light chain variable
 CC region human V-kappa-1 or V-lambda-1 consensus framework residues, and
 CC may be optionally bound to a cytotoxic molecule or detectable label. The
 CC antibody, compositions and methods are useful for treating asthma or a
 CC human disorder in which stem cell factor protein is expressed in certain
 CC cells. This sequence is a human stem cell factor-binding antibody A2-G8
 CC heavy chain constant region.
 XX Sequence 330 AA;
 SQ

Query Match 99.5%; Score 1756; DB 10; Length 330;
 Best Local Similarity 99.4%; Pred. No. 2.4e-123;
 Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
 QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
 DB 61 GLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELGG 120
 QY 121 PSVELFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVFNATKPREEQYN 180
 DB 121 PSVELFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVFNATKPREEQYN 180
 QY 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSRDE 240
 DB 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSRDE 240
 QY 241 LTKQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
 DB 241 LTKQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
 QY 301 QQGNVFCSCVMHEALHNHYTKLSLSPGK 330
 DB 301 QQGNVFCSCVMHEALHNHYTKLSLSPGK 330

RESULT 78
 AEF16289
 ID AEF16289 standard; protein; 330 AA.
 XX AEF16289;
 AC AEF16289;
 DT 09-MAR-2006 (first entry)
 DE Humanized antibody, Hu1D10, heavy chain constant region.
 XX monoclonal antibody; humanized antibody; immunoglobulin; Hu1D10; IgG;
 KW heavy chain constant region; antibody engineering; therapeutic; vaccine;
 KW cancer; neoplasm; inflammation; asthma; autoimmune disease;
 KW viral infection; cytostatic; antiinflammatory; antiasthmatic;
 KW immunosuppressive; virucide.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO2005123780-A2.
 FN 29-DEC-2005.
 PD 08-APR-2005; 2005WO-US011996.
 PF 09-APR-2004; 2004US-00822300.
 PR 09-APR-2004; 2004WO-US011213.
 XX (PROT-) PROTEIN DESIGN LABS INC.
 XX Hinton PR, Tsurushita N, Tso YJ, Vasquez M;
 PI WPI; 2006-067459/07.
 DR
 XX New modified monoclonal antibody of class IgG with altered FcRn binding
 PT affinity, useful for treating a condition, e.g. cancer, inflammatory
 PT conditions such as asthma, autoimmune diseases, or viral infections.
 XX
 PS Disclosure; SEQ ID NO 7; 310pp; English.
 XX
 CC The invention relates to modified monoclonal antibodies of class IgG with
 CC FcRn binding affinity altered relative to that of an unmodified
 CC monoclonal antibody of class IgG. The modified monoclonal antibody of
 CC class IgG comprises a heavy chain constant region where at least amino
 CC acid residues 250 and 428 are different from the residues present in the
 CC unmodified monoclonal antibody and where the unmodified monoclonal
 CC antibody is selected from the group consisting of an anti-CD25, an anti-
 CC CD3, an anti-IFNgamma, or an anti-alphasbeta1 integrin. Also disclosed
 CC are: (1) a method of modifying an antibody of class IgG; (2) a method of

CC producing a modified antibody of class IgG with an altered binding
CC affinity for FcRn and/or an altered serum half life as compared with an
CC unmodified antibody; (3) a vector comprising a polynucleotide encoding
CC one or more heavy or light chain sequences; (4) a host cell comprising
CC the vector; and (5) polynucleotide sequences encoding the modified
CC antibodies. The unmodified monoclonal antibody is an anti-CD25 of IgG1 or
CC IgG2M3 isotype. The modified antibodies of the invention can be used in
CC prophylactic and therapeutic compositions, such as vaccines, for treating
CC a condition, e.g. cancer, inflammatory conditions such as asthma,
CC autoimmune diseases, or viral infections. The antibodies can also be used
CC in diagnostic applications. This sequence represents a region of a
CC humanized antibody.

XX Sequence 330 AA;
Query Match 99.5%; Score 1756; DB 10; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHHTCPPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHHTCPPCPAPELGG 120
QY 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QGQNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QGQNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 79
AEF16285
ID AEF16285 standard; protein; 330 AA.
XX AEF16285;
AC AEF16285;
XX
XX 09-MAR-2006 (first entry)
DE Human OST577-IgG1 antibody, heavy chain constant region.
XX
XX monoclonal antibody; immunoglobulin; OST577; IgG1;
KW heavy chain constant region; antibody engineering; therapeutic; vaccine;
KW cancer; neoplasm; inflammation; asthma; autoimmune disease;
KW viral infection; cytostatic; antiinflammatory; antiasthmatic;
KW immunosuppressive; virucide.
XX
OS Homo sapiens.
XX
XX WO2005123780-A2.
XX
XX 29-DEC-2005.
XX
XX 08-APR-2005; 2005WO-US011996.
XX
XX 09-APR-2004; 2004US-00822300.
XX
XX 09-APR-2004; 2004WO-US011213.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.

PI Hinton PR, Tsurushita N, Tso YJ, Vasquez M;
DR WPI; 2006-067459/07.
XX
XX New modified monoclonal antibody of class IgG with altered FcRn binding
PT affinity, useful for treating a condition, e.g. cancer, inflammatory
PT conditions such as asthma, autoimmune diseases, or viral infections.
XX
XX Disclosure; SEQ ID NO 3; 310pp; English.
XX
CC The invention relates to modified monoclonal antibodies of class IgG with
CC FcRn binding affinity altered relative to that of an unmodified
CC monoclonal antibody of class IgG. The modified monoclonal antibody of
CC class IgG comprises a heavy chain constant region where at least amino
CC acid residues 250 and 428 are different from the residues present in the
CC unmodified monoclonal antibody and where the unmodified monoclonal
CC antibody is selected from the group consisting of an anti-CD25, an anti-
CC CD3, an anti-IFNgamma, or an anti-alphabeta1 integrin. Also disclosed
CC are: (1) a method of modifying an antibody of class IgG; (2) a method of
CC producing a modified antibody of class IgG with an altered binding
CC affinity for FcRn and/or an altered serum half life as compared with an
CC unmodified antibody; (3) a vector comprising a polynucleotide encoding
CC one or more heavy or light chain sequences; (4) a host cell comprising
CC the vector; and (5) polynucleotide sequences encoding the modified
CC antibodies. The unmodified monoclonal antibody is an anti-CD25 of IgG1 or
CC IgG2M3 isotype. The modified antibodies of the invention can be used in
CC prophylactic and therapeutic compositions, such as vaccines, for treating
CC a condition, e.g. cancer, inflammatory conditions such as asthma,
CC autoimmune diseases, or viral infections. The antibodies can also be used
CC in diagnostic applications. This sequence represents a region of the
CC human anti-hepatitis B virus antibody OST577-IgG1.

XX Sequence 330 AA;

Query Match 99.5%; Score 1756; DB 10; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHHTCPPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHHTCPPCPAPELGG 120
QY 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QGQNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QGQNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 80
AEF51200
ID AEF51200 standard; protein; 330 AA.
XX AEF51200;
XX
XX 23-MAR-2006 (first entry)
XX
XX Human immunoglobulin G1 Fc amino acid sequence SEQ ID NO:1.
XX

KW immunoglobulin; antibody; immunoglobulin G1; IgG1; immunosuppressive;
KW antinflammatory; antibacterial; virucide; fungicide; protozoacide;
KW antiparasitic; cytostatic; antibody therapy; autoimmune disease;
KW inflammation; infectious disease; cancer.
XX Homo sapiens.
XX US2006024298-A1.
XX PD 02-FEB-2006.
XX PF 05-MAY-2005; 2005US-00124620.
XX PR 03-MAR-2003; 2003US-00379392.
XX PR 26-SEP-2003; 2003US-00672280.
XX PR 26-MAR-2004; 2004US-00822231.
XX PA (XENC-) XENCOR INC.
XX PI Lazar GA, Dang W, Desjarlais JJ, Karki SB, Vafa O, Hayes R;
XX DR WPI; 2006-117602/12.
XX New protein comprising an Fc variant of a human Fc polypeptide, where the
PT variant exhibits altered binding to an Fc ligand as compared to human Fc
PT polypeptide, useful for treating or preventing autoimmune or inflammatory
PT diseases.
XX Claim 1; SEQ ID NO 1; 138pp; English.
XX The invention relates to a protein comprising an Fc variant of a human Fc
CC polypeptide comprising the 330 amino acid sequence of AEF51200, where the
CC variant exhibits altered binding to an Fc ligand as compared to human Fc
CC polypeptide, where the variant comprises Formula (I), and where the
CC variant comprises 1-4 amino acid substitutions as compared to AEF51200.
CC Also described: (1) a method for engineering optimized Fc variants; (2)
CC an isolated nucleic acid encoding the Fc variants; (3) vectors containing
CC the nucleic acids; (4) host cells containing the vectors; (5) a method
CC for producing the Fc variants; and (6) a composition comprising the Fc
CC polypeptides. The protein is useful for diagnosing, treating, and
CC preventing autoimmune and inflammatory diseases, infectious diseases, and
CC cancers. It can also be used for preventing or treating congestive heart
CC failure, myocarditis, acne, osteoporosis, periodontal disease,
CC osteomalacia, bone metastasis, bone pain management, humoral malignant
CC hypercalcaemia, periodontal reconstruction, spinal cord injury, and bone
CC fractures; metabolic conditions such as Gaucher's disease; endocrine
CC conditions such as Cushing's syndrome; and neurological conditions. The
CC present sequence represents a human immunoglobulin G1 (IgG1) Fc amino
CC acid sequence, which is used in the exemplification of the present
CC invention.
XX Sequence 330 AA;
SQ

Query Match 99.5%; Score 1756; DB 10; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0,
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPPSSSLGQTQYICNVNHPKSTKVDKKVEPKSCDKTHRTCPCPAPELAGA 120
DB 61 GLYSLSVVTVPPSSSLGQTQYICNVNHPKSTKVDKKVEPKSCDKTHRTCPCPAPELGG 120
QY 121 PSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVEVHNAKTKPREQYN 180
DB 121 PSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVEVHNAKTKPREQYN 180
QY 181 STYRVSVSLTVLHQDLNGKEYCKCKSNKALPAPIEKTISKAKGQRPFPVYITPPSRDE 240
DB 181 STYRVSVSLTVLHQDLNGKEYCKCKSNKALPAPIEKTISKAKGQRPFPVYITPPSRDE 240

QY 241 LTKQVSLTCLVKGFPYPSDIAVEHESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
DB 241 LTKQVSLTCLVKGFPYPSDIAVEHESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
QY 301 QQGNVFCSCVMHEALHNNHYTKSLSLSPGK 330
DB 301 QQGNVFCSCVMHEALHNNHYTKSLSLSPGK 330
RESULT 81
AEF82207
ID AEF82207 standard; protein; 330 AA.
XX AC AEF82207;
XX DT 06-APR-2006 (first entry)
XX DE Human immunoglobulin G1 heavy chain constant region protein.
XX KW immunogenicity; fusion protein; immunoglobulin;
KW heavy chain constant region.
XX OS Homo sapiens.
XX PN US2006025573-A1.
XX PD 02-FEB-2006.
XX PF 23-SEP-2005; 2005US-00233683.
XX PR 30-MAR-2001; 2001US-0280625P.
XX PR 29-MAR-2002; 2002US-00112582.
XX PA (MERE) MERCK PATENT GMBH.
XX PI Gillies SD, Way J, Hamilton AA;
XX DR WPI; 2006-201465/21.
XX Reducing immunogenicity of fusion protein, by identifying T-cell epitope
PT within a junction region, and making amino acid substitutions or
PT deletions to reduce the ability of T-cell epitope to interact with T cell
PT receptor.
XX Disclosure; SEQ ID NO 1; 34pp; English.
XX The invention relates to a method for reducing the immunogenicity of a
CC fusion protein. The method comprises: (a) identifying a candidate T-cell
CC epitope within a junction region spanning a fusion junction of a fusion
CC protein, where the fusion protein comprises an immunoglobulin moiety
CC fused to a non-immunoglobulin moiety; and (b) making one or more amino
CC acid substitutions or deletions within the junction region to reduce the
CC ability of the candidate T-cell epitope to interact with a T cell
CC receptor. Also described: (1) a fusion protein produced by the method
CC above; (2) a fusion protein with reduced immunogenicity comprising a non-
CC immunoglobulin protein and an immunoglobulin protein fused to the non-
CC immunoglobulin protein via a fusion junction, where the amino acid
CC sequence of a junction region surrounding the fusion junction is modified
CC by substitution or deletion of one or more amino acids to remove a non-
CC self T-cell epitope; and (3) a nucleic acid encoding a fusion protein
CC with reduced immunogenicity, the fusion protein comprising an
CC immunoglobulin protein, and a non-immunoglobulin protein fused to the
CC immunoglobulin protein via a fusion junction, where the amino acid
CC sequence of a junction region spanning the fusion junction is modified to
CC remove a non-self T-cell epitope. The compositions and methods are useful
CC for producing fusion proteins, e.g. immunocytokines, immunofusins,
CC immunoligands, other antibody and Fc fusion proteins, cytokine-cytokine
CC fusion proteins, and albumin fusion proteins, with reduced
CC immunogenicity, which are useful in therapy. The present sequence
CC represents a human immunoglobulin gamma 1 (IgG1) heavy chain constant
CC (Fc) region amino acid sequence, which is used in the exemplification of
CC the present invention.
XX

SQ Sequence 330 AA;
Query Match 99.5%; Score 1756; DB 10; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNITKVDKVEPKSCDKTHTCPPCPAPELAGA 120
DB 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNITKVDKVEPKSCDKTHTCPPCPAPELAGG 120
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNNYVGVGVVHNAKTKPREEQYN 180
DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNNYVGVGVVHNAKTKPREEQYN 180
QY 181 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 181 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKGRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKGRW 300
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
RESULT 82
ID AEG11432 standard; protein; 330 AA.
AC AEG11432;
XX
DT 20-APR-2006 (first entry)
DE Immunoglobulin G1 (IgG1) kappa constant domain SEQ ID NO 81.
XX
KW cytostatic; neuroprotective; virucide; immunosuppressive; antiarthritic;
KW anti-HIV; procoagulant; antiinflammatory; gastrointestinal-gen.;
KW antiallergic; vasotropic; diagnosis; prognosis; therapeutic; screening;
KW antibody; cancer; neoplasm; hyperproliferation; inflammation;
KW autoimmune disease; immune disorder; rheumatoid arthritis; antirheumatic;
KW musculoskeletal disease; graft versus host disease; Crohns disease;
KW gastrointestinal disease; Wegener granulomatosis;
KW neurodegenerative disease; neuroprotective; neurological disease;
KW viral infection; infection; HIV infection; cytomegalovirus infection;
KW Pneumocystitis carinii infection; Kaposi's sarcoma; dermatological disease;
KW light chain constant region.
XX
OS Homo sapiens.
XX
FN WO2005105841-A2.
XX
PD 10-NOV-2005.
XX
PF 11-MAR-2005; 2005WO-US008377.
XX
PR 12-MAR-2004; 2004US-0552184P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Roschke V, Rosen CA, Ruben SM;
XX
DR WPI; 2006-231015/24.
XX
PT New antibody that immunospecifically binds G-protein Chemokine Receptor
PT (CCR5) polypeptide, useful in preparing a composition for treating or
PT preventing e.g., rheumatoid arthritis, neurodegenerative disease or viral
PT infection.

XX Disclosure; SEQ ID NO 81; 523pp; English.
XX The invention describes a new isolated antibody that immunospecifically
CC binds G-protein Chemokine Receptor (CCR5) polypeptide comprising a first
CC or second amino acid sequence that is at least 85, 90, 95, 96, 97, 98, 99
CC or 100% identical to an amino acid sequence of the VH or VL domain,
CC respectively, of the antibody expressed by the hybridoma cell line
CC deposited under ATCC Deposit No. PTA-5861. Also described are: a
CC polynucleotide encoding at least the VH or VL domain of the isolated
CC antibody; a vector comprising the polynucleotide; a host cell comprising
CC the vector or polynucleotide; a cell line engineered to express the
CC antibody; a method of making an antibody; a method of detecting the
CC expression of a CCR5 polypeptide; a method of detecting, diagnosing,
CC prognosing or monitoring cancer or other hyperproliferative disorders;
CC and a kit comprising the antibody. The isolated antibody is useful in
CC preparing a composition for treating or preventing a disease or disorder,
CC e.g., a disease or disorder associated with inflammation, defective or
CC aberrant chemotaxis of immune cells or T-cell antigen presenting cell
CC interaction, a disease or disorder associated with lack of CCR5 function
CC or of aberrant CCR5 ligand expression, autoimmune disease, rheumatoid
CC arthritis, graft-versus-host disease, Crohn's disease, Wegner's
CC granulomatosis, neurodegenerative disease, or viral, HIV,
CC cytomegalovirus, poxvirus, Pneumocystitis carinii infection or Kaposi's
CC sarcoma. This is the amino acid sequence of human IgG1 kappa constant
CC domain.
XX
SQ Sequence 330 AA;
Query Match 99.5%; Score 1756; DB 10; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNITKVDKVEPKSCDKTHTCPPCPAPELAGA 120
DB 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNITKVDKVEPKSCDKTHTCPPCPAPELAGG 120
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNNYVGVGVVHNAKTKPREEQYN 180
DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNNYVGVGVVHNAKTKPREEQYN 180
QY 181 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 181 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKGRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKGRW 300
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
RESULT 83
ADL35095
ID ADL35095 standard; protein; 332 AA.
XX
AC ADL35095;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human IgG1 (hOAT) kappa heavy chain constant domain protein SeqID 98.
XX
KW antibody; variable domain; framework region; FR; huFR;
KW immune system molecule; kappa; anti-tissue factor; hOAT; human.
XX
OS Homo sapiens.
XX

PN WO2004020579-A2.
XX
PD 11-MAR-2004.
XX
PF 06-AUG-2003; 2003WO-US024637.
XX
PR 29-AUG-2002; 2002US-00230880.
XX
PA (SUNO-) SUNOL MOLECULAR CORP.
XX
XX Wong HC, Stinson JR, Mosquera LA;
XX WPI; 2004-239169/22.
XX
PT Producing humanized antibodies for diagnostic and therapeutic purposes
PT comprises optimizing similarity between individual antibody framework
PT regions to help identify human framework regions suitable for making the
PT antibodies.
XX
PS Disclosure; SEQ ID NO 98; 137pp; English.
XX
XX This invention relates to a novel method for producing a humanised
CC antibody variable (V) domain or its fragment by optimising sequence
CC similarity between individual antibody framework regions (FRs) in order
CC to identify suitable human FRs (huFRs). Specifically, it refers to novel
CC immune system molecules i.e. humanised monoclonal antibodies that exhibit
CC suitable binding affinity with reduced immunogenicity in humans. The
CC present invention describes a method of mutagenising DNA of non-human FRs
CC to encode humanised FRs having an amino acid sequence that is
CC substantially identical to the selected human FR previously identified
CC through sequence similarity searching. As such, this method provides
CC a humanised light or heavy chain V domains of the sequence huFR1-huFR2
CC -CDR2-huFR3-CDR3-huFR4, which can be used as therapeutic or diagnostic
CC products to treat and/or diagnose diseases in humans and animals.
CC Furthermore, the method expands the number of best fit possibilities that
CC can be generated and provides a rational basis for assembling nearly all
CC humanised immune system molecules of interest. This polypeptide sequence
CC is the human IgG1 kappa heavy chain constant domain protein of the
CC invention.
XX
SQ Sequence 332 AA;

Query Match 99.5%; Score 1756; DB 8; Length 332;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
DB 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 62
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 63 GLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTCPCPAPELGG 122
QY 121 PSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
DB 123 PSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQIN 182
QY 181 STYRVSVSLTVLHQLDLNGKEYCKKVSNKALPAPIEKTISKAKGQPREPQVYVTPPSRDE 240
DB 183 STYRVSVSLTVLHQLDLNGKEYCKKVSNKALPAPIEKTISKAKGQPREPQVYVTPPSRDE 242
QY 241 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFLYSKLTVDKSRW 300
DB 243 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFLYSKLTVDKSRW 302
QY 301 QGQNVFSCVMHEALHNYHTQKSLSPGK 330
DB 303 QGQNVFSCVMHEALHNYHTQKSLSPGK 332
RESULT 84
ADM07455

ID ADM07455 standard; protein; 332 AA.
XX
AC ADM07455;
XX
DT 07-APR-2005 (first entry)
XX
DE Human IgG1 heavy chain constant domain.
XX
KW Blood-clotting; heavy chain constant region; inflammation;
KW antiinflammatory; antibody; tissue factor; sepsis;
KW disseminated intravascular coagulation; anticoagulant;
KW hematological disease; thrombosis; lung injury; respiratory-gen.;
KW respiratory distress syndrome; immunosuppressive; Antibacterial;
KW Antiarthritic; Antianemic; anemia; rheumatoid arthritis;
KW glomerulonephritis; multiple sclerosis; psoriasis; Sjogren's syndrome;
KW inflammatory bowel disease.
XX
OS Homo sapiens.
XX
XX WO2005004793-A2.
PN
XX 20-JAN-2005.
PD
XX 04-JUN-2004; 2004WO-US017900.
PF
XX 19-JUN-2003; 2003US-0480254P.
PR
XX 22-JAN-2004; 2004US-0538892P.
PR
XX (SUNO-) SUNOL MOLECULAR CORP.
PA
XX Jiao J, Wong HC, Egan JO;
PI
XX WPI; 2005-091964/10.
DR
XX
XX Preventing or treating sepsis or inflammation in mammals comprises
PT administering a humanized or chimeric antibody that binds to a human
PT tissue factor to form a complex in which factor X or IX binding to the
PT complex is inhibited.
XX
PS Example 1; Fig 5; 109pp; English.
XX
XX The invention relates to preventing or treating a sepsis or inflammatory
CC disease in a mammal comprising administering to the mammal a therapeutic
CC amount of at least one humanized antibody, chimeric antibody, or their
CC fragment that binds specifically to tissue factor (TF) to form a complex,
CC where factor X or IX binding to the complex is inhibited and the
CC administration prevents or treats the sepsis in the mammal. Also included
CC are a kit for performing the above method and reducing an inflammatory
CC cytokine production in a mammal. The inflammatory disease is associated
CC with arthritis (preferably rheumatoid arthritis), glomerulonephritis,
CC multiple sclerosis, psoriasis, Sjogren's syndrome, or inflammatory bowel
CC disease. The method also treats or prevents a sepsis-induced anemia or a
CC sepsis-related condition in a mammal, where the sepsis-related condition
CC is DIC, fibrin deposition, thrombosis, lung injury, or sepsis-associated
CC renal disorder. The lung injury is acute lung injury (ALI) or acute
CC respiratory distress syndrome (ARDS). The sepsis-associated renal
CC disorder is acute tubular necrosis. The methods and kit are useful for
CC preventing or treating sepsis or sepsis-related conditions (e.g. DIC or
CC anemia) or inflammatory diseases (e.g. arthritis). The humanized
CC antibodies are based on the chimeric antibody ch36 which comprises the
CC light and heavy chain variable regions (VL or VH) of an anti-TF antibody
CC fused to the human IgG4 heavy and kappa light constant regions. The CDRs
CC (complementarity determining region) and FRs (framework regions) are then
CC humanized. The present sequence represents a human heavy chain constant
CC region used to make the chimeric antibody.
XX
SQ Sequence 332 AA;

Query Match 99.5%; Score 1756; DB 9; Length 332;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60

Db 3 ASTKGPSVFPLAPSSKSTGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 62
Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCCPPCPAPELAGA 120
Db 63 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCCPPCPAPELJGG 122
Qy 121 PSVFLFPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 123 PSVFLFPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
Qy 181 STYRVSVSLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 183 STYRVSVSLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
Db 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 302
Qy 301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
Db 303 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332

RESULT 85
ADJ95912
ID ADJ95912 standard; protein; 333 AA.
XX AC ADJ95912;
XX DT 06-MAY-2004 (first entry)
XX DE Human IgG heavy chain constant region.
XX KW cytostatic; antibody therapy; immunoglobulin cassette construct;
KW immunoglobulin leader molecule; immunoglobulin domain;
KW immunoglobulin therapeutic molecule; monobody; cancer; immunoglobulin G;
KW IgG; heavy chain constant region; human.
XX OS Homo sapiens.
XX PN US2004033561-A1.
XX PD 19-FEB-2004.
XX PF 17-OCT-2002; 2002US-00272899.
XX PR 19-OCT-2001; 2001US-0350166P.
XX PR 26-JUN-2002; 2002US-0392364P.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI O'keefe TL, Healey JJ, Newman W, Ponath PD, Keyt BA;
XX WPI; 2004-180050/17.
XX DR N-PSDB; ADJ95911.
XX PT New isolated nucleic acid molecules having an immunoglobulin cassette
PT construct, useful for producing immunoglobulin therapeutic molecules
PT termed monobodies, used as a therapeutic group in cancer disorders.
XX PS Example 2; SEQ ID NO 8; 84pp; English.
XX CC The invention describes an isolated nucleic acid molecule comprising an
CC immunoglobulin cassette construct, wherein the immunoglobulin cassette
CC comprises an immunoglobulin leader molecule operably linked to a stable
CC immunoglobulin domain region. The methods and compositions of the present
CC invention are useful for producing immunoglobulins, in particular
CC immunoglobulin therapeutic molecules termed monobodies, used as a
CC therapeutic group in cancer disorders. This is the amino acid sequence of
CC the human immunoglobulin G (IgG) heavy chain constant region used in the
CC creation of immunoglobulin DNA cassette constructs.

SQ Sequence 333 AA;
Query Match 99.5%; Score 1756; DB 8; Length 333;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ASTKGPSVFPLAPSSKSTGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
Db 4 ASTKGPSVFPLAPSSKSTGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 63
Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCCPPCPAPELAGA 120
Db 64 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCCPPCPAPELJGG 123
Qy 121 PSVFLFPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 124 PSVFLFPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 183
Qy 181 STYRVSVSLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 184 STYRVSVSLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 243
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
Db 244 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 303
Qy 301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
Db 304 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 333
RESULT 86
ADL22761
ID ADL22761 standard; protein; 333 AA.
XX AC ADL22761;
XX DT 20-MAY-2004 (first entry)
XX DE Human antibody heavy chain variable region.
XX KW antibody; human; heavy chain variable region; therapeutic.
XX OS Homo sapiens.
XX PN WO2004013278-A2.
XX PD 12-FEB-2004.
XX PF 01-AUG-2003; 2003WO-KR001555.
XX PR 02-AUG-2002; 2002KR-00045765.
XX PR 02-AUG-2002; 2002KR-00045767.
XX PR 02-AUG-2002; 2002KR-00045768.
XX PA (YUHA-) YUHAN CORP.
XX PI Lee J, Ko I, Song M, Kim C, Lee J, Yoo T, Kim J, Park S;
XX WPI; 2004-157108/15.
XX DR N-PSDB; ADL22760.
XX PT New expression vectors for an antibody heavy chain variable region,
PT lambda light chain variable region or kappa light chain variable region,
PT useful in developing therapeutic antibodies, e.g. humanized or chimeric
PT antibodies.
XX PS Example 3; Page 34-35; 39pp; English.
XX CC The present invention relates to an expression vector for an antibody
CC heavy chain variable region, a lambda light chain variable region or a
CC kappa light chain variable region. The expression vectors are useful in
CC the development of therapeutic antibodies, e.g. humanized or chimeric

CC antibodies. The present sequence is a human heavy chain variable region
CC of the invention.
XX
SQ Sequence 333 AA;
Query Match 99.5%; Score 1756; DB 8; Length 333;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db 4 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 63
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 64 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGG 123
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 124 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 183
Qy 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 184 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 243
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 300
Db 244 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 303
Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 304 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 333
RESULT 87
AEC22665
ID AEC22665 standard; protein; 335 AA.
XX
AC AEC22665;
XX
DT 20-OCT-2005 (first entry)
XX
DE Secreted IgG constant domain.
XX
KW multispecific antibody; promoter; bispecific antibody; immunoglobulin.
XX
OS Homo sapiens.
XX
FN WO2005072112-A2.
XX
PD 11-AUG-2005.
XX
PF 30-DEC-2004; 2004WO-US043806.
XX
PR 31-DEC-2003; 2003US-0533241P.
XX
PA (VACC-) VACCINEX INC.
XX
FI Zauderer M, Paris M;
XX
DR WPI; 2005-648912/66.
DR N-PSDB; AEC22664.
XX
PT Identifying polynucleotides encoding a bispecific antibody by introducing
PT a first library of polynucleotides encoding immunoglobulin subunit
PT polypeptides into eukaryotic host cells capable of expressing the
PT bispecific antibody.
XX
PS Example 1; SEQ ID NO 35; 254pp; English.
XX
CC The invention relates to a method of identifying polynucleotides which
CC encode a bispecific antibody which comprises introducing a library of
CC polynucleotides encoding first and second heavy chain and light chain

CC immunoglobulin subunit polypeptides into eukaryotic host cells,
CC expression and recovery of the antibodies or their antigen-binding
CC fragments. The method is useful in identifying polynucleotides which
CC encode a bispecific antibody or its bispecific antigen-binding fragment.
CC The present sequence represents an immunoglobulin constant domain.
XX
SQ Sequence 335 AA;
Query Match 99.5%; Score 1756; DB 9; Length 335;
Best Local Similarity 99.4%; Pred. No. 2.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db 6 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 65
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 66 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGG 125
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 126 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 185
Qy 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 186 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 245
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 300
Db 246 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 305
Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 306 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 335
RESULT 88
AAR43685
ID AAR43685 standard; protein; 351 AA.
XX
AC AAR43685;
XX
DT 25-MAR-2003 (revised)
DT 25-MAY-1994 (first entry)
XX
DE Human kappa immunoglobulin light chain constant domain.
XX
FN Human; immunoglobulin; constant; region; humanised; P-selectin; light;
KW blocking; antibody; heavy; chain; variable; murine; thrombotic disease;
KW monoclonal; PBL.3; CDR; complementarity determining region; leukocyte;
KW expression vector; coexpression; pHCMV-1748RHA-gammaCi-dhfr; epitope;
KW pHCMV-1748RLA-KR-neo; PBL.3/Humanised version A; vascular endothelium;
KW pHCMV-1747CH-gammaCi-neo; pHCMV-1747-CL-KR-neo; PBL.3 chimera;
KW acute lung injury; ischaemia reperfusion injury; inflammation.
XX
OS Homo sapiens.
XX
FI Key Location/Qualifiers
FH Domain 22..119
FT /note= "CH1 domain"
FT Region 120..134
FT /note= "Hinge region"
FT Domain 135..244
FT /note= "CH2 domain"
FT Domain 245..352
FT /note= "CH3 domain"
XX
FN WO9321956-A1.
XX
PD 11-NOV-1993.
XX
PF 04-MAY-1993; 93WO-US004274.

XX 05-MAY-1992; 92US-00880196.
XX (CYTE-) CYTEL CORP.
XX Chestnut RW, Polley MJ, Paulson JC;
XX WPI; 1993-368423/46.
XX N-PSDB; AAQ51547.
XX Anti-P-selectin antibody for ischaemia acute lung injury treatment -
XX useful to treat inflammation and pathological conditions of intercellular
XX adhesion by competitive inhibition assay.
XX Example 10; Fig 9; 82pp; English.
XX The sequences given in AAR43685-86 represent human immunoglobulin
XX constant regions which were used in the production of the humanised P-
XX selectin blocking antibody, along with the heavy and light chain variable
XX region coding sequences of the murine monoclonal antibody PBI.3, given in
XX AAR43687-88. The CDRs from PBI.3 heavy and light chains were substituted
XX for the CDRs of human heavy and light chains. The humanised variable
XX regions were inserted into expression vectors. By coexpression of
XX appropriate combinations of heavy and light chains, several humanised
XX antibodies can be expressed. Coexpression of pHCMV-1748RHA-gammaCI-dhfr
XX and pHCMV-1748RLA-KR-neo gives rise to the PBI.3/Humanised version A.
XX Coexpression of pHCMV-1747CH- gammaCI-neo and pHCMV-1747-CL-KR-neo gives
XX rise to the PBI.3 chimera. These humanised antibodies selectively bind
XX epitopes on P-selectin and block adhesion of leukocytes to the vascular
XX endothelium. They may be used to treat inflammatory and thrombotic
XX diseases and other pathological conditions involving P-selectin and
XX antibodies to it, esp. acute lung injury and ischaemia reperfusion
XX injury. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 351 AA;
Query Match 99.5%; Score 1756; DB 2; Length 351;
Best Local Similarity 99.4%; Pred. No. 2.6e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNNGALTSGVHTFPAVLQSS 60
DB 22 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNNGALTSGVHTFPAVLQSS 81
QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPPELAGA 120
DB 82 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPPELAGG 141
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPREEQYN 180
DB 142 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPREEQYN 201
QY 181 STYRVSVVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 202 STYRVSVVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 261
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
DB 262 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 321
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
DB 322 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 351
RESULT 89
ADJ95976
ID ADJ95976 standard; protein; 356 AA.
XX AC ADJ95976;
XX DT 06-MAY-2004 (first entry)
XX

DE Immunoglobulin DNA cassette polypeptide seqid 72.
XX cytostatic; antibody therapy; immunoglobulin cassette construct;
XX immunoglobulin leader molecule; immunoglobulin domain;
XX immunoglobulin therapeutic molecule; monobody; cancer.
XX Synthetic.
XX US2004033561-A1.
XX 19-FEB-2004.
XX 17-OCT-2002; 2002US-00272899.
XX 19-OCT-2001; 2001US-0350166P.
XX 26-JUN-2002; 2002US-0392364P.
XX (MILL-) MILLENNIUM PHARM INC.
XX O'keefe TL, Healey JJ, Newman W, Ponath PD, Keyt BA;
XX WPI; 2004-180050/17.
XX N-PSDB; ADJ95975.
XX New isolated nucleic acid molecules having an immunoglobulin cassette
XX construct, useful for producing immunoglobulin therapeutic molecules
XX termed monobodies, used as a therapeutic group in cancer disorders.
XX Disclosure; SEQ ID NO 72; 84pp; English.
XX The invention describes an isolated nucleic acid molecule comprising an
XX immunoglobulin cassette construct, wherein the immunoglobulin cassette
XX comprises an immunoglobulin leader molecule operably linked to a stable
XX immunoglobulin domain region. The methods and compositions of the present
XX invention are useful for producing immunoglobulins, in particular
XX immunoglobulin therapeutic molecules termed monobodies, used as a
XX therapeutic group in cancer disorders. This is the amino acid sequence of
XX an immunoglobulin DNA cassette construct.
XX SQ Sequence 356 AA;
Query Match 99.5%; Score 1756; DB 8; Length 356;
Best Local Similarity 99.4%; Pred. No. 2.6e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNNGALTSGVHTFPAVLQSS 60
DB 27 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNNGALTSGVHTFPAVLQSS 86
QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPPELAGA 120
DB 87 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPPELAGG 146
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPREEQYN 180
DB 147 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPREEQYN 206
QY 181 STYRVSVVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 207 STYRVSVVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 266
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
DB 267 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 326
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
DB 327 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 356
RESULT 90
AAP91918
ID AAP91918 standard; protein; 371 AA.

XX AAP91918;
AC 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 14-MAY-1990 (first entry)
DE Sequence of the linked immunoglobulin gamma chain fragment.
XX Immunoglobulin gamma chain; IgG1 heavy chain constant region.
KW Homo sapiens.
XX Key Location/Qualifiers
FH Misc-difference 42..43
FT /note= "Insert site"
FT Misc-difference 144..145
FT /note= "Insert site"
XX EP314317-A.
PN 03-MAY-1989.
XX 03-OCT-1988; 88EP-00309194.
XX 02-OCT-1987; 87US-00104329.
PR 28-SEP-1988; 88US-00250785.
XX (GETH) GENENTECH INC.
XX Capon DJ, Gregory TJ;
PI WPI; 1989-131855/18.
DR N-PSDB; AAN90779.
XX
XX Compens. contg. adhesion variants - useful in therapy and diagnostics,
PT e.g. CD4 variants which are therapeutically useful for treating human
PT immuno-deficiency virus.
XX
XX Disclosure; Fig 4a-4b; 36pp; English.
XX
XX It may be fused to the first 180 N-terminal residues of CD4 at the C-
CC terminus. The fusion protein may be used for antiviral of
CC immunomodulatory therapy particularly in treatment of HIV infection.
CC (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003
CC to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 371 AA;
Query Match 99.5%; Score 1756; DB 1; Length 371;
Best Local Similarity 99.4%; Pred. No. 2.8e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db 42 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 101
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
Db 102 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGG 161
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 162 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 221
QY 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISAKAGQPREPQVYITLPPSRDE 240
Db 222 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISAKAGQPREPQVYITLPPSRDE 281
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 282 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 341

QY 301 QQGNVFSCVMHEALHNHYTOKSLSLSPCK 330
Db 342 QQGNVFSCVMHEALHNHYTOKSLSLSPCK 371
RESULT 91
ABR39465
ID ABR39465 standard; protein; 442 AA.
XX AC ABR39465;
XX 12-JUN-2003 (first entry)
XX Humanised anti-Abeta antibody 266 heavy chain.
XX Amyloid-beta; Abeta; antibody 266; nootropic; neuroprotective; CDR;
KW immunostimulant.
XX OS Homo sapiens.
XX WO2003016467-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US021324.
XX PR 17-AUG-2001; 2001US-0313576P.
PR 28-MAY-2002; 2002US-0383851P.
XX (ELITL) LILLY & CO ELI.
XX Bales KR, Paul SM;
PI WPI; 2003-289975/28.
DR
XX
XX Treating or reducing the progression of diseases associated with amyloid-
PT beta peptide, e.g. Alzheimer's disease, vascular dementia or mild
PT cognitive impairment, comprises administering an anti-amyloid-beta
PT peptide antibody.
XX
XX Disclosure; Page 20-22; 84pp; English.
XX The invention relates to treating cognitive symptoms or reducing disease
CC progression in a subject having a condition or disease associated with
CC amyloid-beta peptide (Abeta). The method involves administering an amount
CC of an anti-Abeta antibody that has greater affinity for soluble Abeta
CC than 10⁻⁹ M, that has affinity (KD) for soluble Abeta1-40 or Abeta1-42
CC higher than 10⁻⁹ M, or that has greater affinity for soluble Abeta than
CC antibody 266 has. The method or the anti-Abeta antibody is useful in
CC preparing a medicament for treating cognitive symptoms or reducing
CC disease progression in a subject having a condition or disease associated
CC with Abeta. The condition or disease is Alzheimer's disease, Down's
CC syndrome, cerebral amyloid angiopathy, vascular dementia, or mild
CC cognitive impairment. The present sequence represents a humanised anti-
CC Abeta antibody 266 heavy chain
XX
XX Sequence 442 AA;
Query Match 99.5%; Score 1756; DB 6; Length 442;
Best Local Similarity 99.4%; Pred. No. 3.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db 113 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 172
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
Db 173 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGG 232
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 233 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 292


```

ABR39793
ID ABR39793 standard; peptide; 442 AA.
XX
AC ABR39793;
XX
DT 18-AUG-2003 (first entry)
XX
DE Humanised anti-Abeta antibody 266 heavy chain.
XX
KW Amyloid-beta; Abeta; antibody 266; neurotropic; neuroprotective; CDR;
KW immunostimulant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 56
FT /note= "Xaa is any amino acid, provided that if Xaa at
FT position 57 is neither Asp nor Pro and Xaa at position 59
FT is Ser or Thr, then Xaa at position 56 is not Asn"
FT
FT Misc-difference 57
FT /note= "Xaa is any amino acid, provided that if Xaa at
FT position 56 is Asn and Xaa at position 58 is Ser or Thr,
FT then Xaa at position 57 is Asp or Pro"
FT
FT Misc-difference 58
FT /note= "Xaa is any amino acid, provided that if Xaa at
FT position 56 is Asn and Xaa at position 57 is neither Asp
FT nor Pro, then Xaa at position 58 is neither Ser nor Thr"
XX
XX WO2003016466-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US021322.
XX
XX 17-AUG-2001; 2001US-0313224P.
XX
XX (ELIL ) LILLY & CO ELI.
XX
XX Jia AY, Tsurushita N, Vasquez MJ;
XX
XX WPI; 2003-278557/27.
XX
XX New antibodies comprising a heavy chain and a light chain complementarity
XX determining regions from antibody 266, for treating and preventing
XX conditions associated with the A beta peptide, e.g. Alzheimer's disease
XX or Down syndrome.
XX
XX Disclosure; Page 21-23; 82pp; English.
XX
XX The invention relates to an anti-Abeta (amyloid-beta peptide) antibody
XX 266. The antibodies are useful for treating and preventing conditions
XX associated with the Abeta peptide, such as Alzheimer's disease, Down
XX syndrome, and cerebral amyloid angiopathy; for diagnosing diseases in
XX humans; for determining whether a human subject will respond to treatment
XX using humanized antibodies against Abeta; for treating, preventing and
XX reversing cognitive decline in clinical or pre-clinical Alzheimer's
XX disease, Down's syndrome or cerebral amyloid angiopathy; for inhibiting
XX formation of amyloid plaques of the effects of toxic soluble Abeta
XX species in humans. Treatment of the patients with antibody will inhibit
XX or prevent cognitive decline typically associated with disease
XX progression and reverses it. The present sequence represents a preferred
XX heavy chain of the humanised anti-Abeta antibody 266
XX
XX Sequence 442 AA;
XX
XX Query Match 99.5%; Score 1756; DB 6; Length 442;
XX Best Local Similarity 99.4%; Pred. No. 3.4e-123;
XX Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
XX 113 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 172

```

```

QY 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNNTKVDKKVEPKSCDKTHTCTPPCPAPELAGA 120
DB 173 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNNTKVDKKVEPKSCDKTHTCTPPCPAPELGG 232
QY 121 PSVFLFPKPKDXTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 233 PSVFLFPKPKDXTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 292
QY 181 STYRVSVLVLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 293 STYRVSVLVLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 352
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
DB 353 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 412
QY 301 QGQNVFSCVMHEALHNYTKQSLSPGK 330
DB 413 QGQNVFSCVMHEALHNYTKQSLSPGK 442
RESULT 96
ABR80113
ID ABR80113 standard; protein; 442 AA.
XX
AC ABR80113;
XX
DT 13-JUN-2003 (first entry)
XX
DE Deglycosylated heavy chain.
XX
KW Complementarity determining region; CDR; humanised; mouse; 266; light;
KW heavy; variable; domain; antibody; preclinical; clinical;
KW Alzheimer's disease; epitope; amyloid beta peptide; Abeta;
KW central nervous system; plasma.
XX
XX Homo sapiens.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Misc-difference 56
XX /label= Any amino acid
XX /note= "Provided that if Xaa57 is neither Asp nor Pro and
XX Xaa58 is Ser or Thr, then Xaa56 is not Asn"
XX
XX Misc-difference 57
XX /label= Any amino acid
XX /note= "Provided that if Xaa56 is Asn and Xaa58 is Ser or
XX Thr, then Xaa57 is Asp or Pro"
XX
XX Misc-difference 58
XX /label= Any amino acid
XX /note= "Provided that if Xaa56 is Asn and Xaa57 is
XX neither Asp nor Pro, then Xaa58 is neither Ser nor Thr"
XX
XX WO2003015617-A2.
XX
XX 27-FEB-2003.
XX
XX 16-AUG-2002; 2002WO-US026321.
XX
XX 17-AUG-2001; 2001US-0313221P.
XX
XX 17-AUG-2001; 2001US-0313224P.
XX
XX 23-OCT-2001; 2001US-0334987P.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX (ELIL ) LILLY & CO ELI.
XX
XX Holtzman DM, Demattos R, Bales KR, Cummins DJ, Paul SM;
XX WPI; 2003-278505/27.
XX
XX Diagnosing preclinical or clinical Alzheimer's disease in a subject by
XX administering an antibody which specifically binds an epitope.
XX
XX

```

PS Claim 8; Page 20-22; 64pp; English.

XX This sequence represents the preferred heavy chain from a deglycosylated

CC version of the humanised mouse antibody 266 heavy chain of the invention.

CC The antibody of the invention specifically binds an epitope, preferably

CC the amyloid beta peptide (Abeta). The antibodies sequester Abeta from its

CC bound, circulating form in blood and alter clearance of soluble and bound

CC forms of Abeta in central nervous system and plasma. The antibodies

CC specifically bind an epitope representing amino acids 13-28 of the Abeta

CC molecule. Deglycosylation of the heavy chain CDR2, as in this sequence,

CC causes higher affinity for Abeta. The antibody of the invention may be

XX used for diagnosing preclinical or clinical Alzheimer's disease

SQ Sequence 442 AA;

Query Match 99.5%; Score 1756; DB 6; Length 442;

Best Local Similarity 99.4%; Pred. No. 3.4e-123;

Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSQVHTFPAVLQSS 60

DB 113 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSQVHTFPAVLQSS 172

QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPELAGA 120

DB 173 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPELAGG 232

QY 121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

DB 233 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 292

QY 181 STYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240

DB 293 STYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 352

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300

DB 353 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 412

QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

DB 413 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 442

RESULT 97

ID ABB80109 standard; protein; 442 AA.

AC ABB80109;

DT 13-JUN-2003 (first entry)

XX Heavy chain.

XX Complementarity determining region; CDR: humanised; mouse; 266; light;

KW heavy; variable; domain; antibody; preclinical; clinical;

KW Alzheimer's disease; epitope; amyloid beta peptide; Abeta;

KW central nervous system; plasma.

XX Homo sapiens.

OS Mus musculus.

PN WO2003015617-A2.

XX 27-FEB-2003.

XX 16-AUG-2002; 2002WO-US026321.

XX 17-AUG-2001; 2001US-0313221P.

PR 17-AUG-2001; 2001US-0313224P.

PR 23-OCT-2001; 2001US-0334987P.

XX (UNIW) UNIV WASHINGTON.

PA

PA (ELIL) LILLY & CO ELI.

XX Holtzman DM, Denattos R, Bales KR, Cummins DJ, Paul SM;

XX WPI; 2003-278505/27.

XX Diagnosing preclinical or clinical Alzheimer's disease in a subject by

XX administering an antibody which specifically binds an epitope.

XX Disclosure; Page 15-16; 64pp; English.

XX The sequences given in AAG80104-09 represent preferred antibodies of the

CC invention. This sequence represents the preferred heavy chain. The

CC humanised antibody of the invention may be used for diagnosing

CC preclinical or clinical Alzheimer's disease. The antibody specifically

CC binds an epitope, preferably the amyloid beta peptide (Abeta). The

CC antibodies sequester Abeta from its bound, circulating form in blood and

CC alter clearance of soluble and bound forms of Abeta in central nervous

CC system and plasma. The antibodies specifically bind an epitope

CC representing amino acids 13-28 of the Abeta molecule

XX Sequence 442 AA;

Query Match 99.5%; Score 1756; DB 6; Length 442;

Best Local Similarity 99.4%; Pred. No. 3.4e-123;

Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSQVHTFPAVLQSS 60

DB 113 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSQVHTFPAVLQSS 172

QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPELAGA 120

DB 173 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPELAGG 232

QY 121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

DB 233 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 292

QY 181 STYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240

DB 293 STYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 352

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300

DB 353 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 412

QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

DB 413 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 442

RESULT 98

ID ADE94066 standard; protein; 442 AA.

XX ADE94066;

AC ADE94066;

XX 12-FEB-2004 (first entry)

XX Humanised anti-Abeta antibody 266 heavy chain SEQ ID NO:12.

XX anxiety disorder; mood disorder; anti-Abeta antibody; Abeta; nootropic;

KW neuroprotective; antidepressant; neuroleptic; tranquilliser;

KW gene therapy; Alzheimer's disease; chronic amyloid angiopathy;

KW depression; major depressive episode; unipolar major depression;

KW schizophrenia; simple phobia; social phobia; agoraphobia; panic disorder;

KW obsessive-compulsive disorder; post-traumatic stress disorder.

XX Synthetic.

OS Mus sp.

OS Homo sapiens.

XX

PN WO2003090772-A1.
XX 06-NOV-2003.
XX 17-APR-2003; 2003WO-US010473.
XX 25-APR-2002; 2002US-0375462P.
XX (ELIL) LILLY & CO ELI.
XX Gerlai RT;
XX WPI; 2003-865528/80.
XX Treating, preventing and/or diagnosing a condition related to Abeta
XX expression, such as anxiety or mood disorders, including Alzheimer's
XX disease, depression, and schizophrenia, by administering an anti-Abeta
XX antibody to the subject.
XX Claim 24; SEQ ID NO 12; 64pp; English.
XX The present invention describes a method for treating an anxiety disorder
XX or a mood disorder in an elderly subject. The method comprises
XX administering an anti-Abeta antibody to the subject. Also described are
XX Abeta nucleic acids, polypeptides, antibodies and pharmaceutical
XX compositions used in the methods of the invention. Abeta has nootropic,
XX neuroprotective, antidepressant, neuroleptic and tranquilliser
XX activities, and can be used in gene therapy. The methods and compositions
XX of the present invention are useful for treating, preventing and/or
XX diagnosing a condition related to Abeta expression, such as anxiety or
XX mood disorders, including Alzheimer's disease, chronic amyloid
XX angiopathy, depression, major or minor depression, a major depressive
XX episode, a unipolar major depression, schizophrenia, simple phobia,
XX social phobia, agoraphobia, panic disorder, obsessive-compulsive disorder
XX or post-traumatic stress disorder. The present sequence is used in the
XX exemplification of the present invention.
XX Sequence 442 AA;
Query Match 99.5%; Score 1756; DB 7; Length 442;
Best Local Similarity 99.4%; Pred. No. 3.4e-123;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWGALTSGVHTFPVAVLQSS 60
Db |||||
QY 61 GLYSLSVVTVPSLSLGTQTYICNVNHPKPSNTKVDKVEPKSCDTHTCPPCPAPELAGA 120
Db |||||
QY 173 GLYSLSVVTVPSLSLGTQTYICNVNHPKPSNTKVDKVEPKSCDTHTCPPCPAPELGG 232
QY 121 PSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVNAKTKPREEOVN 180
Db 233 PSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVNAKTKPREEQIN 292
QY 181 STYRVSVLTVLHQDLNKGKEYCKVSKNKAIPAEIKTISKAKGPQRPQVYTLPPSRDE 240
Db 293 STYRVSVLTVLHQDLNKGKEYCKVSKNKAIPAEIKTISKAKGPQRPQVYTLPPSRDE 352
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKGRW 300
Db 353 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKGRW 412
QY 301 OQGNVFCSCVWHEALHNNHYTKLSLSLSPGK 330
Db 413 OQGNVFCSCVWHEALHNNHYTKLSLSLSPGK 442
RESULT 99
ADE94075
ID ADE94075 standard; protein; 442 AA.
XX
AC ADE94075;

XX 12-FEB-2004 (first entry)
XX Humanised anti-Abeta antibody heavy chain SEQ ID NO:21.
XX anxiety disorder; mood disorder; anti-Abeta antibody; Abeta; nootropic;
XX neuroprotective; antidepressant; neuroleptic; tranquilliser;
XX gene therapy; Alzheimer's disease; chronic amyloid angiopathy;
XX depression; major depressive episode; unipolar major depression;
XX schizophrenia; simple phobia; social phobia; agoraphobia; panic disorder;
XX obsessive-compulsive disorder; post-traumatic stress disorder.
XX Synthetic.
XX Mus sp.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Misc-difference 56 /note= "X at position 56 is any amino acid, provided that
XX if X at position 57 is neither Asp nor Pro and X at
XX position 59 is Ser or Thr, then X at position 56 is not
XX Asn"
XX Misc-difference 57 /note= "X at position 57 is any amino acid, provided that
XX if X at position 56 is Asn and X at position 58 is Ser or
XX Thr, then X at position 57 is Asp or Pro"
XX Misc-difference 58 /note= "X at position 58 is any amino acid, provided that
XX if X at position 56 is Asn and X at position 57 is
XX neither Asp nor Pro, then X at position 58 is neither Ser
XX nor Thr"
XX WO2003090772-A1.
XX 06-NOV-2003.
XX 17-APR-2003; 2003WO-US010473.
XX 25-APR-2002; 2002US-0375462P.
XX (ELIL) LILLY & CO ELI.
XX Gerlai RT;
XX WPI; 2003-865528/80.
XX Treating, preventing and/or diagnosing a condition related to Abeta
XX expression, such as anxiety or mood disorders, including Alzheimer's
XX disease, depression, and schizophrenia, by administering an anti-Abeta
XX antibody to the subject.
XX Claim 24; SEQ ID NO 21; 64pp; English.
XX The present invention describes a method for treating an anxiety disorder
XX or a mood disorder in an elderly subject. The method comprises
XX administering an anti-Abeta antibody to the subject. Also described are
XX Abeta nucleic acids, polypeptides, antibodies and pharmaceutical
XX compositions used in the methods of the invention. Abeta has nootropic,
XX neuroprotective, antidepressant, neuroleptic and tranquilliser
XX activities, and can be used in gene therapy. The methods and compositions
XX of the present invention are useful for treating, preventing and/or
XX diagnosing a condition related to Abeta expression, such as anxiety or
XX mood disorders, including Alzheimer's disease, chronic amyloid
XX angiopathy, depression, major or minor depression, a major depressive
XX episode, a unipolar major depression, schizophrenia, simple phobia,
XX social phobia, agoraphobia, panic disorder, obsessive-compulsive disorder
XX or post-traumatic stress disorder. The present sequence is used in the
XX exemplification of the present invention.
XX Sequence 442 AA;
Query Match 99.5%; Score 1756; DB 7; Length 442;
Best Local Similarity 99.4%; Pred. No. 3.4e-123;

Matches	328:	Conservative	0:	Mismatches	2:	Indels	0:	Gaps	0:
Qy	1	ASTKGPSVFPLAPASKSTSGGTAALGCLIKVDYFFPEPTVTSWNSGALTSGVHTFPFAVLQSS	60						
Db	113	ASTKGPSVFPLAPASKSTSGGTAALGCLIKVDYFFPEPTVTSWNSGALTSGVHTFPFAVLQSS	172						
Qy	61	GLYSLSSVTVTPSSSLGTQTQYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPCPAPELAGA	120						
Db	173	GLYSLSSVTVTPSSSLGTQTQYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPCPAPELLGG	232						
Qy	121	PSVFLLPFPKPKDITLMI SRTPEVTCVVDVSHEDPEVKFNWTVDGVENVNAKTKPREEOYN	180						
Db	233	PSVFLLPFPKPKDITLMI SRTPEVTCVVDVSHEDPEVKFNWTVDGVENVNAKTKPREEOYN	292						
Qy	181	STYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTI SKAKGPQREPQVYTLPPSRDE	240						
Db	293	STYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTI SKAKGPQREPQVYTLPPSRDE	352						
Qy	241	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFPLYSKLTVDKSRW	300						
Db	353	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFPLYSKLTVDKSRW	412						
Qy	301	QQGNVFSCSVMHEALHNHYTOKSLSLSPGK	330						
Db	413	QQGNVFSCSVMHEALHNHYTOKSLSLSPGK	442						

RESULT 100	
ADN61714	
ID	ADN61714 standard; protein; 442 AA.
XX	
XX	
AC	ADN61714;
XX	
DT	01-JUL-2004 (first entry)
XX	
DE	Humanised antibody heavy chain variable region #3.
DE	
XX	
KW	antibody; humanised antibody;
KW	light chain complementarity determining region; CDR; amyloid plaque;
KW	amyloid beta; Abeta; cognitive decline; Alzheimer's disease;
KW	Down's syndrome; cerebral amyloid angiopathy; cognition;
KW	heavy chain variable region.
XX	
OS	Homo sapiens.
OS	Mus sp.
XX	
PN	US2004043418-A1.
XX	
PD	04-MAR-2004.
XX	
PF	21-AUG-2002; 2002US-00226435.
XX	
PR	21-AUG-2002; 2002US-00226435.
XX	
PA	(HOLT/) HOLTZMAN D M.
PA	(DEMA/) DEMATTOS R.
PA	(BALE/) BALES K R.
PA	(PAUL/) PAUL S M.
PA	(TSUR/) TSURUSHITA N.
PA	(VASQ/) VASQUEZ M.
XX	
PI	Holtzman DM, Demattos R, Bales KR, Paul SM, Tsurushita N;
PI	Vasquez M;
XX	
DR	WPI; 2004-238334/22.
DR	N-PSDB; ADN61720.
XX	
PT	New humanized antibody or its fragment that sequesters amyloid beta
PT	peptide, useful for treating, preventing or reversing cognitive decline
PT	in Alzheimer's disease and Down's syndrome.
XX	
PS	Claim 5; SEQ ID NO 12; 35pp; English.
XX	

The invention relates to a humanised antibody or its fragment comprising a light chain comprising three light chain complementarity determining regions (CDRs) and a light chain framework sequence from a humanised immunoglobulin light chain, a heavy chain comprising three heavy chain CDRs and a heavy chain framework sequence from a humanised immunoglobulin heavy chain. Also described are the following: (i) a polynucleic acid comprising a sequence coding for the light chain or the heavy chain of the humanised antibody; (ii) an expression vector for expressing the antibody or its fragment comprising nucleotide sequences encoding the antibody or fragment; and (iii) a cell transfected with the expression vector or two expression vectors, where a first vector comprises the polynucleotide sequence coding for the light chain and a second vector comprises the sequence coding for the heavy chain, and capable of expressing the humanised antibody or its fragment. The humanised antibody or its fragment is useful in inhibiting or reducing the formation of amyloid plaques or the effects of toxic soluble amyloid beta (A β) species in humans, for treating, preventing, or reversing cognitive decline in clinical or pre-clinical Alzheimer's disease, Down's syndrome, or clinical or pre-clinical cerebral amyloid angiopathy, and for improving cognition in a subject. The present sequence represents humanised antibody heavy chain variable region #3.

Sequence 442 AA:
 SO

Search completed: June 12, 2006, 17:10:01
Job time : 228.707 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.
OM protein - protein search, using sw model
Run on: June 10, 2006, 11:56:42 ; Search time 35.1802 Seconds
(without alignments)
902.540 Million cell updates/sec
Title: US-10-733-563-110
Perfect score: 1765
Sequence: 1 ASTKGPSVFPLAPSSKSTG.....MHEALHNHYTQKSLSLSPGK 330
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR 80: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1756	99.5	330	1 GHU	Ig gamma-1 chain C
2	1619.5	91.8	377	2 A23511	Ig gamma-3 chain C
3	1617.5	91.6	377	2 A60764	Ig gamma-3 chain C
4	1608	91.1	326	1 G2HU	Ig gamma-2 chain C
5	1579.5	89.5	327	1 G4HU	Ig gamma-4 chain C
6	1259	71.3	328	2 I47159	Ig gamma 2a chain
7	1253	71.0	328	2 I47160	Ig gamma 2b chain
8	1252.5	71.0	374	2 S69339	Ig heavy chain V r
9	1249	70.8	255	4 S31866	Ig gamma-1 chain C
10	1243	70.4	234	2 PT0207	Ig gamma chain C r
11	1235	70.0	328	2 I47158	Ig gamma 1 chain c
12	1231	69.7	328	2 I47161	Ig gamma chain C r
13	1219.5	69.1	323	1 GHRB	Ig gamma-2 chain C
14	1201.5	68.1	329	1 G2GP	Ig gamma-1 chain -
15	1195.5	67.7	472	2 S31459	Ig heavy chain pre
16	1176.5	66.7	470	2 S22080	Ig heavy chain C r
17	1157.5	65.6	308	2 C30554	monoclonal antibod
18	1156	65.5	444	2 PC4436	Ig gamma-1 chain C
19	1154	65.4	326	2 S00017	Ig gamma-1 chain C
20	1144	64.8	324	1 G1MS	Ig gamma-3 heavy C
21	1140	64.6	289	1 G3HUI.	Ig gamma-1 chain C
22	1139	64.5	393	1 G1NSM	Ig gamma-2b chain
23	1135.5	64.3	333	2 PS0018	Ig gamma-3 chain C
24	1130	64.0	329	1 G3MSC	Ig gamma-3 chain C
25	1119	63.4	398	1 G3MSM	Ig gamma-2a chain
26	1115	63.2	330	1 G2MSA	Ig gamma-2a chain
27	1115	63.2	469	2 S37483	Ig gamma-2c chain
28	1114.5	63.1	329	2 S00847	Ig gamma-2a chain
29	1114	63.1	322	2 PS0019	Ig gamma-2a chain

RESULT 1
GHU

Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004
C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238; PMID:6287432
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <ELL>
A:Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034COE; EMBL:Z17370
A:Note: this sequence has the Gm(17) allotypic marker, 97-Lys, and the Gm(1) markers, R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: UNIPARC:UPI000013CGFE; EMBL:Z17370
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A:Reference number: S33887; MUID:83001943; PMID:6811139
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113;235-330 <TAK>
A:Cross-references: UNIPARC:UPI000017378B; UNIPARC:UPI000017378C; EMBL:Z17370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
A:Reference number: A90563; MUID:71064024; PMID:5489771
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: protein
A:Residues: 1-96, R', 98-135 <CUN>
A:Cross-references: UNIPARC:UPI000017378D
A:Note: this sequence has the Gm(3) marker, 97-Arg
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen
A:Reference number: A90564; MUID:71064025; PMID:5530842
A:Contents: Eu
A:Accession: A90564
A:Molecule type: protein
A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240, '
A:Cross-references: UNIPARC:UPI000017378E
A:Note: this sequence has the Gm(non-1) markers, 239-Glu and 241-Met
R:Ponstingl, H.; Hilschmann, N.

Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2 chain C
Ig gamma-2b chain
Ig gamma-2b chain
Ig gamma 4 chain c
Ig gamma-2b chain
Ig epsilon chain C
Ig epsilon chain C
Ig heavy chain VHI
Ig heavy chain V-I
Ig gamma-1 chain C
Ig heavy chain pre
Ig heavy chain (DO
Ig gamma-1 heavy c

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
igen Primaerstruktur.
A:Reference number: A91668; MUID:77070269; PMID:826475
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A:Cross-references: UNIPARC:UPI000017378F
A>Note: this sequence has the G1m(17) and G1m(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOI
A:Reference number: A91723; MUID:83289131; PMID:6884994
A:Contents: myeloma protein KOI; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A:Cross-references: UNIPARC:UPI0000173790
A>Note: this sequence has the G1m(3) and G1m(non-1) markers
R:Gall, W.E.; Edelman, G.W.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267; PMID:1002129
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:120-85/Domain: immunoglobulin homology <IM1>
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83, 144-204, 250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (co light chain) #status experimental
F:109,112/Disulfide bonds: interchain (co heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 99.5%; Score 1756; DB 1; Length 330;
Best Local Similarity 99.4%; Pred. No. 9.8e-114; Mismatches 0; Indels 0; Gaps 0;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVVPSLSLGTQTYICNVNHPKPSNTKVDKQVPEKSCDTHTCPPCPAPELLAG 120
DB 61 GLYSLSVVTVVPSLSLGTQTYICNVNHPKPSNTKVDKQVPEKSCDTHTCPPCPAPELLAG 120
QY 121 PSVFLPPPKDKTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVEVHNATKPREEOYN 180
DB 121 PSVFLPPPKDKTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVEVHNATKPREEOYN 180
QY 181 STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 181 STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFELYSLKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFELYSLKLTVDKSRW 300
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

||||| 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: con
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: UNIPARC:UPI000004718F; GB:X03604; GB:M12958; NID:g33070; PIDN:CAA2726
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>
Query Match 91.8%; Score 1619.5; DB 2; Length 377;
Best Local Similarity 81.4%; Pred. No. 2.9e-104;
Matches 307; Conservative 10; Mismatches 13; Indels 47; Gaps 1;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVVPSLSLGTQTYICNVNHPKPSNTKVDKQV----- 98
DB 61 GLYSLSVVTVVPSLSLGTQTYICNVNHPKPSNTKVDKRVELKTLPLGDTTHTCPRCEPKSC 120
QY 99 -----EPKSCDKHTTCTPPCPAPELAGAPSVLFFPKPKDT 133
DB 121 DTPPPCPAPELAGAPSVLFFPKPKDT 180
QY 134 LMISRTPEVTCVVDVSHEDPEVKFNWYDGVVEVHNATKPREEOYNSTYRVSVLTVLH 193
DB 181 LMISRTPEVTCVVDVSHEDPEVKFNWYDGVVEVHNATKPREEOYNSTYRVSVLTVLH 240
QY 194 QDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 253
DB 241 QDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 300
QY 254 GFYPDSIAVEWESNGQPENNYKTTTPVLDSDGSEFELYSLKLTVDKSRWQGNVFSCVMHE 313
DB 301 GFYPDSIAVEWESNGQPENNYKTTTPVLDSDGSEFELYSLKLTVDKSRWQGNVFSCVMHE 360
QY 314 ALHNHYTQKSLSLSPGK 330
DB 361 ALHNRYTQKSLSLSPGK 377
RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 31-Dec-2004
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-377 <HUC>
A:Cross-references: UNIPROT:Q8N4Y9; UNIPARC:UPI0000176F0B
C:Superfamily: immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 91.6%; Score 1617.5; DB 2; Length 377;
Best Local Similarity 81.4%; Pred. No. 4e-104;
Matches 307; Conservative 10; Mismatches 13; Indels 47; Gaps 1;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKV----- 98
DB 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVPLGLDTHTCPRCPKSC 120
QY 99 -----EPKSCDTHTCPPCPAPELAGAPSVFLPPPKPKDT 133
DB 121 DTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPAPELLAGPSVFLPPPKPKDT 180
QY 134 LMISTPEVTCVVDVSHEDPEVKNNVYDGVGVHNAKTKPREQYNSTYRVVSVLTVLH 193
DB 181 LMISTPEVTCVVDVSHEDPEVQPKWYDGVGVHNAKTKPREQYNSTYRVVSVLTVLH 240
QY 194 QDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDELTKNQVSLTCLVK 253
DB 241 QDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDEMTKNQVSLTCLVK 300
QY 254 GYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRWQGQGNVFPSCSVHME 313
DB 301 GYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRWQEGNVFPSCSVHME 360
QY 314 ALHNHYTQKSLSLSPGK 330
DB 361 ALHNRYTQKSLSLSPGK 377

RESULT 4
G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A:Reference number: A93906; MUID:82197621; PMID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: UNIPROT:P01859; UNIPARC:UPI000003BFCC; GB:V00554; GB:J00230; NID:g32
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A:Reference number: A92809; MUID:81007873; PMID:6774012
A:Contents: myeloma protein Til
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A:Cross-references: UNIPARC:UPI0000173791
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:80001357; PMID:113060
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-
A:Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793

A:Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Contents: Zie
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
A:Cross-references: UNIPARC:UPI0000173794
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500; PMID:4940472
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:133-306/Domain: immunoglobulin homology <IM3>
F:147-83,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.1%; Score 1608; DB 1; Length 326;
Best Local Similarity 91.5%; Pred. No. 1.5e-103;
Matches 302; Conservative 12; Mismatches 12; Indels 4; Gaps 2;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDTHTCPPCPAPELAGA 120
DB 61 GLYSLSSVTVTPSSNFGTQTYICNVDHKPSNTKVDKTVKRCVVE--CPPCPAPVAG- 116
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVGVHNAKTKPREQYN 180
DB 117 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVGVHNAKTKPREQFN 176
QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
DB 177 STFRVSVLTVVHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 236
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
DB 237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 296
QY 301 QGQNVFSCSVNHEALHNHYTQKSLSLSPGK 330
DB 297 QGQNVFSCSVNHEALHNHYTQKSLSLSPGK 326

RESULT 5
G4HU

Ig gamma-4 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C:Accession: A90933; A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A:Reference number: A90933; MUID:83157104; PMID:6299662
A:Accession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELL>
A:Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190
A:Note: the sequence was determined from the germline gene
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant
A:Reference number: A90249; MUID:70207560; PMID:4192699
A:Accession: A90249
A:Molecule type: protein
A:Residues: 1-30; 81-326 <PIN>
A:Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796
C:Genetics:
A:Gene: GDB:IGHG4
A:Cross-references: GDB:119340; OMIM:147130
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 111/1; 221/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.5%; Score 1579.5; DB 1; Length 327;
Best Local Similarity 90.3%; Pred. No. 1.4e-101;
Matches 298; Conservative 12; Mismatches 17; Indels 3; Gaps 1;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNPKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNPKVDKVEPKSCDKTHTCPCPAPELAGA 117

QY 121 PSVFLFPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
DB 118 PSVFLFPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQFN 177

QY 181 STYRVSVLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 240
DB 178 STYRVSVLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 237

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
DB 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 297

QY 301 QGQNVFSCSVMEALHNNHYTKQSLSPGK 330
DB 298 QGQNVFSCSVMEALHNNHYTKQSLSPGK 327

RESULT 6
147159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C:Accession: I47159
R:Kaczkovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine Igg identified from the cDNA sequences of a s
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: UNIPARC:UPI0000115524; EMBL:U03779; NID:G433123; PIDN:AAAS2217.1; PII
C:Genetics:
A:Gene: IGG2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 71.3%; Score 1259; DB 2; Length 328;
Best Local Similarity 70.2%; Pred. No. 1.6e-79;
Matches 233; Conservative 42; Mismatches 51; Indels 6; Gaps 3;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
DB 1 AKTAPSVYPLAPCSRDTSGPNVALGCLASSYFPEPTVTWNSGALSSGVHTFPAVLQPS 60

QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNPKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNPKVDKVEPKSCDKTHTCPCPAPELAGA 116

QY 121 PSVFLFPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
DB 117 PSVFLFPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQFN 176

QY 181 STYRVSVLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 240
DB 177 STYRVSVLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 236

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 298
DB 237 LSRKVSITCLVIGFYPPDIDVEWQRNGQPEPGRYRTTPQDQVDGTYFLYSKFSVDKA 296

QY 299 RWQGNVFCSCVMHEALHNNHYTKQSLSPGK 330
DB 297 SWQGGIFQCAVMHEALHNNHYTKQSLSPGK 328

RESULT 7
147160
Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C:Accession: I47160
R:Kaczkovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine Igg identified from the cDNA sequences of a s
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47160
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: UNIPARC:UPI0000115525; EMBL:U03780; NID:G433125; PIDN:AAAS2218.1; PII
C:Genetics:
A:Gene: IGG2b
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 71.0%; Score 1253; DB 2; Length 328;
Best Local Similarity 69.9%; Pred. No. 4.2e-79;
Matches 232; Conservative 41; Mismatches 53; Indels 6; Gaps 3;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
DB 1 AKTAPLVYPLAPCSRDTSGPNVALGCLASSYFPEPTVTWNSGALSSGVHTFPAVLQPS 60

QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNPKVDKVEPKSCDKTHTCPCPAPELAGA 120

Db	61	GLYSLSGMSTVPSASSLSKSYTCNVNHPATTTKDKRGVTKT---	KPPCPICFACSPG-	116
Qy	121	PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKPNWYVDGVEVHNAKTKPRREQYN	180	
Db	117	PSYFIIPPPKPTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTQATRPKEQFN	176	
Qy	181	STRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKTISKAKGQPREPOVYTLPPSRDE	240	
Db	177	STRVVSVVLPPIQHDWNLGKFKCKVNNKNDLPAPITRIISKAKGQTPREPOVYTLPPHAE	236	
Qy	241	LTKNQVSLTCLVKGYGPPSDIAVEAESNQ--PENNYKTTTPPLVDSGDSFLYKSLTVDKS	298	
Db	237	LGRSKVITCLVIGYPPDIDVEMQRNGQPEGGYRTTPPQQVDGTGYFLYSKFSVDKA	296	
Qy	299	RWQQGVFSCSVNHEALHNHYTQKSLSLSPGK	330	
Db	297	SWGGGIFOCVAMHEALHNHYTQKSISKTPGK	328	

RESULT 8
S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; PMID:95262687; PMID:7744049
A:Accession: S69339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695
R:Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140, 'C', 142-374 <KH2>
A:Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match	71.0%;	Score 1252.5;	DB 2;	Length 374;
Best Local Similarity	89.0%;	Pred. No. 5.4e-79;		
Matches 235;	Conservative 3;	Mismatches 15;	Indels 11;	Gaps 2;

Qy	78	TQTYICNVN-----HK-PSNTVVDKVKVEPKSCDKTHTCPCPAPELAGAPSVFLF	126
Db	111	TATYICGYSVEGQGYRFHSGGGTLVTVSSPEPKSCDKTHTCPCPAPELLGGPSVFLF	170
Qy	127	PPPKPKDTLMISRPETVCVVVDVSHEDPEVKFKFNMYVDGVEVHNAKTRPREEQYNSTYRVV	186
Db	171	PPPKPKDTLMISRPETVCVVVDVSHEDPEVKFKFNMYVDGVEVHNAKTRPREEQYNSTYRVV	230
Qy	187	SVLTIVLHODWLNGKEYCKVKSNNKALPAPIEKTISKAKGQPREPOVYITLPPSRDELTKNQV	246
Db	231	SVLTIVLHODWLNGKEYCKVKSNNKALPAPIEKTISKAKGQPREPOVYITLPPSRDEMTKNQV	290
Qy	247	SLTCLVKGFYPSPDIAVESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF	306
Db	291	SLTCLVKGFYPSPDIAVESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF	350
Qy	307	SCSVMHEALHNHYTQKSLSLSPGK	330
Db	351	SCSVMHEALHNHYTQKSLSLSPGK	374

RESULT 9
S31866
Iq gamma-1 chain C region - synthetic

C/Species: synthetic
A/Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C/Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C/Accession: S31866
R/Filpula, D.
submitted to the EMBL Data Library, February 1993
A/Description: Screening method for protein-protein interactions of cloned gene products.
A/Reference number: S31866
A/Accession: S31866
A/Molecule type: mRNA
A/Residues: 1-255 <Fil>
A/Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID
C/Keywords: immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region

	Query Match	70.8%	Score 1249;	DB 4;	Length 255;
	Best Local Similarity	96.74;	Pred. No. 5.9e-79;		
	Matches 231;	Conservative	0;	Mismatches 8;	Indels 0; Gaps 0
Qy	92	TKVDKKVEPKSCDKTHTCCPCPAPELAGASVFLFPKPKDTLMISRTPEVTCVVDVSH	151		
Db	17	TVAQADVESCSDKTHTCCPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSH	76		
Qy	152	EDPEVFNWYVDGVGVHNAKTKPREEOYNSTRYVSVLTVLHQDWLNGKEYCKKCVSKNAL	211		
Db	77	EDPEVFNWYVDGVGVHNAKTKPREEOYNSTRYVSVLTVLHQDWLNGKEYCKKCVSKNAL	136		
Qy	212	PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGPYPSDIAVWEWESNGQPE	271		
Db	137	PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGPYPSDIAVWEWESNGQPE	196		
Qy	272	NNYKTTTPVLDSDGSFPLYSKLTVDKSRWQOGNNVFCSCVMHEALHNHYTKQSLSPGK	330		
Db	197	NNYKTTTPVLDSDGSFPLYSKLTVDKSRWQOGNNVFCSCVMHEALHNHYTKQSLSPGK	255		

RESULT 10
PT0207
Ig gamma
C:Species
C:Date: 2
C:Accessi
R:Ehrlich
Mol. Immu
A:Title:
A:Referen
A:Accessi
A:Molecul
A:Residue
A:Cross-r
C:Superfa
C:Keyword
F:48-117/

Query Match	70.4%	Score 1243;	DB 2;	Length 234;
Best Local Similarity	97.94;	Pred. No. 1.4e-78;		
Matches 229;	Conservative 1;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	90	SNTKVDKKBPKSCDTHHTCCPCAPDELAGAPSVFLPPPKPDKDTLMISRTPEVTCVVVDV	149	
Db	1	SNTKVDKKBPKSCDTHHTCCPCAPDELGGPSVFLPPPKPDKDTLMISRTPEVTCVVVDV	60	
Qy	150	SHEDPEVKPNWYVDGVEVHNNAKTKPREEQYNSTRYVVSVLTVLHODMLNGKEYKCKVSNK	209	
Db	61	SHEDPEVKPNWYVDGVEVHNNAKTKPREEQYNSTRYVVSVLTVLHODMLNGKEYKCKVSNK	120	
Qy	210	ALPAPIETKITSKAGQPREPOVTLTPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQ	269	
Db	121	ALPAPIETKITSKAGQPREPOVTLTPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQ	180	
Qy	270	PENNYKTTPEVLDSDGSEFFLYSKLTVDKSKRWQGNVFSCSMHEALNNHYTQKS	323	

Db 181 PENNYKTPPVLDSGDSFFLYSKLTVDKSRWQGNVFSVMSVHEALHNNHYTKS 234

RESULT 11

I47158

Ig gamma 1 chain constant region - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C:Accession: I47158

R:Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a

A:Reference number: I47158; MUID:95015845; PMID:7930579

A:Accession: I47158

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-328 <KAC>

A:Cross-references: UNIPARC:UPI0000115523; EMBL:U03778; NID:G433121; PIDN:AAA52216.1; PI

C:Genetics:

A:Gene: IgG1

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 70.0%; Score 1235; DB 2; Length 328;

Best Local Similarity 69.6%; Pred. No. 7 4e-78;

Matches 231; Conservative 39; Mismatches 56; Indels 6; Gaps 3;

QY 1 ASTKGPSVPLAPSSKSTGGTAALGCLVKDYFPEPTVMSWGALTSGVHTFPAVLQSS 60

Db 1 APTKAPSVVPLAPCGRDVSGPNVALGLASSYFPEPTVTWNSGALTSGVHTFSPVLQPS 60

QY 61 GLYSLSSVTVPSSSIGTQYICNVNHPKSNKTKVDKVEPKSCDKTHTCTPCCPAPELAGA 120

Db 61 GLYSLSSMTVPASSLSKSYTCNVNHPATTKVDKRV---GIHQDTCPICPGCEVAG- 116

QY 121 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQN 180

Db 117 PSVFIFFPKPKDTLMISQTPEVTCVVVDVSKHAHQVQSVYDGVGVHTAETRPKEEQN 176

QY 181 STYRVSVLTCLVKGFPSPDIADVWESNGO--PENNYKTPPVLDSGDSFFLYSKLTVDKS 240

Db 177 STYRVSVLPIQHQLVKGFPSPDIADVWESNGQPEPNYRTTPPQQDVGDTFFLYSKLAVDKA 236

QY 241 LTKNQVSLTCLVKGFYPSDIAVWESNGO--PENNYKTPPVLDSGDSFFLYSKLTVDKS 298

Db 237 LRSKVTLLCLVIGFPPDIHVEWKSNGQPEPNYRTTPPQQDVGDTFFLYSKLAVDKA 296

QY 299 RWOQGNVFSVMSVHEALHNNHYTKSLSPGK 330

Db 297 RWDHDKGKFECAVMHEALHNNHYTKSISKTKGK 328

RESULT 12

I47161

Ig gamma 3 chain constant region - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C:Accession: I47161

R:Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a

A:Reference number: I47158; MUID:95015845; PMID:7930579

A:Accession: I47161

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-328 <KAC>

A:Cross-references: UNIPARC:UPI0000115526; EMBL:U03781; NID:G433127; PIDN:AAA52219.1; PI

C:Genetics:

A:Gene: IgG3

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 69.7%; Score 1231; DB 2; Length 328;

Best Local Similarity 69.3%; Pred. No. 1 4e-77;

Matches 230; Conservative 40; Mismatches 56; Indels 6; Gaps 3;

QY 1 ASTKGPSVPLAPSSKSTGGTAALGCLVKDYFPEPTVMSWGALTSGVHTFPAVLQSS 60

Db 1 APTKAPSVVPLAPCGRDVSGPNVALGLASSYFPEPTVTWNSGALTSGVHTFSPVLQPS 60

QY 61 GLYSLSSVTVPSSSIGTQYICNVNHPKSNKTKVDKVEPKSCDKTHTCTPCCPAPELAGA 120

Db 61 GLYSLSSMTVPASSLSKSYTCNVNHPATTKVDKRVGKT---KPPCPICPGCEVAG- 116

QY 121 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQN 180

Db 117 PSVFIFFPKPKDTLMISQTPEVTCVVVDVSKHAHQVQSVYDGVGVHTAETRPKEEQN 176

QY 181 STYRVSVLTCLVKGFPSPDIADVWESNGO--PENNYKTPPVLDSGDSFFLYSKLTVDKS 240

Db 177 STYRVSVLPIQHQLVKGFPSPDIADVWESNGQPEPNYRTTPPQQDVGDTFFLYSKLAVDKA 236

QY 241 LTKNQVSLTCLVKGFYPSDIAVWESNGO--PENNYKTPPVLDSGDSFFLYSKLTVDKS 298

Db 237 LRSKVTLLCLVIGFPPDIHVEWKSNGQPEPNYRTTPPQQDVGDTFFLYSKLAVDKA 296

QY 299 RWOQGNVFSVMSVHEALHNNHYTKSLSPGK 330

Db 297 RWDHDKGKFECAVMHEALHNNHYTKSISKTKGK 328

RESULT 13

GHRB

Ig gamma chain C region - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004

C:Accession: A91749; A90290; A93928; A90245; A94416; A02161

R:Bernstein, K.E.; Alexander, C.B.; Mage, R.G.

Immunogenetics 18, 387-397, 1983

A:Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haploty

A:Reference number: A91749; MUID:84030930; PMID:6313520

A:Accession: A91749

A:Molecule type: mRNA

A:Residues: 1-323 <BER>

A:Cross-references: UNIPROT:P01870; UNIPARC:UPI000012B37D

A>Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr

R:Pratt, D.M.; Mole, L.E.

Biochem. J. 151, 337-349, 1975

A:Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob

A:Reference number: A90290; MUID:76135469; PMID:1243651

A:Accession: A90290

A:Molecule type: protein

A:Residues: 1-47, 'E', 49-71, 'PV', 72-128 <PRA>

A:Cross-references: UNIPARC:UPI00001737AB

R:Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.

Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982

A:Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain

A:Reference number: A93928; MUID:83299917; PMID:6193512

A:Accession: A93928

A:Molecule type: mRNA

A:Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <WAR>

A:Cross-references: UNIPARC:UPI000016C5ED; GB:M16426; NID:g165111; PIDN:AAA31289.1; PID:9

A>Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker

R:Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.

Biochem. J. 116, 249-259, 1970

A:Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin C

A:Reference number: A90245; MUID:70110015; PMID:5461106

A:Accession: A90245

A:Molecule type: protein

A:Residues: 132-143, 'E', 145-161 <FRU>

A:Cross-references: UNIPARC:UPI00001737AC

R:Hilli, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.

in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,

A:Reference number: A94416

A:Accession: A94416

A:Molecule type: protein

A;Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q',234-243,'G',245-251,'S',253-260,'D',262-270,'E',272-280,'D',282-290,'E',292-299,'D',301-308,'E',310-317,'D',319-326,'E',328-335,'D',337-344,'E',346-353,'D',355-362,'E',364-371,'D',373-380,'E',382-389,'D',391-398,'E',400-407,'D',409-416,'E',418-425,'D',427-434,'E',436-443,'D',445-452,'E',454-461,'D',463-470,'E',472-479,'D',481-488,'E',490-497,'D',499-506,'E',508-515,'D',517-524,'E',526-533,'D',535-542,'E',544-551,'D',553-560,'E',562-569,'D',571-578,'E',580-587,'D',589-596,'E',598-605,'D',607-614,'E',616-623,'D',625-632,'E',634-641,'D',643-650,'E',652-659,'D',661-668,'E',670-677,'D',679-686,'E',688-695,'D',697-704,'E',706-713,'D',715-722,'E',724-731,'D',733-740,'E',742-749,'D',751-758,'E',760-767,'D',769-776,'E',778-785,'D',787-794,'E',796-803,'D',805-812,'E',814-821,'D',823-830,'E',832-839,'D',841-848,'E',850-857,'D',859-866,'E',868-875,'D',877-884,'E',886-893,'D',895-902,'E',904-911,'D',913-920,'E',922-929,'D',931-938,'E',940-947,'D',949-956,'E',958-965,'D',967-974,'E',976-983,'D',985-992,'E',994-1001,'D',1003-1010,'E',1012-1019,'D',1021-1028,'E',1030-1037,'D',1039-1046,'E',1048-1055,'D',1057-1064,'E',1066-1073,'D',1075-1082,'E',1084-1091,'D',1093-1100,'E',1102-1109,'D',1111-1118,'E',1120-1127,'D',1129-1136,'E',1138-1145,'D',1147-1154,'E',1156-1163,'D',1165-1172,'E',1174-1181,'D',1183-1190,'E',1192-1199,'D',1201-1208,'E',1210-1217,'D',1219-1226,'E',1228-1235,'D',1237-1244,'E',1246-1253,'D',1255-1262,'E',1264-1271,'D',1273-1280,'E',1282-1289,'D',1291-1298,'E',1300-1307,'D',1309-1316,'E',1318-1325,'D',1327-1334,'E',1336-1343,'D',1345-1352,'E',1354-1361,'D',1363-1370,'E',1372-1379,'D',1381-1388,'E',1390-1397,'D',1399-1406,'E',1408-1415,'D',1417-1424,'E',1426-1433,'D',1435-1442,'E',1444-1451,'D',1453-1460,'E',1462-1469,'D',1471-1478,'E',1480-1487,'D',1489-1496,'E',1498-1505,'D',1507-1514,'E',1516-1523,'D',1525-1532,'E',1534-1541,'D',1543-1550,'E',1552-1559,'D',1561-1568,'E',1570-1577,'D',1579-1586,'E',1588-1595,'D',1597-1604,'E',1606-1613,'D',1615-1622,'E',1624-1631,'D',1633-1640,'E',1642-1649,'D',1651-1658,'E',1660-1667,'D',1669-1676,'E',1678-1685,'D',1687-1694,'E',1696-1703,'D',1705-1712,'E',1714-1721,'D',1723-1730,'E',1732-1739,'D',1741-1748,'E',1750-1757,'D',1759-1766,'E',1768-1775,'D',1777-1784,'E',1786-1793,'D',1795-1802,'E',1804-1811,'D',1813-1820,'E',1822-1829,'D',1831-1838,'E',1840-1847,'D',1849-1856,'E',1858-1865,'D',1867-1874,'E',1876-1883,'D',1885-1892,'E',1894-1901,'D',1903-1910,'E',1912-1919,'D',1921-1928,'E',1930-1937,'D',1939-1946,'E',1948-1955,'D',1957-1964,'E',1966-1973,'D',1975-1982,'E',1984-1991,'D',1993-2000,'E',2002-2009,'D',2011-2018,'E',2020-2027,'D',2029-2036,'E',2038-2045,'D',2047-2054,'E',2056-2063,'D',2065-2072,'E',2074-2081,'D',2083-2090,'E',2092-2099,'D',2101-2108,'E',2110-2117,'D',2119-2126,'E',2128-2135,'D',2137-2144,'E',2146-2153,'D',2155-2162,'E',2164-2171,'D',2173-2180,'E',2182-2189,'D',2191-2198,'E',2200-2207,'D',2209-2216,'E',2218-2225,'D',2227-2234,'E',2236-2243,'D',2245-2252,'E',2254-2261,'D',2263-2270,'E',2272-2279,'D',2281-2288,'E',2290-2297,'D',2299-2306,'E',2308-2315,'D',2317-2324,'E',2326-2333,'D',2335-2342,'E',2344-2351,'D',2353-2360,'E',2362-2369,'D',2371-2378,'E',2380-2387,'D',2389-2396,'E',2398-2405,'D',2407-2414,'E',2416-2423,'D',2425-2432,'E',2434-2441,'D',2443-2450,'E',2452-2459,'D',2461-2468,'E',2470-2477,'D',2479-2486,'E',2488-2495,'D',2497-2504,'E',2506-2513,'D',2515-2522,'E',2524-2531,'D',2533-2540,'E',2542-2549,'D',2551-2558,'E',2560-2567,'D',2569-2576,'E',2578-2585,'D',2587-2594,'E',2596-2603,'D',2605-2612,'E',2614-2621,'D',2623-2630,'E',2632-2639,'D',2641-2648,'E',2650-2657,'D',2659-2666,'E',2668-2675,'D',2677-2684,'E',2686-2693,'D',2695-2702,'E',2704-2711,'D',2713-2720,'E',2722-2729,'D',2731-2738,'E',2740-2747,'D',2749-2756,'E',2758-2765,'D',2767-2774,'E',2776-2783,'D',2785-2792,'E',2794-2801,'D',2803-2810,'E',2812-2819,'D',2821-2828,'E',2830-2837,'D',2839-2846,'E',2848-2855,'D',2857-2864,'E',2866-2873,'D',2875-2882,'E',2884-2891,'D',2893-2900,'E',2902-2909,'D',2911-2918,'E',2920-2927,'D',2929-2936,'E',2938-2945,'D',2947-2954,'E',2956-2963,'D',2965-2972,'E',2974-2981,'D',2983-2990,'E',2992-2999,'D',3001-3008,'E',3010-3017,'D',3019-3026,'E',3028-3035,'D',3037-3044,'E',3046-3053,'D',3055-3062,'E',3064-3071,'D',3073-3080,'E',3082-3089,'D',3091-3098,'E',3100-3107,'D',3109-3116,'E',3118-3125,'D',3127-3134,'E',3136-3143,'D',3145-3152,'E',3154-3161,'D',3163-3170,'E',3172-3179,'D',3181-3188,'E',3190-3197,'D',3199-3206,'E',3208-3215,'D',3217-3224,'E',3226-3233,'D',3235-3242,'E',3244-3251,'D',3253-3260,'E',3262-3269,'D',3271-3278,'E',3280-3287,'D',3289-3296,'E',3298-3305,'D',3307-3314,'E',3316-3323,'D',3325-3332,'E',3334-3341,'D',3343-3350,'E',3352-3359,'D',3361-3368,'E',3370-3377,'D',3379-

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 11:49:06 ; Search time 271.532 Seconds
(without alignments)
1124.198 Million cell updates/sec

Title: US-10-733-563-110
Perfect score: 1765
Sequence: 1 ASTKGPSVPLPSPSKSTSG.....MHEALHNYTKSLSLSPGK 330

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1756	99.5	330	1 IGHG1_HUMAN	P01857 homo sapien
2	1756	99.5	465	2 Q6GMX6_HUMAN	Q6gmx6 homo sapien
3	1756	99.5	469	2 Q569F4_HUMAN	Q569f4 homo sapien
4	1756	99.5	469	2 Q727P5_HUMAN	Q727p5 homo sapien
5	1756	99.5	470	2 Q6PJ44_HUMAN	Q6pj44 homo sapien
6	1756	99.5	470	2 Q725W1_HUMAN	Q725w1 homo sapien
7	1756	99.5	475	2 Q5EFES_HUMAN	Q5efes homo sapien
8	1756	99.5	475	2 Q6GMW7_HUMAN	Q6gmw7 homo sapien
9	1756	99.5	476	2 Q6GMX1_HUMAN	Q6gmx1 homo sapien
10	1753	99.3	466	2 Q6IN78_HUMAN	Q6in78 homo sapien
11	1753	99.3	472	2 Q6N089_HUMAN	Q6n089 homo sapien
12	1752	99.3	473	2 Q6PD55_HUMAN	Q6pd55 homo sapien
13	1752	99.3	475	2 Q6MZQ6_HUMAN	Q6mzq6 homo sapien
14	1752	99.3	480	2 Q6N094_HUMAN	Q6n094 homo sapien
15	1752	99.3	481	2 Q6N097_HUMAN	Q6n097 homo sapien
16	1752	99.3	482	2 Q72351_HUMAN	Q72351 homo sapien
17	1749	99.1	466	2 Q6N096_HUMAN	Q6n096 homo sapien
18	1747	99.0	348	2 Q6PYX1_HUMAN	Q6pyx1 homo sapien
19	1747	99.0	478	2 Q6PJ181_HUMAN	Q6pj181 homo sapien
20	1747	99.0	480	2 Q6PJF1_HUMAN	Q6pjf1 homo sapien
21	1745	98.9	475	2 Q6N095_HUMAN	Q6n095 homo sapien
22	1745	98.9	544	2 Q6PJ95_HUMAN	Q6pj95 homo sapien
23	1737	98.4	473	2 Q6MZV7_HUMAN	Q6mzv7 homo sapien
24	1687	95.6	475	2 Q5RE17_PONPY	Q5re17 pongo pygma
25	1619.5	91.8	518	2 Q6N030_HUMAN	Q6n030 homo sapien
26	1619.5	91.8	519	2 Q5EMB2_HUMAN	Q5emb2 homo sapien
27	1615.5	91.5	521	2 Q8N4Y9_HUMAN	Q8n4y9 homo sapien
28	1608	91.1	326	1 IGHG2_HUMAN	P01859 homo sapien
29	1608	91.1	417	2 Q6N093_HUMAN	Q6n093 homo sapien
30	1604.5	90.9	509	2 Q8NPF17_HUMAN	Q8nfp17 homo sapien
31	1603	90.8	465	2 Q6PE64_HUMAN	Q6pe64 homo sapien

RESULT 1

ID	IGHG1_HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;			
DT	21-JUL-1986,	integrated into UniProtKB/Swiss-Prot.		
DT	21-JUL-1986,	sequence version 1.		
DT	07-FEB-2006,	entry version 62.		
DE	Ig gamma-1 chain C region.			
GN	Name=IGHG1;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RN	NUCLEOTIDE SEQUENCE [GENOMIC DNA].			
RP	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	PROTEIN SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RA	Waxdal M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."			
RL	Biochemistry 9:3161-3170(1970).			
RN	[3]			
RP	PROTEIN SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."			
RL	Biochemistry 9:3171-3181(1970).			
RN	[4]			
RP	PROTEIN SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN	[5]			
RP	PROTEIN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm H.-D., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN	[6]			
RP	DISULFIDE BONDS.			

Q68cn4 homo sapien
Q6mzu6 homo sapien
P01861 homo sapien
Q8tc63 homo sapien
Q6mzx7 homo sapien
Q86tt2 homo sapien
Q95m34 equus caball
Q96pq8 homo sapien
Q65z12 mus sp. fv/
P01870 oryctolagus
P01862 cavia porce
Q99lc4 mus musculu
Q65zq1 homo sapien
P20759 rattus norv

ALIGNMENTS

```

RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=7070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie), I: purification and
RT characterization of the protein, the L- and H-chains, the cyanogen
RT bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=91208100; PubMed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC -I- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the
CC G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the
CC G1M(3) marker and the G1M (non-1) markers.
CC -I- MISCELLANEOUS: Nie also differs in the amidation states of 35,
CC 116, 198, 269 and 272.
CC -I- MISCELLANEOUS: EU also differs in the amidation states of residues
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC 268-272.
CC -I- MISCELLANEOUS: KOL also differs in the amidation states of
CC residues 198, 267 and 272.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs license
CC -----
DR EMBL; J00228; AAC82527.1; ALT_INIT; Genomic_DNA.
DR PIR; A93433; GHU.
DR PDB; 1AJ7; X-ray; H=1-103.
DR PDB; 1AQK; X-ray; H=1-103.
DR PDB; 1DSB; X-ray; B/H=1-101.
DR PDB; 1DS1; X-ray; H=1-101.
DR PDB; 1D6V; X-ray; H=1-101.
DR PDB; 1DN2; X-ray; A/B=120-326.
DR PDB; 1E4K; X-ray; A/B=106-330.
DR PDB; 1FC1; X-ray; A/B=106-329.
DR PDB; 1FC2; X-ray; D=106-329.
DR PDB; 1FCC; X-ray; A=121-326.
DR PDB; 1HZH; X-ray; H/K=1-330.
DR PDB; 1I7Z; X-ray; B/D=1-103.
DR PDB; 1IIS; X-ray; A/B=107-330.
DR PDB; 1IIX; X-ray; A/B=107-330.
DR PDB; 1L6X; X-ray; A=120-326.
DR PDB; 1QXK; X-ray; A/B=119-330.
DR PDB; 1T83; X-ray; A/B=107-330.
DR PDB; 2RCG; X-ray; H=1-103.
DR HGNC; HGNC:5525; IGHG1.
DR MIM; 147100; gene.
DR LinkHub; P01857; -.
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00407; IGH1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW 3D-structure; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin C region; Immunoglobulin domain.
FT CHAIN <1 330
/FTid=PRO_0000153578.

```

```

FT REGION 1 98
FT REGION 99 110
FT REGION 111 223
FT REGION 224 330
FT CARBOHYD 180 180
FT DISULFID 27 83
FT DISULFID 103 103
FT DISULFID 109 109
FT DISULFID 112 112
FT DISULFID 144 204
FT DISULFID 250 308
FT VARIANT 97 97
FT VARIANT 239 239
FT VARIANT 241 241
FT NON TER 1 1
FT STRAND 4 4
FT STRAND 7 11
FT STRAND 13 13
FT STRAND 15 16
FT STRAND 18 18
FT STRAND 20 35
FT STRAND 38 41
FT HELIX 42 44
FT TURN 45 45
FT TURN 48 49
FT STRAND 50 52
FT STRAND 56 57
FT TURN 59 60
FT STRAND 61 61
FT STRAND 63 75
FT TURN 76 78
FT STRAND 82 87
FT HELIX 88 90
FT TURN 91 91
FT STRAND 92 97
FT STRAND 105 106
FT STRAND 108 108
FT STRAND 111 111
FT STRAND 118 120
FT STRAND 122 126
FT HELIX 130 134
FT TURN 136 137
FT STRAND 138 138
FT STRAND 141 149
FT STRAND 151 153
FT STRAND 157 162
FT TURN 163 164
FT STRAND 165 167
FT STRAND 171 172
FT TURN 176 177
FT TURN 179 180
FT STRAND 181 181
FT STRAND 183 190
FT HELIX 193 197
FT TURN 198 199
FT STRAND 202 207
FT TURN 209 210
FT STRAND 211 213
FT STRAND 215 219
FT STRAND 224 224
FT STRAND 227 227
FT STRAND 230 234
FT HELIX 238 242
FT STRAND 243 258
FT STRAND 261 266
FT TURN 267 268
FT STRAND 269 271
FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284

```

CHI.

Hinge.

CH2.

CH3.

N-linked (GlcNAc. . .).

Interchain (with light chain).

Interchain (with heavy chain).

Interchain (with heavy chain).

K -> R (in G1M(3) marker).

/FTid=VAR_003886.

D -> E (in G1M(non-1) marker).

/FTid=VAR_003887.

L -> M (in G1M(non-1) marker).

/FTid=VAR_003888.

RA Stapleton M., Soares M.B., Ronaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; BC092518; AAH92518.1; -; mRNA.
DR SMR; Q589F4; 20-469.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
DR SEQUENCE 469 AA; 51254 MW; AC1348BE3047784F CRC64;
Query Match 99.5%; Score 1756; DB 2; Length 469;
Best Local Similarity 99.4%; Pred. No. 5.2e-125;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 140 ASTKGPSVFPLAPSSKSTSGGTAALCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 199
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
DB 200 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 259
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 260 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 319
QY 181 STYRVSVLTIVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVTLPPSRDE 240
DB 320 STYRVSVLTIVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVTLPPSRDE 379
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
DB 380 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 439
QY 301 QGQNVFSCSMHEALHNHYTQKSLSLSPGK 330
DB 440 QGQNVFSCSMHEALHNHYTQKSLSLSPGK 469
RESULT 4
Q727P5 HUMAN PRELIMINARY; PRT; 469 AA.
ID Q727P5
AC Q727P5;

DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DE 01-FEB-2006, entry version 20.
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; BC051328; AAH51328.1; -; mRNA.
DR HSP; P01857; IGHZ.
DR SMR; Q727P5; 20-469.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
DR SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;
Query Match 99.5%; Score 1756; DB 2; Length 469;
Best Local Similarity 99.4%; Pred. No. 5.2e-125;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 140 ASTKGPSVFPLAPSSKSTSGGTAALCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 199
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
DB 200 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 259
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Db 260 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 319
QY 181 STYRVSVLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRW 300
Db 320 STYRVSVLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRW 379
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRW 300
Db 380 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRW 439
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 440 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 469
RESULT 5
Q6PJA4 HUMAN
ID Q6PJA4_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; BC018747; AAH18747.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
DR SMR; Q6PJA4; 20-470.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; C1-set; 3.

DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGC1; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00390; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 470 AA; 51716 MW; 7B49556A11FD7D99 CRC64;
Query Match 99.5%; Score 1756; DB 2; Length 470;
Best Local Similarity 99.4%; Pred. No. 5.2e-125;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVEPLAPSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 141 ASTKGPSVEPLAPSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVKCKVEPKSCDKTHTCTCPCPAPELAGA 120
DB 201 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVKCKVEPKSCDKTHTCTCPCPAPELAGG 260
QY 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 261 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
QY 181 STYRVSVLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRW 240
DB 321 STYRVSVLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRW 380
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRW 300
DB 381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRW 440
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
DB 441 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
RESULT 6
Q7Z5W1 HUMAN
ID Q7Z5W1_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q7Z5W1;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

```

RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR B0053984; AAH53984.1; -, mRNA.
DR HSP5; P01857; 1H2H.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match          99.5%; Score 1756; DB 2; Length 470;
Best Local Similarity 99.4%; Pred. No. 5.2e-125;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 141 ASTKGPSVFPLAPSSKSTSGGTAALCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLAG 120
DB 201 GLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 260
QY 121 PSVFLPPPKDPLMI SRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 261 PSVFLPPPKDPLMI SRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
QY 181 STYRVVSVLTVHLQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 321 STYRVVSVLTVHLQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 380
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
DB 381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 440
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
DB 441 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 470

RESULT 7
QSEFES HUMAN
ID QSEFES_HUMAN PRELIMINARY; PRT; 475 AA.
AC QSEFES;
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 15-MAR-2005, sequence version 1.
DE 07-FEB-2006, entry version 8.
DE Anti-Rhd monoclonal T125 gammal heavy chain precursor.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RA Gaucher C., Klein P., Beliard R.;
RT "Sequence determination of the recombinant human anti-Rhd monoclonal
RT antibody T125.";
```

```

RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR B0053984; AAH53984.1; -, mRNA.
DR SMR; QSEFES; 20-475.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 475 anti-Rhd monoclonal T125 gammal heavy
FT CHAIN chain.
SQ SEQUENCE 475 AA; 52362 MW; 1367D400DC7D2859 CRC64;

Query Match          99.5%; Score 1756; DB 2; Length 475;
Best Local Similarity 99.4%; Pred. No. 5.3e-125;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 146 ASTKGPSVFPLAPSSKSTSGGTAALCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 205
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLAG 120
DB 206 GLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 265
QY 121 PSVFLPPPKDPLMI SRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 266 PSVFLPPPKDPLMI SRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 325
QY 181 STYRVVSVLTVHLQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 326 STYRVVSVLTVHLQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 385
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
DB 386 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 445
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
DB 446 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 475

RESULT 8
Q6GMW7 HUMAN
ID Q6GMW7_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6GMW7;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DE 07-FEB-2006, entry version 16.
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388957; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
```

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; BC073782; AAH73782.1; -; mRNA.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PR07654; Cl-set; 3.
DR SMART; SM00409; IG1; 1.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein_
SQ SEQUENCE 475 AA; 51987 MW; 2A1F55D736860F8 CRC64;

Query Match 99.5%; Score 1756; DB 2; Length 475;
Best Local Similarity 99.4%; Pred. No. 5.3e-125;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 146 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 205
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVKKPEKSCDKTKHTCCPCPAPELAGA 120
DB 206 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVKKPEKSCDKTKHTCCPCPAPELGG 265
QY 121 PSVFLFPFPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYN 180
DB 266 PSVFLFPFPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYN 325
QY 181 STYRVVSVLTVLDHQLWNGKEYCKYKSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 326 STYRVVSVLTVLDHQLWNGKEYCKYKSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 385
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSLKLTVDKSRW 300
DB 386 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSLKLTVDKSRW 445
QY 301 QQGNVFSCSMHEALHNHYTQKSLSLSPGK 330
DB 446 QQGNVFSCSMHEALHNHYTQKSLSLSPGK 475

Q6GMX1 HUMAN PRELIMINARY; PRT; 476 AA.
ID O6GMX1;
AC O6GMX1, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; BC073773; AAH73773.1; -; mRNA.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PR07654; Cl-set; 3.
DR SMART; SM00409; IG1; 1.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein_
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match 99.5%; Score 1756; DB 2; Length 476;
Best Local Similarity 99.4%; Pred. No. 5.3e-125;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 147 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 206
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVKKPEKSCDKTKHTCCPCPAPELAGA 120
DB 207 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVKKPEKSCDKTKHTCCPCPAPELGG 266

```

QY 121 PSVFLPPPKDQTLMSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 267 PSVFLPPPKDQTLMSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
QY 181 STYRVVSVLTVLHQDLWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 327 STYRVVSVLTVLHQDLWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 386
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 300
Db 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 446
QY 301 OQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 447 OQGNVFSCVMHEALHNHYTQKSLSLSPGK 476

RESULT 10
Q6IN78 HUMAN
ID Q6IN78_HUMAN PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System; DOI=10.1073/pnas.242603899;
RX MEDLINE=2238257; PubMed=12477932;
RA Klausner R.D., Feingold E.A., Grouse L.H., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; BC072419; AAH72419.1; -; mRNA.
DR HSSP; P01861; 1A0Q.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGcl; 2.

```

```

DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS0290; IG MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50854 MW; 53EB0BCED81076E CRC64;

Query Match 99.3%; Score 1753; DB 2; Length 466;
Best Local Similarity 99.1%; Pred. No. 8.7e-125;
Matches 327; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLSS 60
Db 137 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLSS 196
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKHTHTCPCPAPELAGA 120
Db 197 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKHTHTCPCPAPELGG 256
QY 121 PSVFLPPPKDQTLMSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 257 PSVFLPPPKDQTLMSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 316
QY 181 STYRVVSVLTVLHQDLWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 317 STYRVVSVLTVLHQDLWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 376
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 300
Db 377 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 436
QY 301 OQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 437 OQGNVFSCVMHEALHNHYTQKSLSLSPGK 466

RESULT 11
Q6N089 HUMAN
ID Q6N089_HUMAN PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Hypothetical protein DKFP686P15220.
GN Name=DKFP686P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Rectum tumor;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobott G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; BX640627; CAE45781.1; -; mRNA.
DR HSSP; P01861; 1A0Q.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.V.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGv; 1.

```


DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51725 MW; 26CB340D0046D279 CRC64;

Query Match 99.3%; Score 1753; DB 2; Length 472;
Best Local Similarity 99.1%; Pred. No. 8.8e-125;
Matches 327; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db |||||
QY 143 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 202
Db |||||
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVKKVEPKSCDKTHTCPPCPAPELAG 120
Db |||||
QY 203 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVKKVEPKSCDKTHTCPPCPAPELGG 262
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db |||||
QY 263 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 322
QY 181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240
Db |||||
QY 323 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 382
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRW 300
Db |||||
QY 383 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRW 442
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db |||||
QY 443 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 472

RESULT 12
Q6P055 HUMAN PRELIMINARY; PRT; 473 AA.
AC Q6P055;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; BC065820; AAH65820.1; -; mRNA.
DR HSSP; P01861; IADO.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-CL.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG-V.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; CL-set; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGCL; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match 99.3%; Score 1752; DB 2; Length 473;
Best Local Similarity 99.1%; Pred. No. 1.1e-124;
Matches 327; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db |||||
QY 144 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 203
Db |||||
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVKKVEPKSCDKTHTCPPCPAPELAG 120
Db |||||
QY 204 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVKKVEPKSCDKTHTCPPCPAPELGG 263
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db |||||
QY 264 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 323
QY 181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240
Db |||||
QY 324 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 383
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRW 300
Db |||||
QY 384 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRW 443
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db |||||
QY 444 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 473

RESULT 13
Q6WZQ6 HUMAN PRELIMINARY; PRT; 475 AA.
ID Q6WZQ6 HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6WZQ6;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Hypothetical protein DKFZp686G11190.
GN Name=DKFZp686G11190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German cDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Oeanger A., Fobo G.,
RA Han M., Wiemann S.;

```

RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: BX640947; CAE45972.1; -; mRNA.
DR HSSP: P01861; IADQ.
DR SMR: O6MZQ6; 20-475.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig cl.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR InterPro: IPR013106; V-set.
DR Pfam: PF07654; C1-set; 3.
DR SMART: SM00409; IG1.
DR SMART: SM00409; IG1.
DR SMART: SM00406; IG1.
DR SMART: SM00406; IG1.
DR PROSITE: PS00835; IG_LIKE; 4.
DR PROSITE: PS00230; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE25A26F4B8E CRC64;

Query Match 99.3%; Score 1752; DB 2; Length 475;
Best Local Similarity 99.1%; Pred. No. 1.1e-124;
Matches 327; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 60
Db 146 ASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 205
QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNVTVDKVPKSCDKTHTCPPCPAPELLGG 120
Db 206 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNVTVDKVPKSCDKTHTCPPCPAPELLGG 265
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 266 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 325
QY 181 STYRVVSVLTVLDHQMNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 326 STYRVVSVLTVLDHQMNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 385
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
Db 386 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 445
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 446 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 475

RESULT 14
Q6N094 HUMAN PRELIMINARY; PRT; 480 AA.
AC Q6N094;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Hypothetical protein DKFZp686O01196.
GN Name=DKFZp686O01196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RA Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
RL -----

```

```

CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: BX640622; CAE45776.1; -; mRNA.
DR HSSP: P01861; IADQ.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig cl.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR InterPro: IPR013106; V-set.
DR Pfam: PF07654; C1-set; 3.
DR SMART: SM00409; IG1.
DR SMART: SM00409; IG1.
DR SMART: SM00406; IG1.
DR SMART: SM00406; IG1.
DR PROSITE: PS00835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 52613 MW; 225247P3D35ABC18 CRC64;

Query Match 99.3%; Score 1752; DB 2; Length 480;
Best Local Similarity 99.1%; Pred. No. 1.1e-124;
Matches 327; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 60
Db 151 ASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 210
QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNVTVDKVPKSCDKTHTCPPCPAPELLGG 120
Db 211 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNVTVDKVPKSCDKTHTCPPCPAPELLGG 270
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 271 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 330
QY 181 STYRVVSVLTVLDHQMNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 331 STYRVVSVLTVLDHQMNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 390
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
Db 391 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 450
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 451 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 480

RESULT 15
Q6N097 HUMAN PRELIMINARY; PRT; 481 AA.
AC Q6N097;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Hypothetical protein DKFZp686H20196.
GN Name=DKFZp686H20196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RA Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
RL -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC -----

```

```
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BX640619; CAB45773.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGC1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52759 MW; 47220D9E64BDF98B CRC64;

Query Match          99.3%; Score 1752; DB 2; Length 481;
Best Local Similarity 99.1%; Pred. No. 1.le-124;
Matches 327; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASTKGPSVPLAPSSKSTGGTAALGCLVKDYPPPEPTVTVSNWNSGALTSGVHTFPVAVLQSS 60
Db |||||
QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKKVPKSCDKTHTCPCPAPELAGA 120
Db |||||
QY 212 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKKVPKSCDKTHTCPCPAPELLGG 271
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db |||||
QY 272 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 331
QY 181 STYRVVSVLTVTLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db |||||
QY 332 STYRVVSVLTVTLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 391
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db |||||
QY 392 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 451
QY 301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
Db |||||
QY 452 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 481
```

Search completed: June 10, 2006, 12:05:28
Job time : 272.532 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 12:05:52 ; Search time 56.982 Seconds
(without alignments)
506.917 Million cell updates/sec

Title: US-10-733-563-110

Perfect score: 1765
Sequence: 1 ASTKGSPVFLAPSSKSTSG.....MHEALHNYTKSLSPGK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC Celerra_SIDS3/ptodata/2/iaa/5 COMB.pep.*
- 2: /EMC Celerra_SIDS3/ptodata/2/iaa/6 COMB.pep.*
- 3: /EMC Celerra_SIDS3/ptodata/2/iaa/7 COMB.pep.*
- 4: /EMC Celerra_SIDS3/ptodata/2/iaa/H COMB.pep.*
- 5: /EMC Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pep.*
- 6: /EMC Celerra_SIDS3/ptodata/2/iaa/RE COMB.pep.*
- 7: /EMC Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1765	100.0	444	3	US-09-674-716B-53
2	1756	99.5	330	2	US-10-112-582A-1
3	1756	99.5	371	1	US-08-236-311-7
4	1756	99.5	371	2	US-08-457-918-7
5	1756	99.5	371	2	US-10-157-408-7
6	1756	99.5	444	2	US-10-147-849-7
7	1756	99.5	446	2	US-08-397-411-7
8	1756	99.5	449	1	US-08-458-516-13
9	1756	99.5	467	2	US-08-030-175-41
10	1756	99.5	467	2	US-08-030-175-42
11	1756	99.5	470	2	US-10-104-047-3730
12	1756	99.5	476	1	US-08-378-939-10
13	1756	99.5	547	2	US-09-746-359A-54
14	1756	99.5	567	2	US-09-825-561A-16
15	1756	99.5	571	2	US-09-746-359A-53
16	1756	99.5	951	2	US-09-313-942-9
17	1756	99.5	951	2	US-10-282-162-9
18	1752	99.3	462	2	US-09-289-942A-7
19	1752	99.3	475	2	US-09-740-002-27
20	1752	99.3	476	2	US-08-487-550-4
21	1752	99.3	476	2	US-08-487-550-12
22	1752	99.3	476	2	US-09-526-098-4
23	1752	99.3	476	2	US-09-526-098-12
24	1752	99.3	476	2	US-09-383-916-4
25	1752	99.3	476	2	US-09-383-916-12
26	1752	99.3	476	2	US-09-758-173-4

27	1752	99.3	476	2	US-09-758-173-12	Sequence 12, Appl
28	1752	99.3	476	2	US-09-576-424-4	Sequence 4, Appl
29	1752	99.3	476	2	US-09-576-424-12	Sequence 12, Appl
30	1752	99.3	478	2	US-08-487-550-8	Sequence 8, Appl
31	1752	99.3	478	2	US-09-526-098-8	Sequence 8, Appl
32	1752	99.3	478	2	US-09-383-916-8	Sequence 8, Appl
33	1752	99.3	478	2	US-09-758-173-8	Sequence 8, Appl
34	1752	99.3	478	2	US-09-576-424-8	Sequence 8, Appl
35	1751	99.2	459	1	US-08-157-101A-7	Sequence 7, Appl
36	1751	99.2	470	2	US-09-238-741-4	Sequence 4, Appl
37	1750	99.2	330	2	US-09-301-593-22	Sequence 22, Appl
38	1750	99.2	451	1	US-08-887-352B-14	Sequence 14, Appl
39	1750	99.2	451	1	US-08-887-352B-16	Sequence 16, Appl
40	1750	99.2	451	1	US-08-887-352B-18	Sequence 18, Appl
41	1750	99.2	451	2	US-08-466-151-65	Sequence 65, Appl
42	1750	99.2	451	2	US-09-109-207C-14	Sequence 14, Appl
43	1750	99.2	451	2	US-09-109-207C-16	Sequence 16, Appl
44	1750	99.2	451	2	US-09-109-207C-18	Sequence 18, Appl
45	1750	99.2	451	2	US-09-282-505-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-674-716B-53
; Sequence 53, Application US/09674716B
; Patent No. 7008623
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, Jean-Yves M.P.
; APPLICANT: CROWE, James S.
; APPLICANT: ELLIS, Jonathan H.
; APPLICANT: RAPSON, Nicholas T.
; APPLICANT: SHEARIN, Jean
; TITLE OF INVENTION: Antibodies to CD23, derivatives thereof, and their therapeutic u
; FILE REFERENCE: 1430-2356 / PG3433USwo
; CURRENT APPLICATION NUMBER: US/09/674,716B
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: CA 2,328,606
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: PCT/GB99/01434
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: GB 9809839.5
; PRIOR FILING DATE: 1998-05-09
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: MS Word
; SEQ ID NO 53
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised anti-CD23 antibody

US-09-674-716B-53

Query Match 100.0%; Score 1765; DB 3; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.2e-157;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ASTKGSPVFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS	60
Db	115	ASTKGSPVFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS	174
QY	61	GLYSLSSVVTVSPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSKDKTHTCPCCPAPELAGA	120
Db	175	GLYSLSSVVTVSPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSKDKTHTCPCCPAPELAGA	234
QY	121	PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRBEQYN	180
Db	235	PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRBEQYN	294
QY	181	STYRVVSVLTVLDHQLNGKEVKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE	240
Db	295	STYRVVSVLTVLDHQLNGKEVKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE	354

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 355 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 414
QY 301 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 330
Db 415 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 444

RESULT 2

US-10-112-582A-1
; Sequence 1, Application US/10112582A
; Patent No. 6992174
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
; FILE REFERENCE: LEX-017
; CURRENT APPLICATION NUMBER: US/10/112,582A
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/280,625
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; FEATURE:
; OTHER INFORMATION: human Ig gamma heavy chain C region
US-10-112-582A-1

Query Match 99.5%; Score 1756; DB 2; Length 330;
Best Local Similarity 99.4%; Pred. No. 5.5e-157;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVVTVPSSTSGTQYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSVVTVPSSTSGTQYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPELGG 120

QY 121 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQYN 180
Db 121 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQYN 180

QY 181 STYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300

QY 301 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 330

RESULT 3

US-08-236-311-7
; Sequence 7, Application US/08236311
; Patent No. 5565335
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,311
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 444P1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-236-311-7

Query Match 99.5%; Score 1756; DB 1; Length 371;
Best Local Similarity 99.4%; Pred. No. 6.6e-157;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db 42 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 101

QY 61 GLYSLSVVTVPSSTSGTQYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 102 GLYSLSVVTVPSSTSGTQYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPELGG 161

QY 121 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQYN 180
Db 162 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQYN 221

QY 181 STYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 222 STYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 281

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 282 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 341

QY 301 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 330
Db 342 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 371

RESULT 4
US-08-457-918-7
; Sequence 7, Application US/08457918

```

; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0444PIC3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-457-918-7
Query Match 99.5%; Score 1756; DB 2; Length 371;
Best Local Similarity 99.4%; Pred. No. 6.6e-157;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 60
DB 42 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 101
QY 61 GLYSLSSVTVFPSSSLGTQTYICNVNHPKSNVTVDGVVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 102 GLYSLSSVTVFPSSSLGTQTYICNVNHPKSNVTVDGVVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 161
QY 121 PSVFLPPPKDFTLMSRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 162 PSVFLPPPKDFTLMSRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 221
QY 181 STYRVVSVLTVLDHQLWNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 222 STYRVVSVLTVLDHQLWNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 281
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRW 300

; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0444PIC3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-10-157-408-7
Query Match 99.5%; Score 1756; DB 2; Length 371;
Best Local Similarity 99.4%; Pred. No. 6.6e-157;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 60
DB 42 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 101
QY 61 GLYSLSSVTVFPSSSLGTQTYICNVNHPKSNVTVDGVVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 102 GLYSLSSVTVFPSSSLGTQTYICNVNHPKSNVTVDGVVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 161
QY 121 PSVFLPPPKDFTLMSRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 162 PSVFLPPPKDFTLMSRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 221
QY 181 STYRVVSVLTVLDHQLWNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 222 STYRVVSVLTVLDHQLWNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 281
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRW 341
```


Qy	241	LTKQVSLTCLVKGPYSDIAVWEESNQGPENNYKTTPEVLDSGDGFFLYSKLTVDKSRW	300
Db	357	LTKQVSLTCLVKGPYSDIAVWEESNQGPENNYKTTPEVLDSGDGFFLYSKLTVDKSRW	416
Qy	301	QQGNVFCSCVMHEALHNNHYTKQSLSPCK	330
Db	417	QQGNVFCSCVMHEALHNNHYTKQSLSPCK	446

```

RESULT 8
US-08-458-516-13.
; Sequence 13, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-516-13

```

Query Match	99.5%;	Score 1756;	DB 1;	Length 449;
Best Local Similarity	99.4%;	Pred. No. 8.7e-157;		
Matches 328;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	ASTKGPVVFPLAPSSKSTSGTGAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS	60	
Db	120	ASTKGPVVFPLAPSSKSTSGTGAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS	179	
QY	61	GLYSLSSVWTVPSSSLGTQTVICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA	120	
Db	180	GLYSLSSVWTVPSSSLGTQTVICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELLGG	239	
QY	121	PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNNYVDGVEVHNNAKTKPRRSQYN	180	
Db	240	PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNNYVDGVEVHNNAKTKPRRSQYN	299	
QY	181	STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQQPPEPQVYITLPPSRDE	240	

300	STYRVUSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAQGPQRPQVYTLPPSRDE	359
241	LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW	300
360	LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW	419
301	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	330
420	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	449

RESULT 9
 US-08-030-175-41
 : Sequence 41, Application US/08030175
 : Patent No. 6767996
 : GENERAL INFORMATION:
 : APPLICANT: Gorman, Scott D.
 : APPLICANT: Clark, Michael R.
 : APPLICANT: Cobbold, Stephen P.
 : APPLICANT: Waldmann, Herman
 : TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION
 : NUMBER OF SEQUENCES: 43
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.
 : STREET: 555 13TH ST., NW Suite 701 East
 : CITY: Washington
 : STATE: D. C.
 : COUNTRY: U.S.
 : ZIP: 20004
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk, 5.25 inch, 360 kb storage
 : COMPUTER: IBM AT compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2
 : SOFTWARE: Wordperfect 5.0 (Dos Text)
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/030,175
 : FILING DATE: 17-MAY-1993
 : CLASSIFICATION: 424
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: PCT/GB91/01578
 : FILING DATE: 13-SEP-1991
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Ernst, Barbara G.
 : REGISTRATION NUMBER: 30,377
 : REFERENCE/DOCKET NUMBER: 1768-113
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (202) 783-6040
 : TELEFAX: (202) 783-6031
 : INFORMATION FOR SEQ ID NO: 41:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 467 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-030-175-41

	Query Match	99.5%	Score 1756;	DB 2;	Length 467;
	Best Local Similarity	99.4%;	Pred. No. 9.2e-157;		
	Matches 328;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0
Qy	1	ASTKGPVSFPLPSSKSTSGGTAALGCLVXDYFP	PPVTVS	WNSGALTS	GVHTFP
Db	138	ASTKGPVSFPLPSSKSTSGGTAALGCLVXDYFP	PPVTVS	WNSGALTS	GVHTFP
Qy	61	GLYSLSVWTVPPSSSLGTQTYICNVNHKPSNTK	VDKVPK	SCDKTHT	CPCPAP
Db	198	GLYSLSVWTVPPSSSLGTQTYICNVNHKPSNTK	VDKVPK	SCDKTHT	CPCPAP
Qy	121	PSVFLPPPKDITLMISRTPEVTCVVDVSHED	PEVKFN	VYVDGVEV	HNATK
Db	258	PSVFLPPPKDITLMISRTPEVTCVVDVSHED	PEVKFN	VYVDGVEV	HNATK
Qy	181	STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAP	IEKTI	ISAKAG	PREPQV

Db 318 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 437
QY 301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
Db 438 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 467

RESULT 10
US-08-030-175-42
; Sequence 42, Application US/08030175
; Patent No. 6767996
; GENERAL INFORMATION:
; APPLICANT: Gorman, Scott D.
; APPLICANT: Clark, Michael R.
; APPLICANT: Cobbold, Stephen P.
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.
; STREET: 555 13TH St., NW, Suite 701 East
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage
; COMPUTER: IBM AT compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2
; SOFTWARE: WordPerfect 5.0 (Dos Text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/030,175
; FILING DATE: 17-MAY-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01578
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1768-113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-030-175-42

Query Match 99.5%; Score 1756; DB 2; Length 467;
Best Local Similarity 99.4%; Pred. No. 9.2e-157;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197
QY 61 GLYSLSSVTVTPSSSLGTQYICNVNHPKSNITKVDKKEPKSCDKTHHTCCPCPAPELAGA 120
Db 198 GLYSLSSVTVTPSSSLGTQYICNVNHPKSNITKVDKKEPKSCDKTHHTCCPCPAPELGG 257
QY 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 180
Db 258 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 317

QY 181 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 318 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 437
QY 301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
Db 438 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 467

RESULT 11
US-10-104-047-3730
; Sequence 3730, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cdna
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3730
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3730

Query Match 99.5%; Score 1756; DB 2; Length 470;
Best Local Similarity 99.4%; Pred. No. 9.3e-157;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
QY 61 GLYSLSSVTVTPSSSLGTQYICNVNHPKSNITKVDKKEPKSCDKTHHTCCPCPAPELAGA 120
Db 201 GLYSLSSVTVTPSSSLGTQYICNVNHPKSNITKVDKKEPKSCDKTHHTCCPCPAPELGG 260
QY 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 180
Db 261 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 320
QY 181 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 321 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 380
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 440
QY 301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
Db 441 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470

RESULT 12
US-08-378-939-10
; Sequence 10, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ

```
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-939-10

Query Match 99.5%; Score 1756; DB 1; Length 476;
Best Local Similarity 99.4%; Pred. No. 9.5e-157;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGSPVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 60
Db 147 ASTKGSPVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 206
QY 61 GLYSLSVVTVPSSSLGTTQYICNVNHPKSNKVDKKVPEKSKCDKHTHTCCPCAPAPLAGA 120
Db 207 GLYSLSVVTVPSSSLGTTQYICNVNHPKSNKVDKKVPEKSKCDKHTHTCCPCAPAPLLGG 266
QY 121 PSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 267 PSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
QY 181 STYRVVSVLTVHLQDWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 240
Db 327 STYRVVSVLTVHLQDWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 386
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSLKLTVDKSRW 300
Db 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSLKLTVDKSRW 446
QY 301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
Db 447 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476

RESULT 13
US-09-746-359A-54
; Sequence 54, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
```

```
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekhar, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-54

Query Match 99.5%; Score 1756; DB 2; Length 547;
Best Local Similarity 99.4%; Pred. No. 1.2e-156;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGSPVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 60
Db 218 ASTKGSPVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 277
QY 61 GLYSLSVVTVPSSSLGTTQYICNVNHPKSNKVDKKVPEKSKCDKHTHTCCPCAPAPLAGA 120
Db 278 GLYSLSVVTVPSSSLGTTQYICNVNHPKSNKVDKKVPEKSKCDKHTHTCCPCAPAPLLGG 337
QY 121 PSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 338 PSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 397
QY 181 STYRVVSVLTVHLQDWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 240
Db 398 STYRVVSVLTVHLQDWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 457
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSLKLTVDKSRW 300
Db 458 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSLKLTVDKSRW 517
QY 301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
Db 518 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 547

RESULT 14
US-09-825-561A-16
; Sequence 16, Application US/09825561A
; Patent No. 6777539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 6777539ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 567
; TYPE: PRT
```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: soluble zalphallin/IgGammal polypeptide
US-09-825-561A-16

Query Match          99.5%; Score 1756; DB 2; Length 567;
Best Local Similarity 99.4%; Pred. No. 1.2e-156;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 238 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 297

QY 61 GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
DB 298 GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 357

QY 121 PSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 358 PSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 417

QY 181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 418 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 477

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
DB 478 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 537

QY 301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
DB 538 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 567
```

```

RESULT 15
US-09-746-359A-53
; Sequence 53, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia B.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-53

Query Match          99.5%; Score 1756; DB 2; Length 571;
Best Local Similarity 99.4%; Pred. No. 1.2e-156;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 242 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 301
```

```

QY 61 GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
DB 302 GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 361

QY 121 PSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 362 PSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 421

QY 181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 422 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 481

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
DB 482 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 541

QY 301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
DB 542 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 571

Search completed: June 10, 2006, 12:08:45
Job time : 57.982 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 12, 2006, 17:10:25 ; Search time 307.346 Seconds
(without alignments)
497.358 Million cell updates/sec

Title: US-10-733-563-110
Perfect score: 1765
Sequence: 1 ASTKGPSVFLAPSSKSTSG.....MHEALHNNHYTKSLSPGK 330

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pcp:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pcp:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pcp:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pcp:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pcp:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1765	100.0	330	4	US-10-733-563-110
2	1765	100.0	333	4	US-10-272-899A-10
3	1765	100.0	333	4	US-10-733-563-114
4	1765	100.0	356	4	US-10-272-899A-70
5	1765	100.0	448	4	US-10-171-452A-42
6	1765	100.0	448	4	US-10-171-452A-54
7	1765	100.0	448	4	US-10-353-708-42
8	1765	100.0	448	4	US-10-353-708-54
9	1765	100.0	448	4	US-10-731-984-8
10	1765	100.0	448	4	US-10-731-984-24
11	1765	100.0	448	6	US-11-158-505-8
12	1765	100.0	448	6	US-11-158-505-24
13	1765	100.0	462	6	US-11-177-648-9
14	1765	100.0	462	6	US-11-177-648-26
15	1765	100.0	462	6	US-11-177-648-27
16	1765	100.0	462	6	US-11-177-648-28
17	1765	100.0	462	6	US-11-177-648-29
18	1765	100.0	462	6	US-11-177-648-30
19	1765	100.0	462	6	US-11-177-648-31
20	1765	100.0	462	6	US-11-177-648-32
21	1765	100.0	462	6	US-11-177-648-33
22	1765	100.0	462	6	US-11-177-648-79
23	1765	100.0	462	6	US-11-177-648-92
24	1765	100.0	462	6	US-11-177-648-93
25	1765	100.0	462	6	US-11-177-648-94
26	1765	100.0	462	6	US-11-177-648-95
27	1765	100.0	462	6	US-11-177-648-96

Sequence 97, Appl	US-11-177-648-97	462	100.0	28	1765	100.0
Sequence 98, Appl	US-11-177-648-98	462	100.0	29	1765	100.0
Sequence 53, Appl	US-10-171-452A-53	467	100.0	30	1765	100.0
Sequence 53, Appl	US-10-353-708-53	467	100.0	31	1765	100.0
Sequence 7, Appl	US-10-731-984-7	467	100.0	32	1765	100.0
Sequence 23, Appl	US-10-731-984-23	467	100.0	33	1765	100.0
Sequence 5, Appl	US-11-158-505-5	467	100.0	34	1765	100.0
Sequence 7, Appl	US-11-158-505-7	467	100.0	35	1765	100.0
Sequence 21, Appl	US-11-158-505-21	467	100.0	36	1765	100.0
Sequence 23, Appl	US-11-158-505-23	467	100.0	37	1765	100.0
Sequence 13, Appl	US-10-467-253-13	473	98.7	38	1759	98.7
Sequence 72, Appl	US-10-404-724-72	469	99.6	39	1758	99.6
Sequence 15, Appl	US-09-995-898A-15	330	99.5	40	1756	99.5
Sequence 38, Appl	US-09-892-949-38	330	99.5	41	1756	99.5
Sequence 20, Appl	US-10-047-542-20	330	99.5	42	1756	99.5
Sequence 68, Appl	US-10-269-805-68	330	99.5	43	1756	99.5
Sequence 8, Appl	US-10-310-719-8	330	99.5	44	1756	99.5
Sequence 1, Appl	US-10-112-582-1	330	99.5	45	1756	99.5
Sequence 81, Appl	US-10-320-231A-81	330	99.5	46	1756	99.5
Sequence 6, Appl	US-10-383-902A-6	330	99.5	47	1756	99.5
Sequence 2, Appl	US-10-408-901-2	330	99.5	48	1756	99.5
Sequence 15, Appl	US-10-420-034A-15	330	99.5	49	1756	99.5
Sequence 5, Appl	US-10-257-907-5	330	99.5	50	1756	99.5
Sequence 2, Appl	US-10-656-769-2	330	99.5	51	1756	99.5
Sequence 38, Appl	US-10-772-531-38	330	99.5	52	1756	99.5
Sequence 1, Appl	US-10-479-326-1	330	99.5	53	1756	99.5
Sequence 8, Appl	US-10-815-449-8	330	99.5	54	1756	99.5
Sequence 2, Appl	US-10-684-957-2	330	99.5	55	1756	99.5
Sequence 6, Appl	US-10-886-838-6	330	99.5	56	1756	99.5
Sequence 3, Appl	US-10-822-300-3	330	99.5	57	1756	99.5
Sequence 7, Appl	US-10-822-300-7	330	99.5	58	1756	99.5
Sequence 3, Appl	US-10-687-118-3	330	99.5	59	1756	99.5
Sequence 7, Appl	US-10-687-118-7	330	99.5	60	1756	99.5
Sequence 2, Appl	US-10-901-735-2	330	99.5	61	1756	99.5
Sequence 22, Appl	US-10-698-907-22	330	99.5	62	1756	99.5
Sequence 7, Appl	US-10-928-305-7	330	99.5	63	1756	99.5
Sequence 5, Appl	US-10-480-109-5	330	99.5	64	1756	99.5
Sequence 2, Appl	US-10-891-658-2	330	99.5	65	1756	99.5
Sequence 81, Appl	US-10-867-506-81	330	99.5	66	1756	99.5
Sequence 31, Appl	US-10-937-596-31	330	99.5	67	1756	99.5
Sequence 45, Appl	US-10-893-576-45	330	99.5	68	1756	99.5
Sequence 8, Appl	US-10-868-373-8	330	99.5	69	1756	99.5
Sequence 139, App	US-10-977-369-139	330	99.5	70	1756	99.5
Sequence 60, Appl	US-10-901-736-60	330	99.5	71	1756	99.5
Sequence 38, Appl	US-10-982-555-38	330	99.5	72	1756	99.5
Sequence 20, Appl	US-10-493-909-20	330	99.5	73	1756	99.5
Sequence 68, Appl	US-10-982-440-68	330	99.5	74	1756	99.5
Sequence 1, Appl	US-11-004-054-1	330	99.5	75	1756	99.5
Sequence 22, Appl	US-11-026-998-22	330	99.5	76	1756	99.5
Sequence 44, Appl	US-11-027-309A-22	330	99.5	77	1756	99.5
Sequence 44, Appl	US-11-090-836-44	330	99.5	78	1756	99.5
Sequence 44, Appl	US-11-090-846-44	330	99.5	79	1756	99.5
Sequence 24, Appl	US-11-090-847-44	330	99.5	80	1756	99.5
Sequence 24, Appl	US-11-102-403-24	330	99.5	81	1756	99.5
Sequence 26, Appl	US-11-102-403-26	330	99.5	82	1756	99.5
Sequence 11, Appl	US-11-022-289-11	330	99.5	83	1756	99.5
Sequence 1, Appl	US-11-075-351-1	330	99.5	84	1756	99.5
Sequence 15, Appl	US-11-165-141-15	330	99.5	85	1756	99.5
Sequence 3, Appl	US-11-102-621-3	330	99.5	86	1756	99.5
Sequence 7, Appl	US-11-102-621-7	330	99.5	87	1756	99.5
Sequence 164, App	US-11-005-726-164	330	99.5	88	1756	99.5
Sequence 1, Appl	US-11-124-620-1	330	99.5	89	1756	99.5
Sequence 136, App	US-11-233-683-1	330	99.5	90	1756	99.5
Sequence 98, Appl	US-11-218-813-136	330	99.5	91	1756	99.5
Sequence 167, App	US-09-990-586-98	332	99.5	92	1756	99.5
Sequence 98, Appl	US-10-310-113-167	332	99.5	93	1756	99.5
Sequence 98, Appl	US-10-230-880-98	332	99.5	94	1756	99.5
Sequence 8, Appl	US-11-122-622-98	332	99.5	95	1756	99.5
Sequence 35, Appl	US-10-272-899A-8	333	99.5	96	1756	99.5
Sequence 72, Appl	US-11-024-251-35	335	99.5	97	1756	99.5
Sequence 7, Appl	US-10-272-899A-72	356	99.5	98	1756	99.5
Sequence 7, Appl	US-10-157-408-7	371	99.5	99	1756	99.5
	US-10-097-044A-7	371	99.5	100	1756	99.5

101	1756	99.5	371	4	US-10-769-247-7	Sequence 7, Appli	174	1756	99.5	470	5	US-10-887-230-14	Sequence 14, Appli
102	1756	99.5	442	4	US-10-226-435A-12	Sequence 12, Appli	175	1756	99.5	470	5	US-10-938-353-98	Sequence 98, Appli
103	1756	99.5	442	4	US-10-487-322-12	Sequence 12, Appli	176	1756	99.5	470	6	US-11-072-512-3730	Sequence 3730, Ap
104	1756	99.5	442	5	US-10-487-326-12	Sequence 12, Appli	177	1756	99.5	471	4	US-10-108-260A-4294	Sequence 4294, Ap
105	1756	99.5	442	5	US-10-487-326-21	Sequence 21, Appli	178	1756	99.5	471	4	US-10-108-260A-4073	Sequence 4073, Ap
106	1756	99.5	442	5	US-10-486-908-12	Sequence 12, Appli	179	1756	99.5	472	5	US-10-108-260A-4073	Sequence 20, Appli
107	1756	99.5	442	5	US-10-486-908-12	Sequence 12, Appli	179	1756	99.5	472	5	US-10-497-475-20	Sequence 20, Appli
108	1756	99.5	442	5	US-10-486-908-16	Sequence 16, Appli	180	1756	99.5	473	4	US-10-108-260A-4284	Sequence 4284, Ap
109	1756	99.5	442	5	US-10-512-527-12	Sequence 12, Appli	181	1756	99.5	474	4	US-10-108-260A-4282	Sequence 4282, Ap
110	1756	99.5	442	5	US-10-512-527-21	Sequence 21, Appli	182	1756	99.5	476	3	US-09-747-669A-3	Sequence 3, Appli
111	1756	99.5	442	5	US-10-487-324A-12	Sequence 12, Appli	183	1756	99.5	476	4	US-10-290-703-3	Sequence 3, Appli
112	1756	99.5	442	6	US-10-487-324A-21	Sequence 21, Appli	184	1756	99.5	476	4	US-10-409-938-15	Sequence 15, Appli
113	1756	99.5	442	4	US-11-224-623-12	Sequence 12, Appli	185	1756	99.5	476	4	US-10-108-260A-4288	Sequence 4288, Ap
114	1756	99.5	444	4	US-10-150-475A-6	Sequence 6, Appli	186	1756	99.5	477	4	US-10-108-260A-4289	Sequence 4289, Ap
115	1756	99.5	444	4	US-10-704-522-6	Sequence 6, Appli	187	1756	99.5	485	5	US-10-887-230-26	Sequence 26, Appli
116	1756	99.5	444	6	US-11-136-538-7	Sequence 7, Appli	188	1756	99.5	541	4	US-10-471-151-32	Sequence 32, Appli
117	1756	99.5	444	6	US-11-172-320-6	Sequence 6, Appli	189	1756	99.5	541	4	US-10-807-837-4	Sequence 4, Appli
118	1756	99.5	444	6	US-11-173-969-6	Sequence 6, Appli	190	1756	99.5	547	3	US-09-746-359A-54	Sequence 54, Appli
119	1756	99.5	445	4	US-10-320-231A-79	Sequence 79, Appli	191	1756	99.5	547	3	US-09-951-268-40	Sequence 40, Appli
120	1756	99.5	445	4	US-10-408-901-34	Sequence 34, Appli	192	1756	99.5	547	3	US-09-745-732A-54	Sequence 54, Appli
121	1756	99.5	445	4	US-10-408-901-34	Sequence 42, Appli	193	1756	99.5	547	4	US-10-424-658-54	Sequence 54, Appli
122	1756	99.5	445	5	US-10-867-506-79	Sequence 79, Appli	194	1756	99.5	551	6	US-11-022-289-7	Sequence 7, Appli
123	1756	99.5	445	5	US-10-937-596-3	Sequence 3, Appli	195	1756	99.5	551	6	US-11-022-289-8	Sequence 8, Appli
124	1756	99.5	446	4	US-10-408-901-30	Sequence 30, Appli	196	1756	99.5	557	6	US-11-022-289-4	Sequence 4, Appli
125	1756	99.5	446	4	US-10-408-901-38	Sequence 38, Appli	197	1756	99.5	557	6	US-11-022-289-5	Sequence 5, Appli
126	1756	99.5	446	4	US-10-408-901-46	Sequence 46, Appli	198	1756	99.5	557	6	US-11-022-289-6	Sequence 6, Appli
127	1756	99.5	446	4	US-10-684-957-19	Sequence 19, Appli	199	1756	99.5	558	4	US-10-471-151-31	Sequence 31, Appli
128	1756	99.5	446	4	US-10-408-901-50	Sequence 50, Appli	200	1756	99.5	567	3	US-09-825-561A-16	Sequence 16, Appli
129	1756	99.5	446	4	US-10-435-299-7	Sequence 7, Appli	201	1756	99.5	567	5	US-10-872-087-16	Sequence 16, Appli
130	1756	99.5	446	5	US-10-947-432-2	Sequence 2, Appli	202	1756	99.5	571	3	US-09-746-359A-53	Sequence 53, Appli
131	1756	99.5	447	3	US-09-256-156-1	Sequence 1, Appli	203	1756	99.5	571	3	US-09-951-268-30	Sequence 30, Appli
132	1756	99.5	447	5	US-10-684-957-17	Sequence 17, Appli	204	1756	99.5	571	3	US-09-745-732A-53	Sequence 53, Appli
133	1756	99.5	447	5	US-10-684-957-19	Sequence 19, Appli	205	1756	99.5	571	4	US-10-424-658-53	Sequence 53, Appli
134	1756	99.5	447	5	US-10-684-957-21	Sequence 21, Appli	206	1756	99.5	600	4	US-10-334-235-38	Sequence 38, Appli
135	1756	99.5	447	6	US-11-010-797-2	Sequence 2, Appli	207	1756	99.5	613	5	US-10-769-144-10	Sequence 10, Appli
136	1756	99.5	448	4	US-10-378-567-2	Sequence 2, Appli	208	1756	99.5	613	5	US-10-903-191-10	Sequence 10, Appli
137	1756	99.5	448	5	US-10-985-584-18	Sequence 18, Appli	209	1756	99.5	659	4	US-10-809-790-4	Sequence 4, Appli
138	1756	99.5	448	5	US-10-635-908-16	Sequence 16, Appli	210	1756	99.5	731	3	US-09-825-012-46	Sequence 46, Appli
139	1756	99.5	449	5	US-10-635-908-18	Sequence 18, Appli	211	1756	99.5	741	3	US-09-825-012-55	Sequence 55, Appli
140	1756	99.5	449	5	US-10-476-265-12	Sequence 12, Appli	212	1756	99.5	951	3	US-09-313-942-9	Sequence 9, Appli
141	1756	99.5	449	6	US-11-095-584-10	Sequence 10, Appli	214	1756	99.5	951	4	US-10-287-035-9	Sequence 9, Appli
142	1756	99.5	449	6	US-11-056-776-5	Sequence 5, Appli	215	1756	99.5	951	4	US-10-282-162-9	Sequence 9, Appli
143	1756	99.5	450	5	US-10-503-504-11	Sequence 11, Appli	216	1756	99.5	951	6	US-11-134-114-9	Sequence 9, Appli
144	1756	99.5	450	5	US-10-484-280-18	Sequence 18, Appli	217	1756	99.5	972	4	US-10-418-836-38	Sequence 38, Appli
145	1756	99.5	450	6	US-11-005-726-161	Sequence 161, App	218	1756	99.5	972	6	US-11-007-886-38	Sequence 38, Appli
146	1756	99.5	450	6	US-11-049-536-701	Sequence 701, App	219	1756	99.5	975	6	US-10-418-836-39	Sequence 39, Appli
147	1756	99.5	450	6	US-11-199-739-701	Sequence 701, App	220	1756	99.5	975	6	US-11-007-886-39	Sequence 39, Appli
148	1756	99.5	451	3	US-09-822-698A-26	Sequence 26, Appli	221	1754	99.4	330	5	US-10-966-673-27	Sequence 27, Appli
149	1756	99.5	451	5	US-10-849-615-69	Sequence 69, Appli	222	1754	99.4	330	5	US-10-966-673-29	Sequence 29, Appli
150	1756	99.5	451	5	US-10-822-231-1	Sequence 1, Appli	223	1754	99.4	592	5	US-10-016-686-4	Sequence 4, Appli
151	1756	99.5	451	6	US-11-158-505-33	Sequence 33, Appli	224	1753	99.3	330	4	US-10-679-620-58	Sequence 58, Appli
152	1756	99.5	453	4	US-10-813-483-6	Sequence 6, Appli	225	1753	99.3	330	5	US-10-822-300-71	Sequence 71, Appli
153	1756	99.5	453	5	US-10-484-790A-18	Sequence 18, Appli	226	1753	99.3	330	5	US-10-687-118-71	Sequence 71, Appli
154	1756	99.5	453	5	US-10-891-658-41	Sequence 41, Appli	227	1753	99.3	330	5	US-10-966-673-36	Sequence 36, Appli
155	1756	99.5	453	5	US-10-497-475-12	Sequence 12, Appli	228	1753	99.3	330	5	US-10-966-673-48	Sequence 48, Appli
156	1756	99.5	453	6	US-11-013-966-6	Sequence 6, Appli	229	1753	99.3	330	6	US-11-132-143-58	Sequence 58, Appli
157	1756	99.5	453	6	US-11-208-422-23	Sequence 23, Appli	230	1753	99.3	330	6	US-11-102-621-71	Sequence 71, Appli
158	1756	99.5	457	5	US-10-778-915-1	Sequence 1, Appli	231	1753	99.3	446	5	US-10-822-300-121	Sequence 121, App
159	1756	99.5	464	5	US-10-938-353-102	Sequence 102, App	232	1753	99.3	446	6	US-11-102-621-121	Sequence 121, App
160	1756	99.5	464	6	US-11-218-813-132	Sequence 132, App	233	1753	99.3	447	5	US-10-822-300-132	Sequence 132, App
161	1756	99.5	465	5	US-10-887-230-43	Sequence 43, Appli	234	1753	99.3	447	6	US-11-102-621-132	Sequence 132, App
162	1756	99.5	465	6	US-11-034-655-5	Sequence 5, Appli	235	1753	99.3	448	4	US-10-449-566-107	Sequence 107, App
163	1756	99.5	465	6	US-11-034-655-12	Sequence 12, Appli	236	1753	99.3	465	4	US-10-404-724-8	Sequence 8, Appli
164	1756	99.5	467	4	US-10-108-260A-4293	Sequence 4293, Ap	237	1753	99.3	465	4	US-10-404-724-23	Sequence 23, Appli
165	1756	99.5	467	4	US-10-656-769-32	Sequence 32, Appli	238	1753	99.3	465	5	US-10-816-276-4	Sequence 4, Appli
166	1756	99.5	468	5	US-10-769-144-2	Sequence 2, Appli	239	1753	99.3	465	5	US-10-816-276-19	Sequence 19, Appli
167	1756	99.5	468	5	US-10-476-265-20	Sequence 20, Appli	240	1753	99.3	465	5	US-10-816-276-21	Sequence 21, Appli
168	1756	99.5	468	5	US-10-943-640-4	Sequence 4, Appli	241	1753	99.3	465	5	US-10-429-660-10	Sequence 10, Appli
169	1756	99.5	468	5	US-10-903-191-2	Sequence 2, Appli	242	1753	99.3	469	5	US-10-429-662-10	Sequence 10, Appli
170	1756	99.5	468	6	US-11-056-776-6	Sequence 6, Appli	243	1753	99.3	469	5	US-10-961-567A-9	Sequence 9, Appli
171	1756	99.5	469	4	US-10-656-769-20	Sequence 20, Appli	244	1753	99.3	470	5	US-10-656-769-20	Sequence 9, Appli
172	1756	99.5	469	4	US-10-656-769-26	Sequence 26, Appli	245	1753	99.3	713	4	US-10-679-620-64	Sequence 64, Appli
173	1756	99.5	470	4	US-10-104-047-3730	Sequence 3730, Ap	246	1753	99.3	713	6	US-11-132-143-64	Sequence 64, Appli

247	1753	99.3	715	4	US-10-679-620-62	Sequence 62, Appl	320	1750	99.2	330	5	US-10-822-300-67	Sequence 67, Appl
248	1753	99.3	715	6	US-11-132-143-62	Sequence 62, Appl	321	1750	99.2	330	5	US-10-822-300-68	Sequence 68, Appl
249	1752	99.3	329	6	US-11-186-423-4	Sequence 4, Appl	322	1750	99.2	330	5	US-10-822-300-69	Sequence 69, Appl
250	1752	99.3	330	5	US-10-966-673-16	Sequence 16, Appl	323	1750	99.2	330	5	US-10-687-118-67	Sequence 67, Appl
251	1752	99.3	330	5	US-10-966-673-24	Sequence 24, Appl	324	1750	99.2	330	5	US-10-687-118-68	Sequence 68, Appl
252	1752	99.3	330	5	US-10-966-673-46	Sequence 46, Appl	325	1750	99.2	330	5	US-10-687-118-69	Sequence 69, Appl
253	1752	99.3	330	5	US-10-966-673-55	Sequence 55, Appl	326	1750	99.2	330	5	US-10-901-735-3	Sequence 3, Appl
254	1752	99.3	451	6	US-10-822-231-4	Sequence 4, Appl	327	1750	99.2	330	5	US-10-706-689-3	Sequence 3, Appl
255	1752	99.3	451	6	US-11-124-620-7	Sequence 7, Appl	328	1750	99.2	330	5	US-10-706-689-2	Sequence 2, Appl
256	1752	99.3	451	6	US-11-208-422-25	Sequence 25, Appl	329	1750	99.2	330	5	US-10-988-360-2	Sequence 2, Appl
257	1752	99.3	468	5	US-10-981-738-13	Sequence 13, Appl	330	1750	99.2	330	5	US-10-988-360-3	Sequence 3, Appl
258	1752	99.3	471	4	US-10-108-260A-4285	Sequence 4285, Ap	331	1750	99.2	330	5	US-10-966-673-2	Sequence 2, Appl
259	1752	99.3	475	3	US-09-740-002-27	Sequence 27, Appl	332	1750	99.2	330	5	US-10-966-673-3	Sequence 3, Appl
260	1752	99.3	475	4	US-10-325-698-27	Sequence 27, Appl	333	1750	99.2	330	5	US-10-966-673-4	Sequence 4, Appl
261	1752	99.3	476	3	US-09-758-173-4	Sequence 4, Appl	334	1750	99.2	330	5	US-10-966-673-8	Sequence 8, Appl
262	1752	99.3	476	3	US-09-758-173-12	Sequence 12, Appl	335	1750	99.2	330	5	US-10-966-673-9	Sequence 9, Appl
263	1752	99.3	476	3	US-09-948-4298-4	Sequence 4, Appl	336	1750	99.2	330	5	US-10-966-673-10	Sequence 10, Appl
264	1752	99.3	476	3	US-09-948-4298B-12	Sequence 12, Appl	337	1750	99.2	330	5	US-10-966-673-11	Sequence 11, Appl
265	1752	99.3	476	4	US-10-124-905-4	Sequence 4, Appl	338	1750	99.2	330	5	US-10-966-673-13	Sequence 13, Appl
266	1752	99.3	476	4	US-10-124-905-12	Sequence 12, Appl	339	1750	99.2	330	5	US-10-966-673-14	Sequence 14, Appl
267	1752	99.3	476	4	US-10-124-807-4	Sequence 4, Appl	340	1750	99.2	330	5	US-10-966-673-15	Sequence 15, Appl
268	1752	99.3	476	4	US-10-124-807-12	Sequence 12, Appl	341	1750	99.2	330	5	US-10-966-673-28	Sequence 28, Appl
269	1752	99.3	476	4	US-10-291-532-4	Sequence 4, Appl	342	1750	99.2	330	5	US-10-966-673-32	Sequence 32, Appl
270	1752	99.3	476	4	US-10-291-532-12	Sequence 12, Appl	343	1750	99.2	330	5	US-10-966-673-33	Sequence 33, Appl
271	1752	99.3	476	5	US-10-986-780-4	Sequence 4, Appl	344	1750	99.2	330	5	US-10-966-673-34	Sequence 34, Appl
272	1752	99.3	476	5	US-10-986-780-12	Sequence 12, Appl	345	1750	99.2	330	5	US-10-966-673-37	Sequence 37, Appl
273	1752	99.3	476	6	US-11-139-499-4	Sequence 4, Appl	346	1750	99.2	330	5	US-10-966-673-39	Sequence 39, Appl
274	1752	99.3	476	6	US-11-139-499-12	Sequence 12, Appl	347	1750	99.2	330	5	US-10-966-673-40	Sequence 40, Appl
275	1752	99.3	478	3	US-09-758-173-8	Sequence 8, Appl	348	1750	99.2	330	5	US-10-966-673-47	Sequence 47, Appl
276	1752	99.3	478	3	US-09-948-4298B-8	Sequence 8, Appl	349	1750	99.2	330	5	US-10-966-673-52	Sequence 52, Appl
277	1752	99.3	478	4	US-10-124-905-8	Sequence 8, Appl	350	1750	99.2	330	5	US-10-966-673-53	Sequence 53, Appl
278	1752	99.3	478	4	US-10-124-807-8	Sequence 8, Appl	351	1750	99.2	330	5	US-10-966-673-54	Sequence 54, Appl
279	1752	99.3	478	5	US-10-986-780-8	Sequence 8, Appl	352	1750	99.2	330	5	US-10-966-673-56	Sequence 56, Appl
280	1752	99.3	478	5	US-10-986-780-8	Sequence 8, Appl	353	1750	99.2	330	5	US-10-966-673-57	Sequence 57, Appl
281	1752	99.3	478	6	US-11-139-499-8	Sequence 8, Appl	354	1750	99.2	330	6	US-11-022-289-1	Sequence 1, Appl
282	1751	99.2	330	5	US-10-822-300-70	Sequence 70, Appl	355	1750	99.2	330	6	US-11-102-621-67	Sequence 67, Appl
283	1751	99.2	330	5	US-10-687-118-70	Sequence 70, Appl	356	1750	99.2	330	6	US-11-102-621-68	Sequence 68, Appl
284	1751	99.2	330	5	US-10-966-673-1	Sequence 1, Appl	357	1750	99.2	330	6	US-11-102-621-69	Sequence 69, Appl
285	1751	99.2	330	5	US-10-966-673-12	Sequence 12, Appl	358	1750	99.2	330	6	US-11-201-825-55	Sequence 55, Appl
286	1751	99.2	330	5	US-10-966-673-17	Sequence 17, Appl	359	1750	99.2	446	5	US-10-822-300-119	Sequence 119, App
287	1751	99.2	330	5	US-10-966-673-20	Sequence 20, Appl	360	1750	99.2	446	5	US-10-822-300-120	Sequence 120, App
288	1751	99.2	330	5	US-10-966-673-21	Sequence 21, Appl	361	1750	99.2	446	6	US-11-102-621-119	Sequence 119, App
289	1751	99.2	330	5	US-10-966-673-35	Sequence 35, Appl	362	1750	99.2	446	6	US-11-102-621-120	Sequence 120, App
290	1751	99.2	330	5	US-10-966-673-38	Sequence 38, Appl	363	1750	99.2	447	5	US-10-822-300-130	Sequence 130, App
291	1751	99.2	330	5	US-10-966-673-43	Sequence 43, Appl	364	1750	99.2	447	6	US-10-822-300-131	Sequence 131, App
292	1751	99.2	330	5	US-10-966-673-51	Sequence 51, Appl	365	1750	99.2	447	6	US-11-102-621-130	Sequence 130, App
293	1751	99.2	330	6	US-11-102-621-70	Sequence 70, Appl	366	1750	99.2	447	6	US-11-102-621-131	Sequence 131, App
294	1751	99.2	447	4	US-10-474-832-4	Sequence 4, Appl	367	1750	99.2	449	6	US-11-154-337-17	Sequence 17, Appl
295	1751	99.2	447	4	US-10-474-832-6	Sequence 6, Appl	368	1750	99.2	449	6	US-11-182-908-24	Sequence 24, Appl
296	1751	99.2	448	4	US-10-411-037-56	Sequence 56, Appl	369	1750	99.2	451	3	US-09-920-171-14	Sequence 14, Appl
297	1751	99.2	448	4	US-10-411-026-56	Sequence 56, Appl	370	1750	99.2	451	3	US-09-920-171-16	Sequence 16, Appl
298	1751	99.2	448	4	US-10-411-026-56	Sequence 56, Appl	371	1750	99.2	451	3	US-09-920-171-18	Sequence 18, Appl
299	1751	99.2	448	4	US-10-411-049-56	Sequence 56, Appl	372	1750	99.2	451	3	US-09-925-179-65	Sequence 65, Appl
300	1751	99.2	448	4	US-10-410-930-56	Sequence 56, Appl	373	1750	99.2	451	3	US-09-925-179-66	Sequence 66, Appl
301	1751	99.2	448	4	US-10-410-997-56	Sequence 56, Appl	374	1750	99.2	451	3	US-09-925-179-68	Sequence 68, Appl
302	1751	99.2	448	4	US-10-411-012-56	Sequence 56, Appl	375	1750	99.2	451	3	US-09-792-938-2	Sequence 2, Appl
303	1751	99.2	448	4	US-10-287-994-56	Sequence 56, Appl	376	1750	99.2	451	4	US-10-113-996-14	Sequence 14, Appl
304	1751	99.2	448	4	US-10-410-913-56	Sequence 56, Appl	377	1750	99.2	451	4	US-10-113-996-16	Sequence 16, Appl
305	1751	99.2	448	5	US-10-410-980-56	Sequence 56, Appl	378	1750	99.2	451	4	US-10-113-986-18	Sequence 18, Appl
306	1751	99.2	448	5	US-10-410-897-56	Sequence 56, Appl	379	1750	99.2	451	4	US-10-292-869-2	Sequence 2, Appl
307	1751	99.2	448	5	US-10-492-261-56	Sequence 56, Appl	380	1750	99.2	451	4	US-10-423-299-4	Sequence 4, Appl
308	1751	99.2	448	6	US-11-183-205-56	Sequence 56, Appl	381	1750	99.2	451	4	US-10-835-642-2	Sequence 2, Appl
309	1751	99.2	470	4	US-10-108-260A-4292	Sequence 4292, Ap	382	1750	99.2	451	4	US-10-813-483-4	Sequence 4, Appl
310	1751	99.2	470	6	US-11-019-180-4	Sequence 4, Appl	383	1750	99.2	451	4	US-10-813-483-5	Sequence 5, Appl
311	1751	99.2	663	4	US-10-412-406-32	Sequence 32, Appl	384	1750	99.2	451	5	US-10-757-863-2	Sequence 2, Appl
312	1751	99.2	729	3	US-09-825-012-52	Sequence 52, Appl	385	1750	99.2	451	5	US-10-791-619-14	Sequence 14, Appl
313	1751	99.2	729	3	US-09-825-012-61	Sequence 61, Appl	386	1750	99.2	451	5	US-10-791-619-16	Sequence 16, Appl
314	1751	99.2	4852	4	US-10-412-406-33	Sequence 33, Appl	387	1750	99.2	451	5	US-10-791-619-18	Sequence 18, Appl
315	1750	99.2	330	3	US-09-301-593-22	Sequence 22, Appl	388	1750	99.2	451	5	US-10-714-000-2	Sequence 2, Appl
316	1750	99.2	330	4	US-10-121-464-20	Sequence 20, Appl	389	1750	99.2	451	5	US-10-698-073-9	Sequence 9, Appl
317	1750	99.2	330	4	US-10-159-006-22	Sequence 22, Appl	390	1750	99.2	451	5	US-10-968-237-65	Sequence 65, Appl
318	1750	99.2	331	4	US-10-688-925-53	Sequence 53, Appl	391	1750	99.2	451	5	US-10-968-237-66	Sequence 66, Appl
319	1750	99.2	330	4	US-10-741-481-45	Sequence 45, Appl	392	1750	99.2	451	5	US-10-968-237-68	Sequence 68, Appl

393	1750	99.2	451	5	US-10-982-470-2	Sequence 2, Appli	456	1749	99.1	330	5	US-10-966-673-30	Sequence 30, Appl
394	1750	99.2	451	5	US-10-923-327-7	Sequence 7, Appli	467	1749	99.1	330	5	US-10-966-673-31	Sequence 31, Appl
395	1750	99.2	451	5	US-10-923-327-9	Sequence 9, Appli	468	1749	99.1	330	5	US-10-966-673-42	Sequence 42, Appl
396	1750	99.2	451	5	US-10-923-327-11	Sequence 11, Appli	469	1749	99.1	330	5	US-10-966-673-45	Sequence 45, Appl
397	1750	99.2	451	6	US-11-013-966-4	Sequence 4, Appli	470	1749	99.1	330	5	US-10-966-673-49	Sequence 49, Appl
398	1750	99.2	451	6	US-11-013-966-5	Sequence 5, Appli	471	1749	99.1	330	5	US-10-966-673-50	Sequence 50, Appl
399	1750	99.2	451	6	US-11-158-839-2	Sequence 2, Appli	472	1749	99.1	449	6	US-11-080-587-6	Sequence 6, Appli
400	1750	99.2	451	6	US-11-208-432-20	Sequence 20, Appl	473	1749	99.1	450	6	US-11-155-843-176	Sequence 176, App
401	1750	99.2	451	6	US-11-208-422-21	Sequence 21, Appl	474	1748	99.0	330	5	US-10-966-673-22	Sequence 22, Appl
402	1750	99.2	451	6	US-11-208-422-22	Sequence 22, Appl	475	1748	99.0	330	5	US-10-966-673-25	Sequence 25, Appl
403	1750	99.2	452	3	US-09-726-258-71	Sequence 71, Appl	476	1748	99.0	330	5	US-10-966-673-41	Sequence 41, Appl
404	1750	99.2	452	4	US-10-818-765-4	Sequence 4, Appl	477	1748	99.0	330	5	US-10-966-673-44	Sequence 44, Appl
405	1750	99.2	452	5	US-10-861-049-16	Sequence 16, Appl	478	1748	99.0	448	4	US-10-171-452A-48	Sequence 48, Appl
406	1750	99.2	452	5	US-10-861-049-46	Sequence 46, Appl	479	1748	99.0	448	4	US-10-171-452A-60	Sequence 60, Appl
407	1750	99.2	452	6	US-11-021-874-16	Sequence 16, Appl	480	1748	99.0	448	4	US-10-353-708-48	Sequence 48, Appl
408	1750	99.2	452	6	US-11-021-874-46	Sequence 46, Appl	481	1748	99.0	448	4	US-10-353-708-60	Sequence 60, Appl
409	1750	99.2	452	6	US-11-005-677-4	Sequence 4, Appli	482	1748	99.0	448	4	US-10-731-984-16	Sequence 16, Appl
410	1750	99.2	452	6	US-11-006-136-4	Sequence 4, Appli	483	1748	99.0	448	4	US-10-731-984-32	Sequence 32, Appl
411	1750	99.2	452	6	US-11-120-338-14	Sequence 14, Appl	484	1748	99.0	448	6	US-11-158-505-16	Sequence 16, Appl
412	1750	99.2	452	6	US-11-107-028-32	Sequence 32, Appl	485	1748	99.0	448	6	US-11-158-505-32	Sequence 32, Appl
413	1750	99.2	452	6	US-11-108-820-26	Sequence 26, Appl	486	1748	99.0	449	3	US-03-736-371B-21	Sequence 21, Appl
414	1750	99.2	452	6	US-11-143-077-14	Sequence 14, Appl	487	1748	99.0	449	4	US-10-463-442-21	Sequence 21, Appl
415	1750	99.2	452	6	US-11-143-386-14	Sequence 14, Appl	488	1748	99.0	451	5	US-10-698-073-7	Sequence 7, Appli
416	1750	99.2	452	6	US-11-187-364-14	Sequence 14, Appl	489	1748	99.0	467	4	US-10-171-452A-41	Sequence 41, Appl
417	1750	99.2	452	6	US-11-208-422-27	Sequence 27, Appl	490	1748	99.0	467	4	US-10-171-452A-47	Sequence 47, Appl
418	1750	99.2	452	6	US-11-259-232-71	Sequence 71, Appl	491	1748	99.0	467	4	US-10-171-452A-59	Sequence 59, Appl
419	1750	99.2	453	3	US-09-301-593-18	Sequence 18, Appl	492	1748	99.0	467	4	US-10-353-708-41	Sequence 41, Appl
420	1750	99.2	453	4	US-10-159-006-18	Sequence 18, Appl	493	1748	99.0	467	4	US-10-353-708-47	Sequence 47, Appl
421	1750	99.2	454	5	US-10-835-641-22	Sequence 22, Appl	494	1748	99.0	467	4	US-10-353-708-59	Sequence 59, Appl
422	1750	99.2	470	4	US-10-020-786-9	Sequence 9, Appli	495	1748	99.0	467	4	US-10-731-984-15	Sequence 15, Appl
423	1750	99.2	470	4	US-10-227-694-5	Sequence 5, Appli	496	1748	99.0	467	4	US-10-731-984-31	Sequence 31, Appl
424	1750	99.2	470	5	US-10-754-212-6	Sequence 6, Appli	497	1748	99.0	467	6	US-11-158-505-13	Sequence 13, Appl
425	1750	99.2	470	5	US-10-697-995-3	Sequence 3, Appli	498	1748	99.0	467	6	US-11-158-505-15	Sequence 15, Appl
426	1750	99.2	470	5	US-10-697-995-6	Sequence 6, Appli	499	1748	99.0	467	6	US-11-158-505-29	Sequence 29, Appl
427	1750	99.2	470	5	US-10-697-995-18	Sequence 18, Appl	500	1748	99.0	467	6	US-11-158-505-31	Sequence 31, Appl
428	1750	99.2	470	6	US-11-071-291-9	Sequence 9, Appli	501	1748	99.0	467	6	US-11-158-505-72	Sequence 72, Appl
429	1750	99.2	471	5	US-10-877-363-4	Sequence 4, Appli	502	1748	99.0	469	4	US-10-108-260A-4287	Sequence 4287, Ap
430	1750	99.2	471	5	US-10-922-651-4	Sequence 4, Appli	503	1748	99.0	472	4	US-10-108-260A-4295	Sequence 4295, Ap
431	1750	99.2	471	5	US-10-861-049-4	Sequence 4, Appli	504	1748	99.0	475	3	US-09-740-002-25	Sequence 25, Appl
432	1750	99.2	471	6	US-11-021-874-4	Sequence 4, Appli	505	1748	99.0	475	4	US-10-325-698-25	Sequence 25, Appl
433	1750	99.2	471	6	US-11-106-820-25	Sequence 25, Appl	506	1747	99.0	330	4	US-10-366-709-52	Sequence 52, Appl
434	1750	99.2	471	6	US-11-190-364-22	Sequence 22, Appl	507	1747	99.0	330	5	US-10-822-300-76	Sequence 76, Appl
435	1750	99.2	471	6	US-11-147-780-22	Sequence 22, Appl	508	1747	99.0	330	5	US-10-687-118-76	Sequence 76, Appl
436	1750	99.2	476	4	US-10-020-786-11	Sequence 11, Appl	509	1747	99.0	330	5	US-11-102-621-76	Sequence 76, Appl
437	1750	99.2	476	5	US-10-697-995-9	Sequence 9, Appli	510	1747	99.0	446	5	US-10-822-300-122	Sequence 122, App
438	1750	99.2	476	6	US-11-071-291-11	Sequence 11, Appl	511	1747	99.0	446	6	US-11-102-621-122	Sequence 122, App
439	1750	99.2	476	6	US-10-697-995-12	Sequence 12, Appl	512	1747	99.0	447	4	US-10-379-392-116	Sequence 116, App
440	1750	99.2	548	6	US-11-022-289-3	Sequence 3, Appli	513	1747	99.0	447	6	US-10-822-300-133	Sequence 133, App
441	1750	99.2	557	6	US-11-022-289-2	Sequence 2, Appli	514	1747	99.0	447	6	US-11-102-621-133	Sequence 133, App
442	1750	99.2	564	6	US-11-022-289-10	Sequence 10, Appl	515	1747	99.0	448	4	US-10-449-566-111	Sequence 111, App
443	1750	99.2	666	5	US-10-981-356A-25	Sequence 25, Appl	516	1747	99.0	448	4	US-10-449-566-115	Sequence 115, App
444	1750	99.2	666	5	US-10-981-356A-27	Sequence 27, Appl	517	1747	99.0	448	4	US-10-467-546-4	Sequence 4, Appli
445	1750	99.2	666	6	US-11-096-046-27	Sequence 27, Appl	518	1747	99.0	448	5	US-10-666-332-4	Sequence 4, Appli
446	1750	99.2	667	5	US-10-764-428-7	Sequence 7, Appli	519	1747	99.0	449	4	US-10-318-397-22	Sequence 22, Appl
447	1750	99.2	667	5	US-10-764-428-13	Sequence 13, Appl	520	1747	99.0	449	4	US-10-317-747-22	Sequence 22, Appl
448	1750	99.2	667	5	US-10-764-428-25	Sequence 25, Appl	521	1747	99.0	450	3	US-09-796-848A-37	Sequence 37, Appl
449	1750	99.2	667	6	US-11-096-046-25	Sequence 25, Appl	522	1747	99.0	450	3	US-09-796-848A-39	Sequence 39, Appl
450	1750	99.2	669	5	US-10-764-428-21	Sequence 21, Appl	523	1747	99.0	450	3	US-09-796-848A-41	Sequence 41, Appl
451	1750	99.2	669	5	US-10-764-428-23	Sequence 23, Appl	524	1747	99.0	450	3	US-09-796-848A-43	Sequence 43, Appl
452	1750	99.2	670	5	US-10-764-428-5	Sequence 5, Appli	525	1747	99.0	450	3	US-09-796-848A-45	Sequence 45, Appl
453	1750	99.2	670	5	US-10-764-428-9	Sequence 9, Appli	526	1747	99.0	450	3	US-09-796-848A-47	Sequence 47, Appl
454	1750	99.2	670	5	US-10-764-428-11	Sequence 11, Appl	527	1747	99.0	450	3	US-09-796-848A-49	Sequence 49, Appl
455	1750	99.2	670	5	US-10-764-428-27	Sequence 27, Appl	528	1747	99.0	450	3	US-09-796-848A-51	Sequence 51, Appl
456	1750	99.2	692	5	US-10-981-356A-26	Sequence 26, Appl	529	1747	99.0	450	3	US-09-796-848A-53	Sequence 53, Appl
457	1750	99.2	695	6	US-11-096-046-26	Sequence 26, Appl	530	1747	99.0	450	3	US-09-996-288-208	Sequence 208, App
458	1749	99.1	329	4	US-10-370-749-48	Sequence 48, Appl	531	1747	99.0	450	3	US-09-996-288-210	Sequence 210, App
459	1749	99.1	330	5	US-10-966-673-5	Sequence 5, Appli	532	1747	99.0	450	3	US-09-996-288-212	Sequence 212, App
460	1749	99.1	330	5	US-10-966-673-6	Sequence 6, Appli	533	1747	99.0	450	3	US-09-996-288-214	Sequence 214, App
461	1749	99.1	330	5	US-10-966-673-7	Sequence 7, Appli	534	1747	99.0	450	3	US-09-996-288-216	Sequence 216, App
462	1749	99.1	330	5	US-10-966-673-18	Sequence 18, Appl	535	1747	99.0	450	3	US-09-996-288-218	Sequence 218, App
463	1749	99.1	330	5	US-10-966-673-19	Sequence 19, Appl	536	1747	99.0	450	3	US-09-996-288-220	Sequence 220, App
464	1749	99.1	330	5	US-10-966-673-23	Sequence 23, Appl	537	1747	99.0	450	3	US-09-996-288-222	Sequence 222, App
465	1749	99.1	330	5	US-10-966-673-26	Sequence 26, Appl	538	1747	99.0	450	3	US-09-996-288-224	Sequence 224, App

539	1747	99.0	450	3	US-09-996-288-226	Sequence 226, App	1747	612	99.0	450	5	US-10-962-285-226	Sequence 226, App
540	1747	99.0	450	3	US-09-996-288-228	Sequence 228, App	1747	613	99.0	450	5	US-10-962-285-228	Sequence 228, App
541	1747	99.0	450	3	US-09-996-288-232	Sequence 232, App	1747	614	99.0	450	5	US-10-962-285-232	Sequence 232, App
542	1747	99.0	450	3	US-09-996-288-234	Sequence 234, App	1747	615	99.0	450	5	US-10-962-285-234	Sequence 234, App
543	1747	99.0	450	3	US-09-996-288-236	Sequence 236, App	1747	616	99.0	450	5	US-10-962-285-236	Sequence 236, App
544	1747	99.0	450	3	US-09-996-288-238	Sequence 238, App	1747	617	99.0	450	5	US-10-962-285-238	Sequence 238, App
545	1747	99.0	450	3	US-09-996-288-240	Sequence 240, App	1747	618	99.0	450	5	US-10-962-285-240	Sequence 240, App
546	1747	99.0	450	3	US-09-996-288-242	Sequence 242, App	1747	619	99.0	450	5	US-10-962-285-242	Sequence 242, App
547	1747	99.0	450	3	US-09-996-288-244	Sequence 244, App	1747	620	99.0	450	5	US-10-962-285-244	Sequence 244, App
548	1747	99.0	450	3	US-09-996-288-246	Sequence 246, App	1747	621	99.0	450	5	US-10-962-285-246	Sequence 246, App
549	1747	99.0	450	3	US-09-996-288-248	Sequence 248, App	1747	622	99.0	450	5	US-10-962-285-248	Sequence 248, App
550	1747	99.0	450	3	US-09-996-288-250	Sequence 250, App	1747	623	99.0	450	5	US-10-962-285-250	Sequence 250, App
551	1747	99.0	450	3	US-09-996-288-252	Sequence 252, App	1747	624	99.0	450	5	US-10-962-285-252	Sequence 252, App
552	1747	99.0	450	3	US-09-996-288-254	Sequence 254, App	1747	625	99.0	450	5	US-10-962-285-254	Sequence 254, App
553	1747	99.0	450	3	US-09-996-288-256	Sequence 256, App	1747	626	99.0	450	5	US-10-962-285-256	Sequence 256, App
554	1747	99.0	450	3	US-09-996-265-208	Sequence 208, App	1747	627	99.0	450	5	US-10-403-180-208	Sequence 208, App
555	1747	99.0	450	3	US-09-996-265-210	Sequence 210, App	1747	628	99.0	450	5	US-10-403-180-210	Sequence 210, App
556	1747	99.0	450	3	US-09-996-265-212	Sequence 212, App	1747	629	99.0	450	5	US-10-403-180-212	Sequence 212, App
557	1747	99.0	450	3	US-09-996-265-214	Sequence 214, App	1747	630	99.0	450	5	US-10-403-180-214	Sequence 214, App
558	1747	99.0	450	3	US-09-996-265-216	Sequence 216, App	1747	631	99.0	450	5	US-10-403-180-216	Sequence 216, App
559	1747	99.0	450	3	US-09-996-265-218	Sequence 218, App	1747	632	99.0	450	5	US-10-403-180-218	Sequence 218, App
560	1747	99.0	450	3	US-09-996-265-220	Sequence 220, App	1747	633	99.0	450	5	US-10-403-180-220	Sequence 220, App
561	1747	99.0	450	3	US-09-996-265-222	Sequence 222, App	1747	634	99.0	450	5	US-10-403-180-222	Sequence 222, App
562	1747	99.0	450	3	US-09-996-265-224	Sequence 224, App	1747	635	99.0	450	5	US-10-403-180-224	Sequence 224, App
563	1747	99.0	450	3	US-09-996-265-226	Sequence 226, App	1747	636	99.0	450	5	US-10-403-180-226	Sequence 226, App
564	1747	99.0	450	3	US-09-996-265-228	Sequence 228, App	1747	637	99.0	450	5	US-10-403-180-228	Sequence 228, App
565	1747	99.0	450	3	US-09-996-265-232	Sequence 232, App	1747	638	99.0	450	5	US-10-403-180-232	Sequence 232, App
566	1747	99.0	450	3	US-09-996-265-234	Sequence 234, App	1747	639	99.0	450	5	US-10-403-180-234	Sequence 234, App
567	1747	99.0	450	3	US-09-996-265-236	Sequence 236, App	1747	640	99.0	450	5	US-10-403-180-236	Sequence 236, App
568	1747	99.0	450	3	US-09-996-265-238	Sequence 238, App	1747	641	99.0	450	5	US-10-403-180-238	Sequence 238, App
569	1747	99.0	450	3	US-09-996-265-240	Sequence 240, App	1747	642	99.0	450	5	US-10-403-180-240	Sequence 240, App
570	1747	99.0	450	3	US-09-996-265-242	Sequence 242, App	1747	643	99.0	450	5	US-10-403-180-242	Sequence 242, App
571	1747	99.0	450	3	US-09-996-265-244	Sequence 244, App	1747	644	99.0	450	5	US-10-403-180-244	Sequence 244, App
572	1747	99.0	450	3	US-09-996-265-246	Sequence 246, App	1747	645	99.0	450	5	US-10-403-180-246	Sequence 246, App
573	1747	99.0	450	3	US-09-996-265-248	Sequence 248, App	1747	646	99.0	450	5	US-10-403-180-248	Sequence 248, App
574	1747	99.0	450	3	US-09-996-265-250	Sequence 250, App	1747	647	99.0	450	5	US-10-403-180-250	Sequence 250, App
575	1747	99.0	450	3	US-09-996-265-252	Sequence 252, App	1747	648	99.0	450	5	US-10-403-180-252	Sequence 252, App
576	1747	99.0	450	3	US-09-996-265-254	Sequence 254, App	1747	649	99.0	450	5	US-10-403-180-254	Sequence 254, App
577	1747	99.0	450	3	US-09-996-265-256	Sequence 256, App	1747	650	99.0	450	5	US-10-403-180-256	Sequence 256, App
578	1747	99.0	450	4	US-10-135-636-1	Sequence 1, Appli	1747	651	99.0	450	6	US-11-199-739-723	Sequence 723, App
579	1747	99.0	450	5	US-10-900-230-208	Sequence 208, App	1747	652	99.0	451	3	US-09-996-288-230	Sequence 230, App
580	1747	99.0	450	5	US-10-900-230-210	Sequence 210, App	1747	653	99.0	451	3	US-09-996-285-230	Sequence 230, App
581	1747	99.0	450	5	US-10-900-230-212	Sequence 212, App	1747	654	99.0	451	5	US-10-900-230-230	Sequence 230, App
582	1747	99.0	450	5	US-10-900-230-214	Sequence 214, App	1747	655	99.0	451	5	US-10-962-285-230	Sequence 230, App
583	1747	99.0	450	5	US-10-900-230-216	Sequence 216, App	1747	656	99.0	451	5	US-10-403-180-230	Sequence 230, App
584	1747	99.0	450	5	US-10-900-230-218	Sequence 218, App	1747	657	99.0	468	4	US-10-377-109-2	Sequence 2, Appli
585	1747	99.0	450	5	US-10-900-230-220	Sequence 220, App	1747	658	99.0	469	4	US-10-377-121-18	Sequence 18, Appl
586	1747	99.0	450	5	US-10-900-230-222	Sequence 222, App	1747	659	99.0	469	4	US-10-377-121-22	Sequence 22, Appl
587	1747	99.0	450	5	US-10-900-230-224	Sequence 224, App	1747	660	99.0	469	5	US-10-858-186-14	Sequence 14, Appl
588	1747	99.0	450	5	US-10-900-230-226	Sequence 226, App	1747	661	99.0	470	4	US-10-216-484-89	Sequence 89, Appl
589	1747	99.0	450	5	US-10-900-230-228	Sequence 228, App	1747	662	99.0	470	4	US-10-216-484-117	Sequence 117, App
590	1747	99.0	450	5	US-10-900-230-232	Sequence 232, App	1747	663	99.0	470	4	US-10-216-484-143	Sequence 143, App
591	1747	99.0	450	5	US-10-900-230-234	Sequence 234, App	1747	664	99.0	470	4	US-10-216-484-145	Sequence 145, App
592	1747	99.0	450	5	US-10-900-230-236	Sequence 236, App	1747	665	99.0	470	4	US-10-216-484-147	Sequence 147, App
593	1747	99.0	450	5	US-10-900-230-238	Sequence 238, App	1747	666	99.0	470	4	US-10-216-484-157	Sequence 157, App
594	1747	99.0	450	5	US-10-900-230-240	Sequence 240, App	1747	667	99.0	470	4	US-10-384-933-89	Sequence 89, Appl
595	1747	99.0	450	5	US-10-900-230-242	Sequence 242, App	1747	668	99.0	470	4	US-10-384-933-117	Sequence 117, App
596	1747	99.0	450	5	US-10-900-230-244	Sequence 244, App	1747	669	99.0	470	4	US-10-384-933-143	Sequence 143, App
597	1747	99.0	450	5	US-10-900-230-246	Sequence 246, App	1747	670	99.0	470	4	US-10-384-933-145	Sequence 145, App
598	1747	99.0	450	5	US-10-900-230-248	Sequence 248, App	1747	671	99.0	470	4	US-10-384-933-147	Sequence 147, App
599	1747	99.0	450	5	US-10-900-230-250	Sequence 250, App	1747	672	99.0	470	4	US-10-384-933-157	Sequence 157, App
600	1747	99.0	450	5	US-10-900-230-252	Sequence 252, App	1747	673	99.0	470	6	US-11-041-095-22	Sequence 22, Appl
601	1747	99.0	450	5	US-10-900-230-254	Sequence 254, App	1747	674	99.0	472	3	US-09-301-593-30	Sequence 30, Appl
602	1747	99.0	450	5	US-10-900-230-256	Sequence 256, App	1747	675	99.0	472	3	US-09-301-593-43	Sequence 43, Appl
603	1747	99.0	450	5	US-10-962-285-208	Sequence 208, App	1747	676	99.0	472	4	US-10-159-006-30	Sequence 30, Appl
604	1747	99.0	450	5	US-10-962-285-210	Sequence 210, App	1747	677	99.0	472	4	US-10-159-006-43	Sequence 43, Appl
605	1747	99.0	450	5	US-10-962-285-212	Sequence 212, App	1747	678	99.0	473	4	US-10-108-260A-4681	Sequence 4681, Ap
606	1747	99.0	450	5	US-10-962-285-214	Sequence 214, App	1747	679	99.0	474	3	US-09-848-832-3	Sequence 3, Appli
607	1747	99.0	450	5	US-10-962-285-216	Sequence 216, App	1747	680	99.0	474	4	US-10-225-108A-3	Sequence 3, Appli
608	1747	99.0	450	5	US-10-962-285-218	Sequence 218, App	1747	681	99.0	474	4	US-10-291-265-284	Sequence 284, Appl
609	1747	99.0	450	5	US-10-962-285-220	Sequence 220, App	1747	682	99.0	474	4	US-10-108-260A-4640	Sequence 4640, Ap
610	1747	99.0	450	5	US-10-962-285-222	Sequence 222, App	1747	683	99.0	474	4	US-10-461-148-1	Sequence 1, Appli
611	1747	99.0	450	5	US-10-962-285-224	Sequence 224, App	1747	684	99.0	474	6	US-11-000-463-284	Sequence 284, App

685	1747	99.0	475	6	US-11-041-095-16	Sequence 16, Appl	758	1742	98.7	575	4	US-10-737-208A-6	Sequence 6, Appl
686	1747	99.0	476	4	US-10-225-108A-16	Sequence 16, Appl	759	1742	98.7	669	5	US-10-900-928-3	Sequence 3, Appl
687	1747	99.0	477	4	US-10-461-148-9	Sequence 9, Appl	760	1741	98.6	443	6	US-11-040-071-1	Sequence 1, Appl
688	1747	99.0	478	4	US-10-291-265-395	Sequence 395, App	761	1741	98.6	452	5	US-10-861-049-22	Sequence 22, Appl
689	1747	99.0	479	6	US-11-000-463-395	Sequence 395, App	762	1741	98.6	452	6	US-11-021-874-22	Sequence 22, Appl
690	1747	99.0	478	4	US-10-104-047-3812	Sequence 3812, App	763	1741	98.6	473	4	US-10-108-260A-4278	Sequence 4278, Ap
691	1747	99.0	478	6	US-11-072-513-3812	Sequence 3812, Ap	764	1741	98.6	979	6	US-10-418-836-16	Sequence 16, Appl
692	1747	99.0	489	4	US-10-104-047-3329	Sequence 3329, Ap	765	1741	98.6	979	6	US-10-107-886-16	Sequence 16, Appl
693	1747	99.0	489	6	US-11-072-512-3329	Sequence 3329, Ap	766	1740	98.6	466	5	US-11-007-886-11	Sequence 11, Appl
694	1747	99.0	526	6	US-11-041-095-10	Sequence 10, Appl	767	1740	98.6	476	4	US-10-937-046-11	Sequence 11, Appl
695	1747	99.0	579	4	US-10-138-727A-41	Sequence 41, Appl	768	1740	98.6	666	5	US-10-660-128-12	Sequence 12, Appl
696	1747	99.0	579	6	US-11-174-186-41	Sequence 41, Appl	769	1740	98.6	666	5	US-10-981-356A-29	Sequence 29, Appl
697	1747	99.0	979	4	US-10-418-836-10	Sequence 10, Appl	770	1739	98.5	667	6	US-11-096-046-29	Sequence 29, Appl
698	1747	99.0	979	6	US-11-007-886-10	Sequence 10, Appl	771	1739	98.5	453	3	US-09-802-077-8	Sequence 8, Appl
699	1746	98.9	447	4	US-10-379-392-117	Sequence 117, App	772	1739	98.5	453	3	US-09-802-096-8	Sequence 8, Appl
700	1746	98.9	666	5	US-10-981-356A-28	Sequence 28, Appl	773	1739	98.5	453	3	US-09-925-179-8	Sequence 8, Appl
701	1746	98.9	666	5	US-10-981-356A-30	Sequence 30, Appl	774	1739	98.5	468	5	US-10-968-237-8	Sequence 8, Appl
702	1746	98.9	667	6	US-11-096-046-28	Sequence 28, Appl	775	1739	98.5	468	5	US-10-071-485-67	Sequence 67, Appl
703	1746	98.9	667	6	US-11-096-046-30	Sequence 30, Appl	776	1739	98.5	468	5	US-10-985-581-67	Sequence 67, Appl
704	1745	98.9	339	5	US-10-872-932A-36	Sequence 36, Appl	777	1739	98.5	711	4	US-10-071-485-90	Sequence 90, Appl
705	1745	98.9	339	5	US-10-810-881A-35	Sequence 35, Appl	778	1738	98.5	711	5	US-10-985-581-90	Sequence 90, Appl
706	1745	98.9	339	5	US-10-981-936-35	Sequence 35, Appl	779	1738	98.5	342	3	US-09-925-299-1003	Sequence 1003, Ap
707	1745	98.9	339	5	US-10-999-866-35	Sequence 35, Appl	780	1738	98.5	342	3	US-09-925-299-1003	Sequence 1003, Ap
708	1745	98.9	339	5	US-10-935-005B-66	Sequence 66, Appl	781	1736	98.5	447	4	US-10-379-392-141	Sequence 141, App
709	1745	98.9	339	6	US-11-061-821-35	Sequence 35, Appl	782	1736	98.4	329	5	US-10-798-380-37	Sequence 37, Appl
710	1745	98.9	329	6	US-11-149-309-17	Sequence 17, Appl	783	1736	98.4	447	6	US-11-004-590-231	Sequence 231, App
711	1745	98.9	329	6	US-11-153-843-128	Sequence 128, App	784	1735	98.4	449	6	US-11-004-054-21	Sequence 21, Appl
712	1745	98.9	329	6	US-11-155-843-141	Sequence 141, App	785	1735	98.3	443	6	US-11-040-071-5	Sequence 5, Appl
713	1745	98.9	330	5	US-10-822-300-75	Sequence 75, Appl	786	1735	98.3	452	5	US-10-861-049-17	Sequence 17, Appl
714	1745	98.9	330	5	US-10-687-118-75	Sequence 75, Appl	787	1735	98.3	452	5	US-10-861-049-20	Sequence 20, Appl
715	1745	98.9	330	6	US-11-102-621-75	Sequence 75, Appl	788	1735	98.3	452	6	US-11-021-874-17	Sequence 17, Appl
716	1745	98.9	402	6	US-11-024-251-31	Sequence 31, Appl	789	1735	98.3	452	6	US-11-021-874-20	Sequence 20, Appl
717	1745	98.9	446	5	US-10-822-300-123	Sequence 123, App	790	1735	98.3	452	6	US-11-120-338-15	Sequence 15, Appl
718	1745	98.9	446	6	US-11-102-621-123	Sequence 123, App	791	1735	98.3	452	6	US-11-107-028-45	Sequence 45, Appl
719	1745	98.9	447	4	US-10-474-832-5	Sequence 5, Appl	792	1735	98.3	452	6	US-11-106-820-28	Sequence 28, Appl
720	1745	98.9	447	5	US-10-822-300-134	Sequence 134, App	793	1735	98.3	452	6	US-11-143-077-15	Sequence 15, Appl
721	1745	98.9	447	6	US-11-102-621-134	Sequence 134, App	794	1735	98.3	452	6	US-11-143-386-15	Sequence 15, Appl
722	1745	98.9	448	6	US-11-182-908-16	Sequence 16, Appl	795	1735	98.3	452	6	US-11-187-364-15	Sequence 15, Appl
723	1745	98.9	449	4	US-10-253-366-2	Sequence 2, Appl	796	1735	98.3	452	6	US-11-208-422-28	Sequence 28, Appl
724	1745	98.9	449	4	US-10-316-694-2	Sequence 2, Appl	797	1735	98.3	452	6	US-11-208-422-44	Sequence 44, Appl
725	1745	98.9	449	4	US-10-356-974-2	Sequence 2, Appl	798	1735	98.3	471	5	US-10-861-049-11	Sequence 11, Appl
726	1745	98.9	449	4	US-10-423-299-2	Sequence 2, Appl	799	1735	98.3	471	6	US-11-021-874-11	Sequence 11, Appl
727	1745	98.9	449	4	US-10-659-825-2	Sequence 2, Appl	800	1735	98.3	471	6	US-11-106-820-27	Sequence 27, Appl
728	1745	98.9	449	5	US-10-877-532-2	Sequence 2, Appl	801	1735	98.3	471	6	US-11-190-364-23	Sequence 23, Appl
729	1745	98.9	449	5	US-10-949-683-2	Sequence 2, Appl	802	1735	98.3	471	6	US-11-147-780-23	Sequence 23, Appl
730	1745	98.9	449	6	US-11-084-729-2	Sequence 2, Appl	803	1734	98.3	471	6	US-10-688-073-11	Sequence 11, Appl
731	1745	98.9	449	6	US-11-154-337-15	Sequence 15, Appl	804	1734	98.3	450	5	US-10-004-590-230	Sequence 230, App
732	1745	98.9	449	6	US-11-182-908-14	Sequence 14, Appl	805	1734	98.2	449	6	US-11-004-054-20	Sequence 20, Appl
733	1745	98.9	451	6	US-11-120-338-22	Sequence 22, Appl	806	1730	98.0	470	5	US-10-697-995-21	Sequence 21, Appl
734	1745	98.9	451	6	US-11-143-386-22	Sequence 22, Appl	807	1729	98.0	447	4	US-10-379-392-143	Sequence 143, App
735	1745	98.9	467	6	US-11-182-908-18	Sequence 18, Appl	808	1729	98.0	451	6	US-11-187-364-29	Sequence 29, Appl
736	1745	98.9	730	3	US-09-825-012-49	Sequence 49, Appl	809	1729	98.0	452	6	US-11-120-338-17	Sequence 17, Appl
737	1745	98.9	740	3	US-09-825-012-58	Sequence 58, Appl	810	1729	98.0	452	6	US-11-107-028-43	Sequence 43, Appl
738	1744	98.8	332	4	US-10-323-904-1	Sequence 1, Appl	811	1729	98.0	452	6	US-11-107-028-47	Sequence 47, Appl
739	1744	98.8	556	4	US-10-471-151-26	Sequence 26, Appl	812	1729	98.0	452	6	US-11-106-820-30	Sequence 30, Appl
740	1744	98.8	556	3	US-09-746-359A-62	Sequence 62, Appl	813	1729	98.0	452	6	US-11-106-820-45	Sequence 45, Appl
741	1744	98.8	559	3	US-09-951-268-39	Sequence 39, Appl	814	1729	98.0	452	6	US-11-143-077-17	Sequence 17, Appl
742	1744	98.8	559	3	US-09-745-792A-62	Sequence 62, Appl	815	1729	98.0	452	6	US-11-143-386-17	Sequence 17, Appl
743	1744	98.8	559	4	US-10-424-658-62	Sequence 62, Appl	816	1729	98.0	452	6	US-11-208-422-40	Sequence 40, Appl
744	1744	98.8	559	5	US-10-994-116-78	Sequence 78, Appl	817	1729	98.0	452	6	US-11-208-422-46	Sequence 46, Appl
745	1744	98.8	559	5	US-10-994-151-78	Sequence 78, Appl	818	1729	98.0	464	4	US-10-032-037B-26	Sequence 26, Appl
746	1744	98.8	573	4	US-10-471-151-25	Sequence 25, Appl	819	1729	98.0	464	4	US-10-029-988B-26	Sequence 26, Appl
747	1744	98.8	594	3	US-09-746-359A-23	Sequence 23, Appl	820	1729	98.0	464	4	US-10-032-423A-26	Sequence 26, Appl
748	1744	98.8	594	3	US-09-951-268-24	Sequence 24, Appl	821	1729	98.0	464	4	US-10-029-926B-26	Sequence 26, Appl
749	1744	98.8	594	3	US-09-745-792A-23	Sequence 23, Appl	822	1729	98.0	468	5	US-10-723-003-12	Sequence 12, Appl
750	1744	98.8	594	4	US-10-424-658-23	Sequence 23, Appl	823	1729	98.0	468	5	US-10-723-003-20	Sequence 20, Appl
751	1744	98.8	594	5	US-10-994-116-77	Sequence 77, Appl	824	1729	98.0	468	6	US-11-004-639-12	Sequence 12, Appl
752	1744	98.8	594	5	US-10-994-151-77	Sequence 77, Appl	825	1729	98.0	468	6	US-11-004-639-20	Sequence 20, Appl
753	1743	98.8	329	5	US-10-370-749-25	Sequence 25, Appl	826	1729	98.0	470	5	US-10-723-003-40	Sequence 40, Appl
754	1743	98.8	329	5	US-10-426-334-1	Sequence 1, Appl	827	1729	98.0	470	6	US-11-004-639-40	Sequence 40, Appl
755	1743	98.8	447	4	US-10-379-392-119	Sequence 119, App	828	1729	98.0	472	5	US-10-723-003-54	Sequence 54, Appl
756	1743	98.8	472	4	US-10-108-260A-4291	Sequence 4291, Ap	829	1729	98.0	472	6	US-11-004-639-54	Sequence 54, Appl
757	1742	98.7	470	4	US-10-108-260A-4191	Sequence 4191, Ap	830	1729	98.0	624	5	US-10-723-003-24	Sequence 24, Appl

831	1729	98.0	624	5	US-10-723-003-30	Sequence 30, Appl	904	1608	91.1	326	5	US-10-872-932A-37	Sequence 37, Appl
832	1729	98.0	624	6	US-11-004-639-24	Sequence 24, Appl	905	1608	91.1	326	5	US-10-928-305-8	Sequence 8, Appl
833	1729	98.0	624	6	US-11-004-639-30	Sequence 30, Appl	906	1608	91.1	326	5	US-10-891-658-4	Sequence 4, Appl
834	1729	98.0	626	5	US-10-723-003-44	Sequence 44, Appl	907	1608	91.1	326	5	US-10-893-576-45	Sequence 46, Appl
835	1729	98.0	626	5	US-11-004-639-44	Sequence 44, Appl	908	1608	91.1	326	5	US-10-810-881A-36	Sequence 36, Appl
836	1729	98.0	628	5	US-10-723-003-58	Sequence 58, Appl	909	1608	91.1	326	5	US-10-981-936-36	Sequence 36, Appl
837	1729	98.0	628	5	US-11-004-639-58	Sequence 58, Appl	910	1608	91.1	326	5	US-10-999-866-36	Sequence 36, Appl
838	1729	98.0	639	5	US-10-723-003-26	Sequence 26, Appl	911	1608	91.1	326	5	US-10-493-909-22	Sequence 22, Appl
839	1729	98.0	639	5	US-10-723-003-32	Sequence 32, Appl	912	1608	91.1	326	5	US-10-935-005B-67	Sequence 67, Appl
840	1729	98.0	639	6	US-11-004-639-26	Sequence 26, Appl	913	1608	91.1	326	6	US-11-001-980-2	Sequence 2, Appl
841	1729	98.0	639	6	US-11-004-639-32	Sequence 32, Appl	914	1608	91.1	326	6	US-11-001-980-6	Sequence 6, Appl
842	1729	98.0	641	5	US-10-723-003-46	Sequence 46, Appl	915	1608	91.1	326	6	US-11-004-054-4	Sequence 4, Appl
843	1729	98.0	641	5	US-11-004-639-46	Sequence 46, Appl	916	1608	91.1	326	6	US-11-026-998-23	Sequence 23, Appl
844	1729	98.0	643	5	US-10-723-003-60	Sequence 60, Appl	917	1608	91.1	326	6	US-11-027-309A-23	Sequence 23, Appl
845	1729	98.0	643	6	US-11-004-639-60	Sequence 60, Appl	918	1608	91.1	326	6	US-11-144-248-28	Sequence 28, Appl
846	1726	97.8	329	6	US-11-102-403-25	Sequence 25, Appl	919	1608	91.1	326	6	US-11-061-821-36	Sequence 36, Appl
847	1726	97.8	579	4	US-10-310-719-32	Sequence 32, Appl	920	1608	91.1	326	6	US-11-144-222-28	Sequence 28, Appl
848	1724	97.7	447	4	US-10-379-392-142	Sequence 142, Appl	921	1608	91.1	326	6	US-11-182-343-28	Sequence 28, Appl
849	1724	97.7	451	6	US-11-120-338-25	Sequence 25, Appl	922	1608	91.1	326	6	US-11-124-620-2	Sequence 2, Appl
850	1724	97.7	451	6	US-11-143-077-22	Sequence 22, Appl	923	1608	91.1	326	6	US-11-233-683-2	Sequence 2, Appl
851	1724	97.7	451	6	US-11-143-386-25	Sequence 25, Appl	924	1608	91.1	443	3	US-09-256-156-2	Sequence 2, Appl
852	1724	97.7	451	6	US-11-187-364-34	Sequence 34, Appl	925	1608	91.1	444	6	US-11-085-368-89	Sequence 89, Appl
853	1722	97.6	447	4	US-10-379-392-118	Sequence 118, Appl	926	1608	91.1	445	5	US-10-644-277-2	Sequence 2, Appl
854	1719	97.4	447	4	US-10-379-392-120	Sequence 120, Appl	927	1608	91.1	445	5	US-10-644-277-18	Sequence 18, Appl
855	1719	97.4	452	6	US-11-107-028-43	Sequence 43, Appl	928	1608	91.1	445	5	US-10-644-277-38	Sequence 38, Appl
856	1719	97.4	452	6	US-11-208-422-43	Sequence 43, Appl	929	1608	91.1	445	5	US-10-644-277-90	Sequence 90, Appl
857	1718	97.3	330	3	US-09-847-208-2	Sequence 2, Appl	930	1608	91.1	449	5	US-10-891-658-40	Sequence 40, Appl
858	1718	97.3	330	4	US-10-000-439-2	Sequence 2, Appl	931	1608	91.1	451	4	US-10-891-658-40	Sequence 40, Appl
859	1716	97.2	481	4	US-10-409-938-23	Sequence 23, Appl	932	1608	91.1	451	4	US-10-153-382-17	Sequence 17, Appl
860	1700	96.3	451	5	US-10-822-231-5	Sequence 5, Appl	933	1608	91.1	451	5	US-10-612-497-70	Sequence 70, Appl
861	1691	95.8	447	6	US-11-124-620-5	Sequence 5, Appl	934	1608	91.1	451	6	US-11-085-368-17	Sequence 17, Appl
862	1681	95.2	447	4	US-10-379-392-151	Sequence 151, Appl	935	1608	91.1	451	6	US-11-128-900-70	Sequence 70, Appl
863	1678	95.1	380	4	US-10-272-899A-106	Sequence 106, Appl	936	1608	91.1	460	5	US-10-938-353-14	Sequence 14, Appl
864	1639	92.9	580	4	US-10-310-719-37	Sequence 37, Appl	937	1608	91.1	460	5	US-10-938-353-26	Sequence 26, Appl
865	1636	92.7	362	4	US-10-112-582-3	Sequence 3, Appl	938	1608	91.1	460	5	US-10-938-353-74	Sequence 74, Appl
866	1636	92.7	362	6	US-11-233-683-3	Sequence 3, Appl	939	1608	91.1	461	5	US-10-938-353-2	Sequence 2, Appl
867	1632	92.5	580	4	US-10-310-719-35	Sequence 35, Appl	940	1608	91.1	461	5	US-10-938-353-34	Sequence 34, Appl
868	1622	91.9	377	6	US-10-822-300-113	Sequence 113, Appl	941	1608	91.1	461	5	US-10-938-353-66	Sequence 66, Appl
869	1622	91.9	377	6	US-11-102-621-113	Sequence 113, Appl	942	1608	91.1	462	5	US-10-828-782A-18	Sequence 18, Appl
870	1622	91.9	519	4	US-10-312-354-19	Sequence 19, Appl	943	1608	91.1	462	5	US-10-910-901-2	Sequence 2, Appl
871	1619	91.8	377	3	US-09-925-664-45	Sequence 45, Appl	944	1608	91.1	462	5	US-10-910-901-14	Sequence 14, Appl
872	1619	91.8	377	3	US-09-925-192-45	Sequence 45, Appl	945	1608	91.1	462	6	US-11-238-983-2	Sequence 2, Appl
873	1619	91.8	377	4	US-10-047-542-24	Sequence 24, Appl	946	1608	91.1	463	4	US-10-153-382-13	Sequence 13, Appl
874	1619	91.8	377	5	US-10-822-300-115	Sequence 115, Appl	947	1608	91.1	463	4	US-10-656-769-34	Sequence 34, Appl
875	1619	91.8	377	5	US-10-872-932A-38	Sequence 38, Appl	948	1608	91.1	463	5	US-10-612-497-1	Sequence 1, Appl
876	1619	91.8	377	5	US-10-810-881A-37	Sequence 37, Appl	949	1608	91.1	463	5	US-10-612-497-4	Sequence 4, Appl
877	1619	91.8	377	5	US-10-981-936-37	Sequence 37, Appl	950	1608	91.1	463	5	US-10-612-497-63	Sequence 63, Appl
878	1619	91.8	377	5	US-10-999-866-37	Sequence 37, Appl	951	1608	91.1	463	5	US-10-612-497-68	Sequence 68, Appl
879	1619	91.8	377	5	US-10-493-909-24	Sequence 24, Appl	952	1608	91.1	463	5	US-10-612-497-68	Sequence 68, Appl
880	1619	91.8	377	5	US-10-935-005B-68	Sequence 68, Appl	953	1608	91.1	463	5	US-10-776-649-1	Sequence 1, Appl
881	1619	91.8	377	6	US-11-061-821-37	Sequence 37, Appl	954	1608	91.1	463	5	US-10-776-649-4	Sequence 4, Appl
882	1619	91.8	377	6	US-11-102-621-115	Sequence 115, Appl	955	1608	91.1	463	5	US-10-776-649-63	Sequence 63, Appl
883	1619	91.8	377	6	US-11-124-620-3	Sequence 3, Appl	956	1608	91.1	463	5	US-10-776-649-68	Sequence 68, Appl
884	1619	91.8	494	3	US-09-256-156-3	Sequence 3, Appl	957	1608	91.1	463	5	US-10-910-901-10	Sequence 10, Appl
885	1618	91.7	516	4	US-10-108-260A-4283	Sequence 4283, Ap	958	1608	91.1	463	5	US-10-938-353-6	Sequence 6, Appl
886	1617	91.6	339	4	US-10-272-899A-18	Sequence 18, Appl	959	1608	91.1	463	6	US-11-085-368-3	Sequence 3, Appl
887	1617	91.6	359	4	US-10-272-899A-76	Sequence 76, Appl	960	1608	91.1	463	6	US-11-085-368-41	Sequence 41, Appl
888	1615	91.5	516	4	US-10-272-899A-4452	Sequence 4452, Ap	961	1608	91.1	463	6	US-11-085-368-41	Sequence 41, Appl
889	1615	91.5	518	4	US-10-108-260A-4452	Sequence 10, Appl	962	1608	91.1	463	6	US-11-085-368-53	Sequence 53, Appl
890	1615	91.5	518	4	US-10-225-108A-10	Sequence 4, Appl	963	1608	91.1	463	6	US-11-031-485-2	Sequence 2, Appl
891	1615	91.5	520	4	US-10-461-148-4	Sequence 4, Appl	964	1608	91.1	463	6	US-11-031-485-6	Sequence 6, Appl
892	1615	91.5	535	4	US-10-108-260A-4767	Sequence 4767, Ap	965	1608	91.1	463	6	US-11-128-900-1	Sequence 1, Appl
893	1615	91.5	310	4	US-10-060-714-25	Sequence 25, Appl	966	1608	91.1	463	6	US-11-128-900-4	Sequence 4, Appl
894	1610	91.2	376	5	US-10-891-658-26	Sequence 26, Appl	967	1608	91.1	463	6	US-11-128-900-63	Sequence 63, Appl
895	1610	91.2	499	5	US-10-891-658-43	Sequence 43, Appl	968	1608	91.1	463	6	US-11-128-900-68	Sequence 68, Appl
896	1608	91.1	339	4	US-10-272-899A-16	Sequence 16, Appl	969	1608	91.1	464	4	US-10-153-382-9	Sequence 9, Appl
897	1608	91.1	326	4	US-10-047-542-22	Sequence 22, Appl	970	1608	91.1	464	4	US-10-292-088-22	Sequence 22, Appl
898	1608	91.1	326	4	US-10-310-719-9	Sequence 9, Appl	971	1608	91.1	464	5	US-10-612-497-2	Sequence 2, Appl
899	1608	91.1	326	4	US-10-113-582-2	Sequence 2, Appl	972	1608	91.1	464	5	US-10-612-497-66	Sequence 66, Appl
900	1608	91.1	326	4	US-10-038-591-28	Sequence 28, Appl	973	1608	91.1	464	5	US-10-776-649-2	Sequence 2, Appl
901	1608	91.1	326	4	US-10-656-769-6	Sequence 6, Appl	974	1608	91.1	464	5	US-10-776-649-66	Sequence 66, Appl
902	1608	91.1	326	4	US-10-775-444A-28	Sequence 28, Appl	975	1608	91.1	464	5	US-10-938-353-22	Sequence 22, Appl
903	1608	91.1	326	5	US-10-756-153-32	Sequence 32, Appl	976	1608	91.1	464	6	US-11-085-368-9	Sequence 9, Appl

```
977 1608 91.1 464 6 US-11-085-368-45
978 1608 91.1 464 6 US-11-031-485-52
979 1608 91.1 464 6 US-11-128-900-2
980 1608 91.1 464 6 US-11-128-900-66
981 1608 91.1 465 4 US-10-292-088-38
982 1608 91.1 465 4 US-10-656-769-22
983 1608 91.1 465 4 US-10-656-769-28
984 1608 91.1 466 4 US-10-292-088-30
985 1608 91.1 466 4 US-10-292-088-70
986 1608 91.1 466 4 US-10-292-088-86
987 1608 91.1 466 5 US-10-938-353-10
988 1608 91.1 466 5 US-10-938-353-30
989 1608 91.1 466 5 US-10-938-353-62
990 1608 91.1 467 4 US-10-180-648-2
991 1608 91.1 468 6 US-11-031-485-56
992 1608 91.1 468 6 US-11-086-289-14
993 1608 91.1 468 6 US-11-086-289-22
994 1608 91.1 469 4 US-10-292-088-54
995 1608 91.1 469 6 US-11-031-485-34
996 1608 91.1 469 6 US-11-031-485-42
997 1608 91.1 469 6 US-11-031-485-60
998 1608 91.1 470 3 US-09-859-053-28
999 1608 91.1 470 3 US-09-859-053-32
1000 1608 91.1 470 3 US-09-859-053-36
```

ALIGNMENTS

```
RESULT 1
US-10-733-563-110
; Sequence 110, Application US/10733563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Ponath, Paul
; TITLE OF INVENTION: HUMANIZED ANTI-CR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human IgG1-FcRmut protein
US-10-733-563-110

Query Match 100.0%; Score 1765; DB 4; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPREEQYN 180
DB 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPREEQYN 180
QY 181 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 181 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
QY 301 QOQNVFSCVMHEALHNHYTOKSLSPGK 330
DB 301 QOQNVFSCVMHEALHNHYTOKSLSPGK 330
```

```
Query Match 100.0%; Score 1765; DB 4; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPREEQYN 180
DB 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPREEQYN 180
QY 181 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 181 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
QY 301 QOQNVFSCVMHEALHNHYTOKSLSPGK 330
DB 301 QOQNVFSCVMHEALHNHYTOKSLSPGK 330
```

RESULT 3

```
US-10-733-563-114
; Sequence 114, Application US/10733563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Ponath, Paul
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human IgG1-FcRmut protein
US-10-733-563-114

Query Match          100.0%; Score 1765; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTGGTAAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
DB 4 ASTKGPSVFPLAPSSKSTGGTAAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 63
QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 64 GLYSLSVVTVPPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 123
QY 121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 124 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 183
QY 181 STYRVSVSLTVLHQDLWGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 184 STYRVSVSLTVLHQDLWGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 243
QY 241 LTKNQVSLTCLVKGYFPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 300
DB 244 LTKNQVSLTCLVKGYFPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 303
QY 301 QQGNVFCVSMVHEALHNHYTQKSLSLSPGK 330
DB 304 QQGNVFCVSMVHEALHNHYTQKSLSLSPGK 333

RESULT 4
US-10-733-899A-70
; Sequence 70, Application US/10272899A
; Publication No. US20040033561A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa L.
; APPLICANT: Healy, Judith Jacques
; APPLICANT: Newman, Walter
; APPLICANT: Ponath, Paul
; APPLICANT: Bruce Keyt
; TITLE OF INVENTION: IMMUNOGLOBULIN DNA CASSETTE MOLECULES,
; TITLE OF INVENTION: MONOCLONAL CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS OF
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: MP101-244P2RM
; CURRENT APPLICATION NUMBER: US/10/272,899A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/350,166
```

```
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/392,364
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin cassette protein sequence
; OTHER INFORMATION: Leader-HuFCRm_56
US-10-272-899A-70

Query Match          100.0%; Score 1765; DB 4; Length 356;
Best Local Similarity 100.0%; Pred. No. 1.6e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTGGTAAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
DB 27 ASTKGPSVFPLAPSSKSTGGTAAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 86
QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 87 GLYSLSVVTVPPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 146
QY 121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 147 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 206
QY 181 STYRVSVSLTVLHQDLWGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 207 STYRVSVSLTVLHQDLWGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 266
QY 241 LTKNQVSLTCLVKGYFPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 300
DB 267 LTKNQVSLTCLVKGYFPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 326
QY 301 QQGNVFCVSMVHEALHNHYTQKSLSLSPGK 330
DB 327 QQGNVFCVSMVHEALHNHYTQKSLSLSPGK 356

RESULT 5
US-10-171-452A-42
; Sequence 42, Application US/10171452A
; Publication No. US20030108518A1
; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobbold, Stephen
; APPLICANT: Winsor-Hines, Dawn
; TITLE OF INVENTION: TRX1 Antibody and Uses Therefor
; FILE REFERENCE: 695458-59
; CURRENT APPLICATION NUMBER: US/10/171,452A
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 42
```

```
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Heavy chain of humanized antibody
US-10-171-452A-42

Query Match      100.0%; Score 1765; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 2.1e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 119 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 178

Qy 61 GLYSSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELLAG 120
Db 179 GLYSSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELLAG 238

Qy 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 239 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 298

Qy 181 STYRVSVSLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 299 STYRVSVSLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 358

Qy 241 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 359 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 418

Qy 301 QQGNVFSCSVMHAEALHNHYTOKSLSLSPGK 330
Db 419 QQGNVFSCSVMHAEALHNHYTOKSLSLSPGK 448
```

```
RESULT 6
US-10-171-452A-54
; Sequence 54, Application US/10171452A
; Publication No. US20030108518A1
; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobbold, Stephen
; APPLICANT: Winsox-Hines, Dawn
; TITLE OF INVENTION: TRX1 Antibody and Uses Therefor
; FILE REFERENCE: 695458-59
; CURRENT APPLICATION NUMBER: US/10/171,452A
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 54
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Heavy chain of humanized antibody
US-10-171-452A-54
```

```
Query Match      100.0%; Score 1765; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 2.1e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 119 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 178

Qy 61 GLYSSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELLAG 120
Db 179 GLYSSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELLAG 238

Qy 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 239 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 298

Qy 181 STYRVSVSLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 299 STYRVSVSLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 358

Qy 241 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 359 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 418

Qy 301 QQGNVFSCSVMHAEALHNHYTOKSLSLSPGK 330
Db 419 QQGNVFSCSVMHAEALHNHYTOKSLSLSPGK 448

RESULT 7
US-10-353-708-42
; Sequence 42, Application US/10353708
; Publication No. US20030219403A1
; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobbold, Stephen
; APPLICANT: Winsox-Hines, Dawn
; TITLE OF INVENTION: Compositions and Methods of Tolerizing a Primate to an Antigen
; FILE REFERENCE: 695458-73
; CURRENT APPLICATION NUMBER: US/10/353,708
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US10/171,452
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 42
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Heavy chain of humanized antibody
US-10-353-708-42

Query Match      100.0%; Score 1765; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 2.1e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 119 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 178

Qy 61 GLYSSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELLAG 120
Db 179 GLYSSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELLAG 238

Qy 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 239 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 298

Qy 181 STYRVSVSLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 299 STYRVSVSLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 358

Qy 241 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 359 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 418

Qy 301 QQGNVFSCSVMHAEALHNHYTOKSLSLSPGK 330
Db 419 QQGNVFSCSVMHAEALHNHYTOKSLSLSPGK 448
```

```
US-10-353-708-42
; Sequence 42, Application US/10353708
; Publication No. US20030219403A1
; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobbold, Stephen
; APPLICANT: Winsox-Hines, Dawn
; TITLE OF INVENTION: Compositions and Methods of Tolerizing a Primate to an Antigen
; FILE REFERENCE: 695458-73
; CURRENT APPLICATION NUMBER: US/10/353,708
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US10/171,452
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 42
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Heavy chain of humanized antibody
US-10-353-708-42

Query Match      100.0%; Score 1765; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 2.1e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
```

Db 119 ASTKGPSVFPLAPSSKSTGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 178
Qy 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 179 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNNTKVDKVEPKSCDKTHTCPPCPAPELAGA 238
Qy 121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 239 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 298
Qy 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 299 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 358
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKGRW 300
Db 359 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKGRW 418
Qy 301 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 330
Db 419 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 448

RESULT 8

US-10-353-708-54
; Sequence 54, Application US/10353708
; Publication No. US20030219403A1
; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobbold, Stephen
; APPLICANT: Winsor-Hines, Dawn
; TITLE OF INVENTION: Compositions and Methods of Tolerizing a Primate to an Antigen
; FILE REFERENCE: 695458-73
; CURRENT APPLICATION NUMBER: US/10/353,708
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US10/171,452
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 54
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Heavy chain of humanized antibody
US-10-353-708-54

Query Match 100.0%; Score 1765; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 2.1e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASTKGPSVFPLAPSSKSTGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
Db 119 ASTKGPSVFPLAPSSKSTGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 178
Qy 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120

Db 179 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNNTKVDKVEPKSCDKTHTCPPCPAPELAGA 238
Qy 121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 239 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 298
Qy 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 299 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 358
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKGRW 300
Db 359 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKGRW 418
Qy 301 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 330
Db 419 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 448

RESULT 9

US-10-731-984-8
; Sequence 8, Application US/10731984
; Publication No. US20040175381A1
; GENERAL INFORMATION:
; APPLICANT: WINDSOR-HINES, Dawn
; APPLICANT: RAO, Patricia
; APPLICANT: RINGLER, Douglas J.
; TITLE OF INVENTION: INDUCING TOLERANCE IN PRIMATES
; FILE REFERENCE: TLN-022
; CURRENT APPLICATION NUMBER: US/10/731,984
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: 60/431839
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric Sequence
US-10-731-984-8

Query Match 100.0%; Score 1765; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 2.1e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASTKGPSVFPLAPSSKSTGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
Db 119 ASTKGPSVFPLAPSSKSTGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 178
Qy 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 179 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNNTKVDKVEPKSCDKTHTCPPCPAPELAGA 238
Qy 121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 239 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 298
Qy 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 299 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 358
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKGRW 300
Db 359 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKGRW 418
Qy 301 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 330
Db 419 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 448

RESULT 10

```
US-10-731-984-24
; Sequence 24, Application US/10731984
; Publication No. US20040175381A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, Dawn
; APPLICANT: RAO, Patricia
; APPLICANT: RINGLER, Douglas J.
; TITLE OF INVENTION: INDUCING TOLERANCE IN PRIMATES
; FILE REFERENCE: TLN-022
; CURRENT APPLICATION NUMBER: US/10/731,984
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: 60/431839
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric Sequence
US-10-731-984-24

Query Match      100.0%; Score 1765; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 2.le-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 119 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 178
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 179 GLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 238
QY 121 PSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 239 PSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 298
QY 181 STYRVSVLTVLHQDLNGLKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
DB 299 STYRVSVLTVLHQDLNGLKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 358
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 300
DB 359 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 418
QY 301 OQGNVFCSCVMHEALHNNHYTKLSLSPGK 330
DB 419 OQGNVFCSCVMHEALHNNHYTKLSLSPGK 448

RESULT 11
US-11-158-505-8
; Sequence 8, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, Dawn
; APPLICANT: RAO, Patricia
; APPLICANT: RINGLER, Douglas J.
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 8
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: heavy chain construct
US-11-158-505-8

Query Match      100.0%; Score 1765; DB 6; Length 448;
Best Local Similarity 100.0%; Pred. No. 2.le-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 119 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 178
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 179 GLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 238

US-10-733-563-110.rapbm
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: antibody heavy chain construct
US-11-158-505-8

Query Match      100.0%; Score 1765; DB 6; Length 448;
Best Local Similarity 100.0%; Pred. No. 2.le-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 119 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 178
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 179 GLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 238

RESULT 12
US-11-158-505-24
; Sequence 24, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, Dawn
; APPLICANT: RAO, Patricia
; APPLICANT: RINGLER, Douglas J.
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 24
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: heavy chain construct
US-11-158-505-24

Query Match      100.0%; Score 1765; DB 6; Length 448;
Best Local Similarity 100.0%; Pred. No. 2.le-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 119 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 178
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 179 GLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 238
```



```
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H6
US-11-177-648-27

Query Match      100.0%; Score 1765; DB 6; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 133 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 192
Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 120
Db 193 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 252
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 253 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 312
Qy 181 STYRVSVSLTVLHODWLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 313 STYRVSVSLTVLHODWLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 372
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 300
Db 373 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 432
Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 433 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 462
```

```
RESULT 16
US-11-177-648-28
; Sequence 28, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; PRIOR FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H700
US-11-177-648-28
```

```
Query Match      100.0%; Score 1765; DB 6; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 133 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 192
Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 120
Db 193 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 252
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 253 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 312
Qy 181 STYRVSVSLTVLHODWLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 313 STYRVSVSLTVLHODWLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 372
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 300
Db 373 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 432
Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 433 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 462
```

```
RESULT 17
US-11-177-648-29
; Sequence 29, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H14
US-11-177-648-29
```

```
Query Match      100.0%; Score 1765; DB 6; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 133 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 192
Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 120
Db 193 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 252
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 253 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 312
```



```
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H17
US-11-177-648-32

Query Match          100.0%; Score 1765; DB 6; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 133 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 192
QY 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 193 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 252
QY 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 253 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 312
QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 313 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 372
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFELYSLKLTVDKSRW 300
Db 373 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFELYSLKLTVDKSRW 432
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 433 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 462

RESULT 21
US-11-177-648-33
; Sequence 33, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H18
US-11-177-648-33

Query Match          100.0%; Score 1765; DB 6; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 133 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 192
QY 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 193 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 252
QY 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 253 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 312
QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 313 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 372
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFELYSLKLTVDKSRW 300
Db 373 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFELYSLKLTVDKSRW 432
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 433 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 462

RESULT 22
US-11-177-648-79
; Sequence 79, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H1
US-11-177-648-79

Query Match          100.0%; Score 1765; DB 6; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 133 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 192
QY 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 193 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 252
QY 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 253 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 312
QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
```

```
Db 313 STYRVSVLTVLHQDLNKGKCKVSNKALPAPIEKTISKAKGPREPQVYTLPPSRDE 372
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 300
Db 373 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 432
QY 301 QGQNVFSCSVMEALHNHYTQKSLSLSPGK 330
Db 433 QGQNVFSCSVMEALHNHYTQKSLSLSPGK 462

RESULT 23
US-11-177-648-92
; Sequence 92, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H19
US-11-177-648-92

Query Match 100.0%; Score 1765; DB 6; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 133 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 192
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 193 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 252
QY 121 PSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 253 PSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 312
QY 181 STYRVSVLTVLHQDLNKGKCKVSNKALPAPIEKTISKAKGPREPQVYTLPPSRDE 240
Db 313 STYRVSVLTVLHQDLNKGKCKVSNKALPAPIEKTISKAKGPREPQVYTLPPSRDE 372
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 300
Db 373 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 432

RESULT 24
US-11-177-648-93
; Sequence 93, Application US/11177648
```

```
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H20
US-11-177-648-93

Query Match 100.0%; Score 1765; DB 6; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 133 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 192
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 193 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 252
QY 121 PSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 253 PSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 312
QY 181 STYRVSVLTVLHQDLNKGKCKVSNKALPAPIEKTISKAKGPREPQVYTLPPSRDE 240
Db 313 STYRVSVLTVLHQDLNKGKCKVSNKALPAPIEKTISKAKGPREPQVYTLPPSRDE 372
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 300
Db 373 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 432
QY 301 QGQNVFSCSVMEALHNHYTQKSLSLSPGK 330
Db 433 QGQNVFSCSVMEALHNHYTQKSLSLSPGK 462

RESULT 25
US-11-177-648-94
; Sequence 94, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
```

```
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H21
US-11-177-648-94

Query Match          100.0%; Score 1765; DB 6; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db 133 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 192
QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 193 GLYSLSVVTVPPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 252
QY 121 PSVFLFPPKPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 253 PSVFLFPPKPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 312
QY 181 STYRVSVSLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 313 STYRVSVSLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 372
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 373 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRW 432
QY 301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
Db 433 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 462

RESULT 27
US-11-177-648-96
; Sequence 96, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H23
US-11-177-648-96

Query Match          100.0%; Score 1765; DB 6; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db 133 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 192
QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 193 GLYSLSVVTVPPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 252
QY 121 PSVFLFPPKPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 253 PSVFLFPPKPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 312
QY 181 STYRVSVSLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 313 STYRVSVSLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 372
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 373 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRW 432
QY 301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
Db 433 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 462

RESULT 26
US-11-177-648-95
; Sequence 95, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H22
US-11-177-648-95

Query Match          100.0%; Score 1765; DB 6; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 373 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 432
QY 301 OQGNVFCSCVMHEALHNNHYTKSLSPGK 330
Db 433 OQGNVFCSCVMHEALHNNHYTKSLSPGK 462

RESULT 28
US-11-177-648-97
; Sequence 97, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H24
US-11-177-648-97

Query Match 100.0%; Score 1765; DB 6; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSS 60
Db 133 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSS 192
QY 61 GLYSLSSVTVFPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 193 GLYSLSSVTVFPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 252
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 253 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 312
QY 181 STYRVSVLTVLHQLDNLNGKEYCKVSKNKAAPAEIKETISKAKGQPREPQVYTLPPSRDE 240
Db 313 STYRVSVLTVLHQLDNLNGKEYCKVSKNKAAPAEIKETISKAKGQPREPQVYTLPPSRDE 372
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 373 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 432
QY 301 OQGNVFCSCVMHEALHNNHYTKSLSPGK 330
Db 433 OQGNVFCSCVMHEALHNNHYTKSLSPGK 462

RESULT 29
US-11-177-648-98
; Sequence 98, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H25
US-11-177-648-98

Query Match 100.0%; Score 1765; DB 6; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSS 60
Db 133 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSS 192
QY 61 GLYSLSSVTVFPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 193 GLYSLSSVTVFPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 252
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 253 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 312
QY 181 STYRVSVLTVLHQLDNLNGKEYCKVSKNKAAPAEIKETISKAKGQPREPQVYTLPPSRDE 240
Db 313 STYRVSVLTVLHQLDNLNGKEYCKVSKNKAAPAEIKETISKAKGQPREPQVYTLPPSRDE 372
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 373 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 432
QY 301 OQGNVFCSCVMHEALHNNHYTKSLSPGK 330
Db 433 OQGNVFCSCVMHEALHNNHYTKSLSPGK 462

RESULT 29
US-11-177-648-98
; Sequence 98, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H25
US-11-177-648-98

Query Match 100.0%; Score 1765; DB 6; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSS 60
Db 133 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSS 192
QY 61 GLYSLSSVTVFPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 193 GLYSLSSVTVFPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 252
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 253 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 312
QY 181 STYRVSVLTVLHQLDNLNGKEYCKVSKNKAAPAEIKETISKAKGQPREPQVYTLPPSRDE 240
Db 313 STYRVSVLTVLHQLDNLNGKEYCKVSKNKAAPAEIKETISKAKGQPREPQVYTLPPSRDE 372
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 373 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 432
QY 301 OQGNVFCSCVMHEALHNNHYTKSLSPGK 330
Db 433 OQGNVFCSCVMHEALHNNHYTKSLSPGK 462

RESULT 30
US-10-171-452A-53
; Sequence 53, Application US/10171452A
; Publication No. US20030108518A1
; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobbold, Stephen
; APPLICANT: Winsor-Hines, Dawn
; TITLE OF INVENTION: TRX1 Antibody and Uses Therefor
; FILE REFERENCE: 695458-59
; CURRENT APPLICATION NUMBER: US/10/171,452A
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
```

```
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Heavy chain of humanized antibody
US-10-171-452A-53

Query Match      100.0%; Score 1765; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 2.2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197

Qy 61 GLYSLSSVTVVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 120
Db 198 GLYSLSSVTVVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 257

Qy 121 PSVLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
Db 258 PSVLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 317

Qy 181 STYRVSVSLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 318 STYRVSVSLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 377

Qy 241 LTKQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
Db 378 LTKQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 437

Qy 301 QQGNVFSCVMEALHNHYTOKSLSLSPGK 330
Db 438 QQGNVFSCVMEALHNHYTOKSLSLSPGK 467

RESULT 31
US-10-353-708-53
; Sequence 53, Application US/10353708
; Publication No. US20030219403A1
; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Jadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobbold, Stephen
; APPLICANT: Winsor-Hines, Dawn
; TITLE OF INVENTION: Compositions and Methods of Tolerizing a Primate to an Antigen
; FILE REFERENCE: 695458-73
; CURRENT APPLICATION NUMBER: US/10/353,708
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US10/171,452
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
```

```
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 53
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Heavy chain of humanized antibody
US-10-353-708-53

Query Match      100.0%; Score 1765; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 2.2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197

Qy 61 GLYSLSSVTVVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 120
Db 198 GLYSLSSVTVVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 257

Qy 121 PSVLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
Db 258 PSVLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 317

Qy 181 STYRVSVSLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 318 STYRVSVSLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 377

Qy 241 LTKQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
Db 378 LTKQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 437

Qy 301 QQGNVFSCVMEALHNHYTOKSLSLSPGK 330
Db 438 QQGNVFSCVMEALHNHYTOKSLSLSPGK 467
```

```
RESULT 32
US-10-731-984-7
; Sequence 7, Application US/10731984
; Publication No. US20040175381A1
; GENERAL INFORMATION:
; APPLICANT: WINDSOR-HINES, Dawn
; APPLICANT: RAO, Patricia
; APPLICANT: RINGLER, Douglas J.
; TITLE OF INVENTION: INDUCING TOLERANCE IN PRIMATES
; FILE REFERENCE: TLN-022
; CURRENT APPLICATION NUMBER: US/10/731,984
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: 60/431839
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric Sequence
US-10-731-984-7

Query Match      100.0%; Score 1765; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 2.2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197
```



```
QY 61 GLYSLSSVVTVFPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCPPCPAPELAGA 120
Db 198 GLYSLSSVVTVFPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCPPCPAPELAGA 257
QY 121 PSVELFPKPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 258 PSVELFPKPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 317
QY 181 STYRVSVVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSRDE 240
Db 318 STYRVSVVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSRDE 377
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 300
Db 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 437
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 438 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 467

RESULT 33
US-10-731-984-23
; Sequence 23, Application US/10731984
; Publication No. US20040175381A1
; GENERAL INFORMATION:
; APPLICANT: WINDSOR-HINES, Dawn
; APPLICANT: RAO, Patricia
; APPLICANT: RINGLER, Douglas J.
; TITLE OF INVENTION: INDUCING TOLERANCE IN PRIMATES
; FILE REFERENCE: TLN-022
; CURRENT APPLICATION NUMBER: US/10/731,984
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: 60/431839
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric Sequence
US-10-731-984-23
```

```
Query Match 100.0%; Score 1765; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 2.2e-128; Mismatches 0; Indels 0; Gaps 0;
Matches 330; Conservative 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
Db 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 197
QY 61 GLYSLSSVVTVFPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCPPCPAPELAGA 120
Db 198 GLYSLSSVVTVFPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCPPCPAPELAGA 257
QY 121 PSVELFPKPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 258 PSVELFPKPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 317
QY 181 STYRVSVVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSRDE 240
Db 318 STYRVSVVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSRDE 377
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 300
Db 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 437
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 438 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 467
```

```
RESULT 34
US-11-158-505-5
; Sequence 5, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 5
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: antibody heavy chain construct
US-11-158-505-5

Query Match 100.0%; Score 1765; DB 6; Length 467;
Best Local Similarity 100.0%; Pred. No. 2.2e-128; Mismatches 0; Indels 0; Gaps 0;
Matches 330; Conservative 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
Db 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 197
QY 61 GLYSLSSVVTVFPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCPPCPAPELAGA 120
Db 198 GLYSLSSVVTVFPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCPPCPAPELAGA 257
QY 121 PSVELFPKPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 258 PSVELFPKPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 317
QY 181 STYRVSVVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSRDE 240
Db 318 STYRVSVVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSRDE 377
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 300
Db 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 437
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 438 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 467

RESULT 35
US-11-158-505-7
; Sequence 7, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
```



```

; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-404-724-72

Query Match 99.6%; Score 1758; DB 4; Length 469;
Best Local Similarity 99.7%; Pred. No. 7.7e-128;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAAPSSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFFPAVLQSS 60
Db 140 ASTKGPSVFPLAAPSSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFFPAVLQSS 199
Qy 61 GLYSLSVTVTPSSSLGTQTYICNNHKPNTKVDKKVEPKSCDKTHCTCPCPAPELAGA 120
Db 200 GLYSLSVTVTPSSSLGTQTYICNNHKPNTKVDKKVEPKSCDKTHCTCPCPAPELAGA 259
Qy 121 PSVFLRPKPKDLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNNAKTKPREQYN 180
Db 260 PSVFLRPKPKHTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNNAKTKPREQYN 319
Qy 181 STYRVSVLTVLHQDWLNGKEYCKVKSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 240
Db 320 STYRVSVLTVLHQDWLNGKEYCKVKSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 379
Qy 241 LTRNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 380 LTRNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 439
Qy 301 QOQNVFSCSVMEALHNHYTKQSLSLSPGK 330
Db 440 QOQNVFSCSVMEALHNHYTKQSLSLSPGK 469

RESULT 40
US-09-995-898A-15
; Sequence 15, Application US/09995898A
; Publication No. US20030027253A1
; GENERAL INFORMATION:
; APPLICANT: Preenell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: No. US20030027253A1ak, Julia E.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Grant, Francis J.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
; FILE REFERENCE: 00-108
; CURRENT APPLICATION NUMBER: US/09/995,898A
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/253,561
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/267,211
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-995-898A-15

Query Match 99.5%; Score 1756; DB 3; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAAPSSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFFPAVLQSS 60
Db 1 ASTKGPSVFPLAAPSSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFFPAVLQSS 60
Qy 61 GLYSLSVTVTPSSSLGTQTYICNNHKPNTKVDKKVEPKSCDKTHCTCPCPAPELAGA 120

```

```
Db 61 GLYSLSVVTVFPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPAPELLGG 120
Qy 121 PSVFLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 121 PSVFLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
Qy 301 QGQNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QGQNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 41
US-09-892-949-38
; Sequence 38, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuijper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; TYPE: PRT
; LENGTH: 330
; ORGANISM: Homo sapiens
US-09-892-949-38

Query Match 99.5%; Score 1756; DB 3; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSVVTVFPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPAPELLAGA 120
Db 61 GLYSLSVVTVFPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPAPELLGG 120
Qy 121 PSVFLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 121 PSVFLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
Qy 301 QGQNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QGQNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 42
US-10-047-542-20
; Sequence 20, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.CIP1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-542-20

Query Match 99.5%; Score 1756; DB 4; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSVVTVFPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPAPELLAGA 120
Db 61 GLYSLSVVTVFPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPAPELLGG 120
Qy 121 PSVFLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 121 PSVFLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
Qy 301 QGQNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QGQNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 43
US-10-269-805-68
; Sequence 68, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 330
```

```
Db 301 QGQNVFSCVMHEALHNHYTQKSLSLSPGK 330
Qy 301 QGQNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 44
US-10-047-542-20
; Sequence 20, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.CIP1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-542-20

Query Match 99.5%; Score 1756; DB 4; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSVVTVFPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPAPELLAGA 120
Db 61 GLYSLSVVTVFPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPAPELLGG 120
Qy 121 PSVFLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 121 PSVFLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
Qy 301 QGQNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QGQNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 45
US-10-269-805-68
; Sequence 68, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 330
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-68

Query Match      99.5%; Score 1756; DB 4; Length 330;
Best Local Similarity 99.4%; Pred. No. 7,1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGG 120

Qy 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy 181 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYVTLPPSRDE 240
Db 181 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYVTLPPSRDE 240

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300

Qy 301 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 44
US-10-310-719-8
; Sequence 8, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc
; LOCATION: (1)..(330)
; OTHER INFORMATION: Igg1 constant region
US-10-310-719-8

Query Match      99.5%; Score 1756; DB 4; Length 330;
Best Local Similarity 99.4%; Pred. No. 7,1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGG 120

Qy 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy 181 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYVTLPPSRDE 240
Db 181 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYVTLPPSRDE 240

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300

Qy 301 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 45
US-10-112-582-1
; Sequence 1, Application US/10112582
; Publication No. US20030166877A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
; FILE REFERENCE: LEX-017
; CURRENT APPLICATION NUMBER: US/10/112,582
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/280,625
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: human Ig gamma heavy chain C region
US-10-112-582-1

Query Match      99.5%; Score 1756; DB 4; Length 330;
Best Local Similarity 99.4%; Pred. No. 7,1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGG 120

Qy 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy 181 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYVTLPPSRDE 240
Db 181 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYVTLPPSRDE 240

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300

Qy 301 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 46
US-10-320-231A-81
; Sequence 81, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
```

```
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; FILE REFERENCE: Treatment Of Asthma
; CURRENT APPLICATION NUMBER: 7430*163
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/10/320,231A
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 81
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-320-231A-81

Query Match          99.5%; Score 1756; DB 4; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPELAGA 120
Db 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPELAGG 120

Qy 121 PSVFLFPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 121 PSVFLFPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180

Qy 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300

Qy 301 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 330

RESULT 47
US-10-383-902A-6
; Sequence 6, Application US/10383902A
; Publication No. US20030224408A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Mullberg, Jurgen
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: LIGAND SCREENING AND DISCOVERY
; FILE REFERENCE: 10280-042001
; CURRENT APPLICATION NUMBER: US/10/383,902A
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/362,403
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated plasmid sequence
US-10-383-902A-6

Query Match          99.5%; Score 1756; DB 4; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPELAGA 120
Db 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPELAGG 120

Qy 121 PSVFLFPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 121 PSVFLFPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180

Qy 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300

Qy 301 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 330

RESULT 48
US-10-408-901-2
; Sequence 2, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Elliot, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: MBHB 01-1145-A
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-2

Query Match          99.5%; Score 1756; DB 4; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPELAGA 120
Db 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPELAGG 120

Qy 121 PSVFLFPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 121 PSVFLFPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180

Qy 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
```


QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
QY 181 STYRVSVSLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYVTLPPSRDE 240
Db 181 STYRVSVSLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYVTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
RESULT 52
US-10-772-531-38
; Sequence 38, Application US/10772531
; Publication No. US2004014242A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuitjper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/10/772,531
; PRIOR FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/09/892,949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-772-531-38
Query Match 99.5%; Score 1756; DB 4; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGG 120
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
QY 181 STYRVSVSLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYVTLPPSRDE 240
Db 181 STYRVSVSLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYVTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
RESULT 53
US-10-479-326-1
; Sequence 1, Application US/10479326
; Publication No. US20040198961A1
; GENERAL INFORMATION:
; APPLICANT: Tanox, INC.
; APPLICANT: AN, Ling-Ling
; APPLICANT: WU, Herren
; APPLICANT: FUNG, Michael
; TITLE OF INVENTION: Fce FUSION PROTEINS FOR TREATMENT OF ALLERGY AND ASTHMA
; FILE REFERENCE: TXN01-02PCT
; CURRENT APPLICATION NUMBER: US/10/479,326
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US60/298,710
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(330)
US-10-479-326-1
Query Match 99.5%; Score 1756; DB 4; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGG 120
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
QY 181 STYRVSVSLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYVTLPPSRDE 240
Db 181 STYRVSVSLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYVTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
RESULT 54
US-10-815-449-8
; Sequence 8, Application US/10815449
; Publication No. US20040228859A1
; GENERAL INFORMATION:
; APPLICANT: GRAUS, Yvo
; APPLICANT: KOPETZKI, Erhard
; APPLICANT: KUENKELE, Klaus-Peter
; APPLICANT: MUNDIGL, Olaf
; APPLICANT: PARREN, Paul
; APPLICANT: REERS, Frank
; APPLICANT: SCHUMACHER, Ralf
; APPLICANT: Van de WINKEL, Jan
; APPLICANT: Van VUGT, Martine


```
; TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and uses
; FILE OF INVENTION: thereof
; FILE REFERENCE: 21655 US2
; CURRENT APPLICATION NUMBER: US/10/815,449
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: US 60/459,837
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US 60/463,003
; PRIOR FILING DATE: 2003-04-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-815-449-8

Query Match      99.5%; Score 1756; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 7,1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGG 120
QY 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
QY 301 QCGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QCGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 55
US-10-684-957-2
; Sequence 2, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-957-2
```

```
Query Match      99.5%; Score 1756; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 7,1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGG 120
QY 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300

RESULT 56
US-10-886-838-6
; Sequence 6, Application US/10886838
; Publication No. US20050008642A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and uses
; FILE REFERENCE: 21695
; CURRENT APPLICATION NUMBER: US/10/886,838
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: EP 03015526
; PRIOR FILING DATE: 2003-07-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-886-838-6

Query Match      99.5%; Score 1756; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 7,1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGG 120
QY 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
```

```
QY 301 OQGNVFCVMEALHNNHYTKSLSPGK 330
Db 301 OQGNVFCVMEALHNNHYTKSLSPGK 330

RESULT 57
US-10-822-300-3
; Sequence 3, Application US/10822300
; Publication No. US20050014934A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.CPUS01
; CURRENT APPLICATION NUMBER: US/10/822,300
; CURRENT FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-300-3

Query Match 99.5%; Score 1756; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGG 120
QY 121 PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
Db 121 PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
QY 181 STYRVSVLTIVLHODWLNQKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 181 STYRVSVLTIVLHODWLNQKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300

RESULT 58
US-10-822-300-7
; Sequence 7, Application US/10822300
; Publication No. US20050014934A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.CPUS01
; CURRENT APPLICATION NUMBER: US/10/822,300
; CURRENT FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Humanized antibody
; FEATURE:
; OTHER INFORMATION: Humanized antibody
```

```
US-10-822-300-7

Query Match 99.5%; Score 1756; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGG 120
QY 121 PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
Db 121 PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
QY 181 STYRVSVLTIVLHODWLNQKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 181 STYRVSVLTIVLHODWLNQKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300

RESULT 59
US-10-687-118-3
; Sequence 3, Application US/10687118
; Publication No. US20050032114A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.NPUS04
; CURRENT APPLICATION NUMBER: US/10/687,118
; CURRENT FILING DATE: 2003-10-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-687-118-3

Query Match 99.5%; Score 1756; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGG 120
QY 121 PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
Db 121 PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
QY 181 STYRVSVLTIVLHODWLNQKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 181 STYRVSVLTIVLHODWLNQKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
```

```
QY 301 QQGNVFSCVMHEALHNHYTKSLSPGK 330
      |||||
Db 301 QQGNVFSCVMHEALHNHYTKSLSPGK 330

RESULT 60
US-10-687-118-7
; Sequence 7, Application US/10687118
; Publication No. US20050032114A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.NPUS04
; CURRENT APPLICATION NUMBER: US/10/687,118
; CURRENT FILING DATE: 2003-10-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7
; LENGTH: 330
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody
US-10-687-118-7

Query Match 99.5%; Score 1756; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
      |||||
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELAGA 120
      |||||
Db 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELGG 120

QY 121 PSVFLPPPKPDKTLMISRTPEVTCVVDVSHDEPKFNWYVDGVEVHNATKPREEQYN 180
      |||||
Db 121 PSVFLPPPKPDKTLMISRTPEVTCVVDVSHDEPKFNWYVDGVEVHNATKPREEQYN 180

QY 181 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
      |||||
Db 181 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
      |||||
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300

QY 301 QQGNVFSCVMHEALHNHYTKSLSPGK 330
      |||||
Db 301 QQGNVFSCVMHEALHNHYTKSLSPGK 330

RESULT 62
US-10-698-907-22
; Sequence 22, Application US/10698907
; Publication No. US20050049194A1
; GENERAL INFORMATION:
; APPLICANT: Frisen, Jonas
; APPLICANT: Holmberg, Johan
; TITLE OF INVENTION: Use of Ephrins and Related Molecules to Regulate Cellular
; TITLE OF INVENTION: Proliferation
; FILE REFERENCE: 21882-529 UTIL
; CURRENT APPLICATION NUMBER: US/10/698,907
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/460,488
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 10/291,290
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 60/393,272
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/345,206
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 22
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-698-907-22

Query Match 99.5%; Score 1756; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
      |||||
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELAGA 120
      |||||
Db 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELGG 120
```

```
QY 301 QQGNVFSCVMHEALHNHYTKSLSPGK 330
      |||||
Db 301 QQGNVFSCVMHEALHNHYTKSLSPGK 330

RESULT 60
US-10-687-118-7
; Sequence 7, Application US/10687118
; Publication No. US20050032114A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.NPUS04
; CURRENT APPLICATION NUMBER: US/10/687,118
; CURRENT FILING DATE: 2003-10-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7
; LENGTH: 330
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody
US-10-687-118-7

Query Match 99.5%; Score 1756; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
      |||||
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELAGA 120
      |||||
Db 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELGG 120

QY 121 PSVFLPPPKPDKTLMISRTPEVTCVVDVSHDEPKFNWYVDGVEVHNATKPREEQYN 180
      |||||
Db 121 PSVFLPPPKPDKTLMISRTPEVTCVVDVSHDEPKFNWYVDGVEVHNATKPREEQYN 180

QY 181 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
      |||||
Db 181 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
      |||||
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300

QY 301 QQGNVFSCVMHEALHNHYTKSLSPGK 330
      |||||
Db 301 QQGNVFSCVMHEALHNHYTKSLSPGK 330

RESULT 61
US-10-901-735-2
; Sequence 2, Application US/10901735
; Publication No. US20050032183A1
; GENERAL INFORMATION:
; APPLICANT: AMGEN, Inc.
; APPLICANT: OSSUND, Timothy D.
; APPLICANT: CLOGSTON, Christi
; APPLICANT: CRAMPTON, Shon
; APPLICANT: BASS, Randal
; TITLE OF INVENTION: CRYSTALLINE POLYPEPTIDES
; FILE REFERENCE: A-859
; CURRENT APPLICATION NUMBER: US/10/901,735
; CURRENT FILING DATE: 2004-07-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2
```

```
QY 121 PSVFLPPPKDXTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNNAKTKPREEQYN 180
Db 121 PSVFLPPPKDXTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNNAKTKPREEQYN 180
QY 181 STYRVSVSLTVLHQDLWNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVSLTVLHQDLWNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 63
US-10-928-305-7
; Sequence 7, Application US/10928305
; Publication No. US20050069521A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen D.
; APPLICANT: Lauder, Scott
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ENHANCING THE CIRCULATING HALF-LIFE OF INTERLEUKIN-2 PROTEINS
; FILE REFERENCE: LEX-024
; CURRENT APPLICATION NUMBER: US/10/928,305
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/498,618
; PRIOR FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-928-305-7

Query Match 99.5%; Score 1756; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGLVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGLVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGG 120
QY 121 PSVFLPPPKDXTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNNAKTKPREEQYN 180
Db 121 PSVFLPPPKDXTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNNAKTKPREEQYN 180
QY 181 STYRVSVSLTVLHQDLWNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVSLTVLHQDLWNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 64
US-10-480-109-5
; Sequence 5, Application US/10480109
; Publication No. US20050069540A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Liu, Jinqi
; APPLICANT: Na, Songqing
; APPLICANT: Song, Ho
; APPLICANT: Yang, Derek
; TITLE OF INVENTION: TREATING B-CELL MEDIATED DISEASES BY MODULATING DR6 ACTIVITY
; FILE REFERENCE: X-15237
; CURRENT APPLICATION NUMBER: US/10/480,109
; CURRENT FILING DATE: 2004-06-08
; PRIOR APPLICATION NUMBER: 60/342,632
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-480-109-5

Query Match 99.5%; Score 1756; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGLVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGLVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGG 120
QY 121 PSVFLPPPKDXTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNNAKTKPREEQYN 180
Db 121 PSVFLPPPKDXTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNNAKTKPREEQYN 180
QY 181 STYRVSVSLTVLHQDLWNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVSLTVLHQDLWNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 65
US-10-891-658-2
; Sequence 2, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,431
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-891-658-2
```

Query Match 99.5%; Score 1756; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPELAGA 120
Db 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPELAGA 120

Qy 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

Qy 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRW 300

Qy 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 66
US-10-867-506-81
; Sequence 81, Application US/10867506
; Publication No. US20050112698A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; APPLICANT: Delaria, Kathy
; APPLICANT: Van, Kelly
; APPLICANT: Wong, Teresa
; APPLICANT: Longphre, Malinda
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; FILE REFERENCE: 11334*10
; CURRENT APPLICATION NUMBER: US/10/867,506
; PRIOR FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 10/320,231
; PRIOR FILING DATE: 2002-12-16
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-867-506-81

Query Match 99.5%; Score 1756; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPELAGA 120
Db 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPELAGA 120

Qy 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

Db 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Qy 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRW 300

Qy 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 67
US-10-937-596-31
; Sequence 31, Application US/10937596
; Publication No. US20050118169A1
; GENERAL INFORMATION:
; APPLICANT: BARTKE, ILSE
; APPLICANT: CARR, FRANCIS
; APPLICANT: CHIZZONITE, RICHARD ANTHONY
; APPLICANT: EUGUI, ELSIE M.
; APPLICANT: FERTIG, GEORG
; APPLICANT: HAMILTON, ANITA
; APPLICANT: LANZENDOERFER, MARTIN
; APPLICANT: RUEGER, PETRA
; APPLICANT: SCHUMACHER, RALF
; APPLICANT: TRUITT, THERESA PATRICIA
; TITLE OF INVENTION: ANTIBODIES AGAINST INTERLEUKIN-1 RECEPTOR AND USBS THEREOF
; FILE REFERENCE: CD21842-US1
; CURRENT APPLICATION NUMBER: US/10/937,596
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: 60/501,681
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: EP 03029659.4
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-937-596-31

Query Match 99.5%; Score 1756; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPELAGA 120
Db 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPELAGA 120

Qy 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

Qy 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRW 300

Qy 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

```
RESULT 68
US-10-893-576-45
; Sequence 45, Application US/108933576
; Publication No. US20050118643A1
; GENERAL INFORMATION:
; APPLICANT: BURGESS, TERESA L.
; APPLICANT: COXON, ANGELA
; APPLICANT: GREEN, LARRY L.
; APPLICANT: ZHANG, KE
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR
; FILE REFERENCE: 06843.0051-00000
; CURRENT APPLICATION NUMBER: US/10/893,576
; CURRENT FILING DATE: 2004-07-16
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 45
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Human IgG1
; OTHER INFORMATION: Constant Region
US-10-893-576-45

Query Match          99.5%; Score 1756; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 7,1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 120
DB 61 GLYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELGG 120
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
QY 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
DB 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 69
US-10-868-373-8
; Sequence 8, Application US/10868373
; Publication No. US20050118683A1
; GENERAL INFORMATION:
; APPLICANT: Wood, C. et al.
; TITLE OF INVENTION: METHOD FOR PRODUCING A POLYPEPTIDE
; FILE REFERENCE: 22058-547
; CURRENT APPLICATION NUMBER: US/10/868,373
; CURRENT FILING DATE: 2004-06-14
; PRIOR FILING DATE: 2003-06-11
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1.1
; SEQ ID NO 8
; LENGTH: 330

Query Match          99.5%; Score 1756; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 7,1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 120
DB 61 GLYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELGG 120
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
QY 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
DB 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 70
US-10-977-369-139
; Sequence 139, Application US/10977369
; Publication No. US20050152898A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Hamilton, Anita A.
; TITLE OF INVENTION: MODIFIED ANTI-CD52 ANTIBODY
; FILE REFERENCE: ILEX:095US
; CURRENT APPLICATION NUMBER: US/10/977,369
; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: 60/516,210
; PRIOR FILING DATE: 2003-11-01
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 139
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-977-369-139

Query Match          99.5%; Score 1756; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 7,1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 120
DB 61 GLYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELGG 120
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
QY 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
DB 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
```

Qy	241	LTRQVSLTCLVKGFYPSDIAVWESNQGPPNNYKTTTPVLDSDGSGFFLYSKLTVDKSRW	300
Db	241	LTRQVSLTCLVKGFYPSDIAVWESNQGPPNNYKTTTPVLDSDGSGFFLYSKLTVDKSRW	300
Qy	301	QQGVNFCSCVMHEALHNHYTQKSLSLSPGK	330
Db	301	QQGVNFCSCVMHEALHNHYTQKSLSLSPGK	330

```

RESULT 71
US-10-901-736-60
; Sequence 60, Application US/10901736
; Publication No. US20050169909A1
; GENERAL INFORMATION:
; APPLICANT: TANOX, INC.
; APPLICANT: SINGH, Sanjaya
; APPLICANT: HUANG, Danyang
; APPLICANT: FUNG, Sek Chung
; TITLE OF INVENTION: Identification of Unique, High Affinity IgE Epitopes
; FILE REFERENCE: TNX-1030
; CURRENT APPLICATION NUMBER: US/10/901,736
; CURRENT FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: 60/444,229
; PRIOR FILING DATE: 2003-02-01
; PRIOR APPLICATION NUMBER: PCT/US04/02892
; PRIOR FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: PCT/US04/02894
; PRIOR FILING DATE: 2004-02-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 330
; TYPE: PRT
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: CONSTANT REGION OF HUMAN IGH1
US-10-901-736-60

```

RESULT 72
US-10-982-555-38
; Sequence 38, Application US/10982555
; Publication No. US20050214801A1
; GENERAL INFORMATION:

```

; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuijper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/10/982,555
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US/09/892,949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-555-38

Query Match          99.5%; Score 1756; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128; Indels 0; Gaps 0;
Matches 328; Conservative 0; Mismatches 2;

Qy 1  ASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPTVSMNSGALTSVHTFPAVLQSS 60
Db 1  ASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPTVSMNSGALTSVHTFPAVLQSS 60

Qy 61  GLYSLSGVTVPSSSIGTQYICNVNKHPSNTKVDKKVPEKSCDKHTCCPCPAPELAGA 120
Db 61  GLYSLSGVTVPSSSIGTQYICNVNKHPSNTKVDKKVPEKSCDKHTCCPCPAPELLGG 120

Qy 121  PSVFLEPPPKPDKTLMSIRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 121  PSVFLEPPPKPDKTLMSIRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy 181  STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTITISKAKGQPREPOVYITLPSRDE 240
Db 181  STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTITISKAKGQPREPOVYITLPSRDE 240

Qy 241  LTKNQVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241  LTKNQVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300

Qy 301  QQQNVFSCSVMHDAALHNHYTQKSLSLSPGK 330
Db 301  QQQNVFSCSVMHDAALHNHYTQKSLSLSPGK 330

RESULT 73
US-10-493-909-20
; Sequence 20, Application US/10493909
; Publication No. US20060015969A1
; GENERAL INFORMATION:
; APPLICANT: LABRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING TOXICIT
; FILE REFERENCE: 41514-20004.01
; CURRENT APPLICATION NUMBER: US/10/493,909
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1

```

```
; SEQ ID NO 20
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-493-909-20

Query Match      99.5%; Score 1756; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGG 120
Qy 121 PSVFLFPPKPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
Db 121 PSVFLFPPKPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
Qy 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 74
US-10-982-440-68
; Sequence 88, Application US/10982440
; Publication No. US20060018909A1
; GENERAL INFORMATION:
; APPLICANT: Oliner, John
; APPLICANT: Graham, Kevin
; TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
; FILE REFERENCE: 04-881-A
; CURRENT APPLICATION NUMBER: US/10/982,440
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/620,161
; PRIOR FILING DATE: 2004-10-19
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 68
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-440-68

Query Match      99.5%; Score 1756; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGG 120
Qy 121 PSVFLFPPKPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
Db 121 PSVFLFPPKPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
Qy 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
```

```
; SEQ ID NO 20
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-493-909-20

Query Match      99.5%; Score 1756; DB 6; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGG 120
Qy 121 PSVFLFPPKPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
Db 121 PSVFLFPPKPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
Qy 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 75
US-11-004-054-1
; Sequence 1, Application US/11004054
; Publication No. US2005014213A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Dang, Wei
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hammond, Philip W.
; APPLICANT: Vielmetter, Jost
; TITLE OF INVENTION: OPTIMIZED PROTEINS THAT TARGET THE EPIDERMAL GROWTH FACTOR
; FILE REFERENCE: 185834/US/2
; CURRENT APPLICATION NUMBER: US/11/004,054
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/526,799
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-004-054-1

Query Match      99.5%; Score 1756; DB 6; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGG 120
Qy 121 PSVFLFPPKPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
Db 121 PSVFLFPPKPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYN 180
Qy 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 76
US-11-026-998-22
; Sequence 22, Application US/11026998
; Publication No. US2005019221A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen D.
; APPLICANT: Lauder, Scott
```


RESULT 7a

```

RESULI 78
US-11-090-836-44
; Sequence 44, Application US/11090836
; Publication No. US20050214288A1
; GENERAL INFORMATION:
; APPLICANT: Bell, et al.
; TITLE OF INVENTION: Antibodies Against Nogo Receptor
; FILE REFERENCE: PF610
; CURRENT APPLICATION NUMBER: US/11/090.836
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/556,443
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-090-836-44

```

[illegible]

```
RESULT 79
US-11-090-846-44
; Sequence 44, Application US/11090846
; Publication No. US20050214289A1
; GENERAL INFORMATION:
; APPLICANT: Bell, et al.
; TITLE OF INVENTION: Antibodies Against Nogo Receptor
; FILE REFERENCE: PF611
; CURRENT APPLICATION NUMBER: US/11/090,846
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/556,442
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 44
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-090-846-44

Query Match      99.5%; Score 1756; DB 6; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 60
QY 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
DB 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGG 120
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVITLPPSRDE 240
DB 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVITLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 81
US-11-102-403-24
; Sequence 24, Application US/11102403
; Publication No. US20050226876A1
; GENERAL INFORMATION:
; APPLICANT: GRAUS, YVO
; APPLICANT: HIMBER, JACQUES
; APPLICANT: JANSEN-MOLENAAR, MIRANDA
; APPLICANT: KLING, DOROTHEE
; APPLICANT: KOPETZKI, ERHARD
; APPLICANT: PAREN, PAUL
; APPLICANT: REBERS, FRANK
; APPLICANT: STEINER, BEAT
; APPLICANT: STERN, ANNE
; APPLICANT: STUBENRAUCH, KAY-GUNNAR
; APPLICANT: VAN DE WINKEL, JAN
; APPLICANT: VAN VUUT, MARTINE
; TITLE OF INVENTION: ANTI-P SELECTIN ANTIBODIES
; FILE REFERENCE: 22354
; CURRENT APPLICATION NUMBER: US/11/102,403
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: EP 04008722.3
; PRIOR FILING DATE: 2004-04-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patentin ver. 3.3
; SEQ ID NO 24
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-403-24

Query Match      99.5%; Score 1756; DB 6; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 60
QY 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
DB 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGG 120
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVITLPPSRDE 240
DB 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVITLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 80
US-11-090-847-44
; Sequence 44, Application US/11090847
; Publication No. US20050215770A1
; GENERAL INFORMATION:
; APPLICANT: Bell, et al.
; TITLE OF INVENTION: Antibodies Against Nogo Receptor
; FILE REFERENCE: PF609
; CURRENT APPLICATION NUMBER: US/11/090,847
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/556,386
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 249
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 44
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-090-847-44

Query Match      99.5%; Score 1756; DB 6; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 60
QY 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
DB 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGG 120
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVITLPPSRDE 240
DB 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVITLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
```

QY 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 82

US-11-102-403-26
; Sequence 26, Application US/11102403
; Publication No. US20050226876A1
; GENERAL INFORMATION:
; APPLICANT: GRAUS, YVO
; APPLICANT: HIMBER, JACQUES
; APPLICANT: JANSEN-MOLENAAR, MIRANDA
; APPLICANT: KLING, DOROTHEE
; APPLICANT: KOPETZKI, ERHARD
; APPLICANT: PAREN, PAUL
; APPLICANT: REBERS, FRANK
; APPLICANT: STEINER, BEAT
; APPLICANT: STERN, ANNE
; APPLICANT: STREIN, PAMELA
; APPLICANT: STUBENRAUCH, KAY-GUNNAR
; APPLICANT: VAN DE WINKEL, JAN
; APPLICANT: VAN VUGT, MARTINE
; TITLE OF INVENTION: ANTI-P SELECTIN ANTIBODIES
; FILE REFERENCE: 22354
; CURRENT APPLICATION NUMBER: US/11/102,403
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: EP 04008722.3
; PRIOR FILING DATE: 2004-04-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 26
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-403-26

Query Match 99.5%; Score 1756; DB 6; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELAGA 120
DB 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPEAAGG 120
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNATKPREEOYN 180
DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNATKPREEOYN 180
QY 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 83
US-11-022-289-11
; Sequence 11, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: LAZAR, GREGORY ALAN
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-022-289-11

Query Match 99.5%; Score 1756; DB 6; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELAGA 120
DB 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELAGG 120
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNATKPREEOYN 180
DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNATKPREEQYN 180
QY 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 84

US-11-075-351-1
; Sequence 1, Application US/11075351
; Publication No. US20050260716A1
; GENERAL INFORMATION:
; APPLICANT: MOORE, MARGARET D.
; APPLICANT: FOX, BRIAN A.
; TITLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS
; TITLE OF INVENTION: AND METHODS FOR PRODUCING THEM
; FILE REFERENCE: 02-16
; CURRENT APPLICATION NUMBER: US/11/075,351
; CURRENT FILING DATE: 2005-03-08
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-075-351-1
Query Match 99.5%; Score 1756; DB 6; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;

Matches	328;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	1	ASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHFFPAVLQSS	60						
Db	1	ASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHFFPAVLQSS	60						
Qy	61	GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPELAGA	120						
Db	61	GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPELLGG	120						
Qy	121	PSVELFPKPKDITLMI SRTPEVTCVVDVSHEDPEVKFNWTVDGVGVHNAKTKPREQYN	180						
Db	121	PSVELFPKPKDITLMI SRTPEVTCVVDVSHEDPEVKFNWTVDGVGVHNAKTKPREQYN	180						
Qy	181	STYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE	240						
Db	181	STYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE	240						
Qy	241	LTRNQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW	300						
Db	241	LTRNQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW	300						
Qy	301	QQGNVFCSVMHEALHNHYTQKSLSLSPGK	330						
Db	301	QQGNVFCSVMHEALHNHYTQKSLSLSPGK	330						

RESULT 85

```

US-11-153-141-15
; Sequence 15, Application US/1115141
; Publication NO. US20050266485A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenteng
; APPLICANT: Novak, Julia E.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Grant, Francis J.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR1

```

	Query Match	99.5%	Score 1756;	DB 6;	Length 330;
	Best Local Similarity	99.4%;	Pred. No. 7.1e-128;		
	Matches 328;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	ASTKGPVVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAVLQSS	60		
Db	1	ASTKGPVVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAVLQSS	60		
Qy	61	GLYSLSVVTVPSSSLGTQTVICNNHKPSNTKVDKVKPKSCDKHTCCPCPAPELAGA	120		
Db	61	GLYSLSVVTVPSSSLGTQTVICNNHKPSNTKVDKVKPKSCDKHTCCPCPAPELLGG	120		
Qy	121	PSVFELPPKPKDTLMI SRTPEVT CVVDVSHEDDEVFNWTVYDGVVHNNAKTKPREQYN	180		
Db	121	PSVFELPPKPKDTLMI SRTPEVT CVVDVSHEDDEVFNWTVYDGVVHNNAKTKPREQYN	180		
Qy	181	STRVWSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE	240		

```

Db      181  STYRVSVLTVHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Qy      241  LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGDSGFFLYSKLTVDKSRW 300
Db      241  LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGDSGFFLYSKLTVDKSRW 300
Qy      301  QOQNVFSCVMHEALHNNHYTQKLSLSLSPGK 330
Db      301  QOQNVFSCVMHEALHNNHYTQKLSLSLSPGK 330

RESULT 86
US-11-102-621-3
; Sequence 3, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCgRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-3

```

Query Match	99.5%;	Score 1756;	DB 6;	Length 330;
Best Local Similarity	99.4%;	Pred. No. 7.1e-128;		
Matches 326;	Conservative 0;	Mismatches 12;	Indels 0;	Gaps 0;
Qy	1	ASTKGPVFPFLAPSSKSTSGGTAAALGCLVKXDYPPEPVTVSNWNGALTSGVHTFPVAVLQSS	60	
Db	1	ASTKGPVFPFLAPSSKSTSGGTAAALGCLVKXDYPPEPVTVSNWNGALTSGVHTFPVAVLQSS	60	
Qy	61	GLYSLSWVTVPPSSSLGTQYIICNVNHKPSNTKVKKEPKSCDKHTCTCPCPAPELAGA	120	
Db	61	GLYSLSWVTVPPSSSLGTQYIICNVNHKPSNTKVKKEPKSCDKHTCTCPCPAPELLGG	120	
Qy	121	PSVFLPPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRREQYN	180	
Db	121	PSVFLPPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRREQYN	180	
Qy	181	STRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPSSRDE	240	
Db	181	STRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPSSRDE	240	
Qy	241	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSLKLTVDKSRW	300	
Db	241	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSLKLTVDKSRW	300	
Qy	301	QOQNVFSCSVMHREALNHHYTKQSLSLSPGK	330	
Db	301	QOQNVFSCSVMHREALNHHYTKQSLSLSPGK	330	

RESULT 87
US-11-102-621-7
; Sequence 7, Application US/11102621
; Publication No. US2005027679A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya

APPLICANT: Tso, J. Yun
APPLICANT: Vasquez, Maximiliano
TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
FILE OF INVENTION: ANTIBODIES BY MUTAGENESIS
FILE REFERENCE: 05882.0039.00PC03
CURRENT APPLICATION NUMBER: US/11/102,621
CURRENT FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: US 10/822,300
PRIOR FILING DATE: 2004-04-09
NUMBER OF SEQ ID NOS: 146
SOFTWARE: Patentin version 3.2
SEQ ID NO 7
LENGTH: 330
TYPE: PRT
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: Humanized antibody
US-11-102-621-7

Query Match 99.5%; Score 1756; DB 6; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVKPEKSCDKTHTCPPCPAPELAGA 120
DB 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVKPEKSCDKTHTCPPCPAPELAGG 120
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 330

RESULT 88
US-11-005-726-164
Sequence 164, Application US/11005726
Publication No. US20060018903A1
GENERAL INFORMATION:
APPLICANT: HELLENDORN, Koen
APPLICANT: BAKER, Matthew
APPLICANT: CARR, Francis J.
TITLE OF INVENTION: TNF ALPHA-BINDING POLYPEPTIDE
FILE REFERENCE: MER-131
CURRENT APPLICATION NUMBER: US/11/005,726
CURRENT FILING DATE: 2004-12-07
PRIOR APPLICATION NUMBER: 10/495,146
PRIOR FILING DATE: 2004-05-10
PRIOR APPLICATION NUMBER: PCT/EP02/12566
PRIOR FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: EP 01126859.8
PRIOR FILING DATE: 2001-11-12
NUMBER OF SEQ ID NOS: 165
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 164
LENGTH: 330
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: anti-TNF alpha chimeric antibody heavy chain
OTHER INFORMATION: constant region
US-11-005-726-164
Query Match 99.5%; Score 1756; DB 6; Length 330;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVKPEKSCDKTHTCPPCPAPELAGA 120
DB 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVKPEKSCDKTHTCPPCPAPELAGG 120
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 330

RESULT 89
US-11-124-620-1
Sequence 1, Application US/11124620
Publication No. US20060024298A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Dang, Wei
APPLICANT: Desjarlais, John R.
APPLICANT: Karki, Sher Bahadur
APPLICANT: Vafa, Omid
APPLICANT: Hayes, Robert
TITLE OF INVENTION: OPTIMIZED FC VARIANTS
FILE REFERENCE: A-71386-9
CURRENT APPLICATION NUMBER: US/11/124,620
CURRENT FILING DATE: 2005-05-05
PRIOR APPLICATION NUMBER: US 60/568,440
PRIOR FILING DATE: 2004-07-15
PRIOR APPLICATION NUMBER: US 60/589,906
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: US 60/627,026
PRIOR FILING DATE: 2004-11-09
PRIOR APPLICATION NUMBER: US 60/626,991
PRIOR FILING DATE: 2004-11-10
PRIOR APPLICATION NUMBER: US 60/627,774
PRIOR FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: US 10/822,231
PRIOR FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US 10/672,280
PRIOR FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: US 10/379,392
PRIOR FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.3
SEQ ID NO 1
LENGTH: 330
TYPE: PRT
ORGANISM: Homo sapiens
US-11-124-620-1

Query Match	99.5%	Score 1756;	DB 6;	Length 330;
Best Local Similarity	99.4%;	Pred. No. 7.1e-128;		
Matches 328;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS	60	
Db	1	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS	60	
Qy	61	GLYSLSSVTVTPSSSLGTQTQYICNVNHPKPSNTKVDKVEPKSCDKHTHTCPPCPAPELAGA	120	
Db	61	GLYSLSSVTVTPSSSLGTQTQYICNVNHPKPSNTKVDKVEPKSCDKHTHTCPPCPAPELGG	120	
Qy	121	PSVFLPPPKPKDTHMISRTPEVTCVVDVSHEDDEVKFNWYVDGVEVFNNAKTKPREQYN	180	
Db	121	PSVFLPPPKPKDTHMISRTPEVTCVVDVSHEDDEVKFNWYVDGVEVFNNAKTKPREQYN	180	
Qy	181	STYRWSVLTVLHODWLNKGKVKCKVSNKALPAPIEKTIISAKGQPREPQVYTLPPSRDE	240	
Db	181	STYRWSVLTVLHODWLNKGKVKCKVSNKALPAPIEKTIISAKGQPREPQVYTLPPSRDE	240	
Qy	241	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFPLYSKLTVDKSRW	300	
Db	241	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFPLYSKLTVDKSRW	300	
Qy	301	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	330	
Db	301	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	330	

```

RESULT 90
US-11-233-683-1
; Sequence 1, Application US/11233683
; Publication No. US20060025573A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
; FILE REFERENCES: LEX-017
; CURRENT APPLICATION NUMBER: US/11/233,683
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 60/280,625
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: human Ig gamma heavy chain C region
; US-11-233-683-1

```

Query Match	99.5%	Score 1756;	DB 6;	Length 330;
Best Local Similarity	99.4%;	Pred. No. 7.1e-128;		
Matches 328;	Conservative	0;	Mismatches 2;	Indels 0;
Gaps	0;			
Qy	1	ASTKGPSVFPLAPSSKTSGGTAAAGCLGVKDYFPPEPVTVWNSGALTSGVHTFPVAVLOSS	60	
Db	1	ASTKGPSVFPLAPSSKTSGGTAAAGCLGVKDYFPPEPVTVWNSGALTSGVHTFPVAVLOSS	60	
Qy	61	GLYSLSSVTVVPSSSLGTQTIVICNNHHKPSNTKVDKKVEPKSCDKTHTCTPCCPAPELAGA	120	
Db	61	GLYSLSSVTVVPSSSLGTQTIVICNNHHKPSNTKVDKKVEPKSCDKTHTCTPCCPAPELLGG	120	
Qy	121	PSVFLFPPKPKDGLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQVN	180	
Db	121	PSVFLFPPKPKDGLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQVN	180	
Qy	181	STYRVSVSLTVLHQDWLNGKEYCKCKSNKALPAPIEKTISAKAGQPREPQVYTLPPSRDE	240	
Db	181	STYRVSVSLTVLHQDWLNGKEYCKCKSNKALPAPIEKTISAKAGQPREPQVYTLPPSRDE	240	
Qy	241	LTKNOVSLTCLVKGFPYSDIAVEVESNGOPENNYKTTTPVLDSDSGSFFLYSLKLTVDKSRW	300	

```

Db      241  LTRNQVSLTCLVKGFPDSIAVENESGQPENNYKTTTPVLDSGSPFLYSKLTVDKSRW 330
Qy      301  QQGNVFCSCVMHEALHNHYTKSLSLSPGK 330
Db      301  QQGNVFCSCVMHEALHNHYTKSLSLSPGK 330

RESULT 91
US-11-218-813-136
; Sequence 136, Application US/11218813
; Publication No. US20060062793A1
; GENERAL INFORMATION:
; APPLICANT: Webb, Iain J.
; APPLICANT: Horvath, Christopher J.
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 1048-163005
; CURRENT APPLICATION NUMBER: US/11/218,813
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US2004/006543
; PRIOR FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain constant region of deJ591 spans
US-11-218-813-136

```

Query Match	99.5%;	Score 1756;	DB 6;	Length 330;
Best Local Similarity	99.4%;	Pred. No. 7.1e-128;		
Matches 328;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	ASTKGPVFPLAPSSKSTSGTAAALGCLVKDYPPEPVTVSNWSGALTSGVHTFPAVLQSS	60	
Db	1	ASTKGPVFPLAPSSKSTSGTAAALGCLVKDYPPEPVTVSNWSGALTSGVHTFPAVLQSS	60	
Qy	61	GLYSLSWVTVPPSSSLGTQTVICNVNHKPSNTKVDKVEPKSCDKHTTCCPCPAPELAGA	120	
Db	61	GLYSLSWVTVPPSSSLGTQTVICNVNHKPSNTKVDKVEPKSCDKHTTCCPCPAPELLGG	120	
Qy	121	PSVFLFPKPKDITLMI SRTPEVT CVVVDVSHEDDEVFNKTVYDGVGVHNAKTKPREQYN	180	
Db	121	PSVFLFPKPKDITLMI SRTPEVT CVVVDVSHEDDEVFNKTVYDGVGVHNAKTKPREQYN	180	
Qy	181	STYRVVSVLTVLHVDWLNKGEYCKVSNKALPAPIEKTIISKAKGPQREPQVYTLPPSRDE	240	
Db	181	STYRVVSVLTVLHVDWLNKGEYCKVSNKALPAPIEKTIISKAKGPQREPQVYTLPPSRDE	240	
Qy	241	LTKNQVSLTCLIVKGFPYPSDIAVAVESNGQPENNYKTTTPPVLDSDGSFPLYSKLTVDKSRW	300	
Db	241	LTKNQVSLTCLIVKGFPYPSDIAVAVESNGQPENNYKTTTPPVLDSDGSFPLYSKLTVDKSRW	300	
Qy	301	QQGNVFCSVMHEALHNHYTQKSLSLSPGK	330	
Db	301	QQGNVFCSVMHEALHNHYTQKSLSLSPGK	330	

RESULT 92
US-09-990-586-98
: Sequence 98, Application US/09990586
: Publication No. US20030109680A1
: GENERAL INFORMATION:
: APPLICANT: JIAO, JIN-AN
: APPLICANT: WONG, HING C
: TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
: TITLE OF INVENTION: OF USE THEREOF
: FILE REFERENCE: 71758/46943-CIP2
: CURRENT APPLICATION NUMBER: US/09/990,586
: CURRENT FILING DATE: 2001-11-21

; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-98

Query Match
Best Local Similarity 99.5%; Score 1756; DB 3; Length 332;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSS 60
Db 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSS 62
QY 61 GLYSLSSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPCPAPELAGA 120
Db 63 GLYSLSSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPCPAPELGG 122
QY 121 PSVFLFPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 123 PSVFLFPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
QY 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 183 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 302
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 303 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 332

RESULT 93
US-10-310-113-167
; Sequence 167, Application US/10310113
; Publication No. US20030176664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; APPLICANT: NIEVES, ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 167
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-167

Query Match
Best Local Similarity 99.5%; Score 1756; DB 4; Length 332;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSS 60
Db 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSS 62
QY 61 GLYSLSSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPCPAPELAGA 120
Db 63 GLYSLSSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPCPAPELGG 122
QY 121 PSVFLFPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 123 PSVFLFPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
QY 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 183 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 302
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 303 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 332

RESULT 94
US-10-230-880-98
; Sequence 98, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-98

Query Match
Best Local Similarity 99.4%; Score 1756; DB 4; Length 332;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSS 60
Db 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSS 62
QY 61 GLYSLSSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPCPAPELAGA 120
Db 63 GLYSLSSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPCPAPELGG 122
QY 121 PSVFLFPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 123 PSVFLFPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
QY 181 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 183 STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300

```
Db 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 302
QY 301 QQGNVFCSCVMHEALHNNHYTKSLSPGK 330
Db 303 QQGNVFCSCVMHEALHNNHYTKSLSPGK 332

RESULT 95
US-11-122-622-98
; Sequence 98, Application US/11122622
; Publication No. US2006003901A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/11/122,622
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: US/09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-122-622-98

Query Match 99.5%; Score 1756; DB 6; Length 332;
Best Local Similarity 99.4%; Pred. No. 7.1e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 63 GLYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 122
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 123 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 182
QY 181 STYRVSVSLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 183 STYRVSVSLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 242
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 302
QY 301 QQGNVFCSCVMHEALHNNHYTKSLSPGK 330
Db 303 QQGNVFCSCVMHEALHNNHYTKSLSPGK 332

RESULT 96
US-10-272-899A-8
; Sequence 8, Application US/10272899A
; Publication No. US20040033561A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa L.
; APPLICANT: Healy, Judith Jacques
; APPLICANT: Newman, Walter
; APPLICANT: Ponath, Paul
; APPLICANT: Bruce Keyt
; TITLE OF INVENTION: IMMUNOGLOBULIN DNA CASSETTE MOLECULES,
; TITLE OF INVENTION: MONOBODY CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS OF
; TITLE OF INVENTION: USE THEREFOR
```

```
; FILE REFERENCE: MPI01-244P2RM
; CURRENT APPLICATION NUMBER: US/10/272,899A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/350,166
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/392,364
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human IgG1-WT protein
US-10-272-899A-8

Query Match 99.5%; Score 1756; DB 4; Length 333;
Best Local Similarity 99.4%; Pred. No. 7.2e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 4 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 63
QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 64 GLYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 123
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 124 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 183
QY 181 STYRVSVSLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 184 STYRVSVSLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 243
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 244 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 303
QY 301 QQGNVFCSCVMHEALHNNHYTKSLSPGK 330
Db 304 QQGNVFCSCVMHEALHNNHYTKSLSPGK 333

RESULT 97
US-11-024-251-35
; Sequence 35, Application US/11024251
; Publication No. US20050266425A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Paris, Mark
; TITLE OF INVENTION: Methods for Producing and Identifying Multispecific Antibodies
; FILE REFERENCE: 1843.0230001
; CURRENT APPLICATION NUMBER: US/11/024,251
; CURRENT FILING DATE: 2004-12-29
; PRIOR APPLICATION NUMBER: 60/533,241
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: IgG Secreted Constant Domain
US-11-024-251-35

Query Match 99.5%; Score 1756; DB 6; Length 335;
Best Local Similarity 99.4%; Pred. No. 7.2e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```


QY 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
Db 6 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 65
QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 66 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELGG 125
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 126 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 185
QY 181 STYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 186 STYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 245
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 246 LTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 305
QY 301 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 306 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 335
RESULT 98
US-10-272-899A-72
; Sequence 72, Application US/10272899A
; Publication No. US20040033561A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa L.
; APPLICANT: Healy, Judith Jacques
; APPLICANT: Newman, Walter
; APPLICANT: Ponath, Paul
; APPLICANT: Bruce Keyt
; TITLE OF INVENTION: IMMUNOGLOBULIN DNA CASSETTE MOLECULES,
; TITLE OF INVENTION: MONOBODY CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS OF
; FILE OF INVENTION: USE THEREFOR
; FILE REFERENCE: MPI01-244P2RM
; CURRENT APPLICATION NUMBER: US/10/272,899A
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/350,166
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/392,364
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin cassette protein sequence
; OTHER INFORMATION: Leader-HuWT_55
US-10-272-899A-72
Query Match 99.5%; Score 1756; DB 4; Length 356;
Best Local Similarity 99.4%; Pred. No. 7.8e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
Db 27 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 86
QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 87 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELGG 146
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 147 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 206
QY 181 STYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Db 207 STYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 266
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 267 LTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 326
QY 301 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 327 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 356
RESULT 99
US-10-157-408-7
; Sequence 7, Application US/10157408
; Publication No. US20030104535A1
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/157,408
; FILING DATE: 28-May-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0444PIC3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-157-408-7
Query Match 99.5%; Score 1756; DB 4; Length 371;
Best Local Similarity 99.4%; Pred. No. 8.2e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
Db 42 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 101

```
QY 61 GLYSLSSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 102 GLYSLSSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELGG 161
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 162 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 221
QY 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYVTLPPSRDE 240
Db 222 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYVTLPPSRDE 281
QY 241 LTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 282 LTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 341
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 342 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 371
```

RESULT 100

US-10-097-044A-7
; Sequence 7, Application US/10097044A
; Publication No. US20030143220A1

GENERAL INFORMATION:

; APPLICANT: Capon, Daniel J.
; Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/097,044A
FILING DATE: 28-May-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-JUN-1995
APPLICATION NUMBER: 08/236311
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987

ATTORNEY/AGENT INFORMATION:

NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444PIC3
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-10-097-044A-7

Query Match 99.5%; Score 1756; DB 4; Length 371;
Best Local Similarity 99.4%; Pred. No. 8.2e-128;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 ASTKGPSVFPLAPSSKSTSGGTAAIGCLVKKDYFPPEPVTVSNWNSGALTSGVHTFPAVLQSS 60
Db 42 ASTKGPSVFPLAPSSKSTSGGTAAIGCLVKKDYFPPEPVTVSNWNSGALTSGVHTFPAVLQSS 101
QY 61 GLYSLSSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 102 GLYSLSSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELGG 161
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 162 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 221
QY 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYVTLPPSRDE 240
Db 222 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYVTLPPSRDE 281
QY 241 LTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 282 LTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 341
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 342 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 371
```

Search completed: June 12, 2006, 17:30:55

Job time : 314.346 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 12:32:32 ; Search time 11.3964 Seconds
(without alignments)
366.103 Million cell updates/sec

Title: US-10-733-563-110
Perfect score: 1765
Sequence: 1 ASTKGPSVFPLAPSSKSTSG.....MHEALHNHYTQKLSLSLSPGK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 64916 seqs, 12643201 residues

Total number of hits satisfying chosen parameters: 64916

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New.*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	DB ID	Description	
1	1759	99.7	330	7	US-11-221-902-87	Sequence 87, Appl
2	1756	99.5	330	7	US-11-219-563-136	Sequence 136, Appl
3	1756	99.5	453	7	US-11-254-182-44	Sequence 44, Appl
4	1756	99.5	464	7	US-11-219-563-132	Sequence 132, Appl
5	1756	99.5	467	7	US-11-293-697-4293	Sequence 4293, Appl
6	1756	99.5	471	7	US-11-293-697-4294	Sequence 4294, Appl
7	1756	99.5	472	7	US-11-293-697-4073	Sequence 4073, Appl
8	1756	99.5	473	7	US-11-293-697-4284	Sequence 4284, Appl
9	1756	99.5	474	7	US-11-293-697-4282	Sequence 4282, Appl
10	1756	99.5	476	7	US-11-293-697-4288	Sequence 4288, Appl
11	1756	99.5	477	7	US-11-293-697-4289	Sequence 4289, Appl
12	1754	99.4	330	7	US-11-221-902-88	Sequence 88, Appl
13	1752	99.3	471	7	US-11-293-697-4285	Sequence 4285, Appl
14	1751	99.2	448	7	US-11-183-218-56	Sequence 56, Appl
15	1751	99.2	470	7	US-11-293-697-4292	Sequence 4292, Appl
16	1751	99.2	472	6	US-10-546-594-130	Sequence 130, Appl
17	1751	99.2	697	7	US-11-155-444-2	Sequence 2, Appl
18	1751	99.2	701	7	US-11-155-444-8	Sequence 8, Appl
19	1750	99.2	330	7	US-11-221-902-25	Sequence 25, Appl
20	1750	99.2	330	7	US-11-221-902-86	Sequence 86, Appl
21	1750	99.2	447	7	US-11-219-121-30	Sequence 30, Appl
22	1750	99.2	447	7	US-11-219-121-32	Sequence 32, Appl
23	1750	99.2	448	7	US-11-219-121-28	Sequence 28, Appl
24	1750	99.2	449	7	US-11-254-182-24	Sequence 24, Appl
25	1750	99.2	450	7	US-11-221-902-2	Sequence 2, Appl

26	1750	99.2	451	7	US-11-254-182-41	Sequence 41, Appl
27	1750	99.2	451	7	US-11-254-182-42	Sequence 42, Appl
28	1750	99.2	451	7	US-11-254-182-43	Sequence 43, Appl
29	1750	99.2	451	7	US-11-254-182-51	Sequence 51, Appl
30	1750	99.2	451	7	US-11-254-182-53	Sequence 53, Appl
31	1750	99.2	452	7	US-11-254-182-65	Sequence 65, Appl
32	1750	99.2	452	7	US-11-106-762-4	Sequence 4, Appl
33	1750	99.2	452	7	US-11-106-762-26	Sequence 26, Appl
34	1750	99.2	452	7	US-11-238-281-14	Sequence 14, Appl
35	1750	99.2	471	7	US-11-106-762-25	Sequence 25, Appl
36	1749	99.1	330	7	US-11-221-902-85	Sequence 85, Appl
37	1748	99.0	468	7	US-11-155-444-18	Sequence 18, Appl
38	1748	99.0	469	7	US-11-293-697-4287	Sequence 4287, Ap
39	1748	99.0	472	7	US-11-293-697-4295	Sequence 4295, Ap
40	1747	99.0	448	7	US-11-297-317-4	Sequence 4, Appl
41	1747	99.0	450	7	US-11-263-230-208	Sequence 208, App
42	1747	99.0	450	7	US-11-263-230-210	Sequence 210, App
43	1747	99.0	450	7	US-11-263-230-212	Sequence 212, App
44	1747	99.0	450	7	US-11-263-230-214	Sequence 214, App
45	1747	99.0	450	7	US-11-263-230-216	Sequence 216, App

ALIGNMENTS

RESULT 1
US-11-221-902-87
; Sequence 87, Application US/11221902
; Publication No. US20060088522A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGA
; FILE REFERENCE: 040000-0317285
; CURRENT APPLICATION NUMBER: US/11/221,902
; CURRENT FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 87
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-221-902-87

Query Match		99.7%;	Score 1759;	DB 7;	Length 330;				
Best Local Similarity		99.4%;	Pred. No. 8.4e-133;						
Matches 328;		Conservative	2;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS	60						
Db	1	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS	60						
Qy	61	GLYSLSGSVVTVFPSSSLGTQTVICNVNHPKSNTKVDKKVEPKSCDKTHTCPCPAPELAGA	120						
Db	61	GLYSLSGSVVTVFPSSSLGTQTVICNVNHPKSNTKVDKKVEPKSCDKTHTCPCPAPELAGA	120						
Qy	121	PSVFLFPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVFNAKTKPREEQYN	180						
Db	121	PSVFLFPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVFNAKTKPREEQYN	180						
Qy	181	STYRVSVSLTVLHQDLNKGKCYKCVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE	240						
Db	181	STYRVSVSLTVLHQDLNKGKCYKCVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE	240						
Qy	241	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFGFFLYSKLTVDKSRW	300						
Db	241	MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFGFFLYSKLTVDKSRW	300						
Qy	301	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	330						
Db	301	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	330						

RESULT 2

```
US-11-219-563-136
; Sequence 136, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219,563
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Heavy chain constant region of deJ591 spans
US-11-219-563-136

Query Match          99.5%; Score 1756; DB 7; Length 330;
Best Local Similarity 99.4%; Pred. No. 1.5e-132;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCSVMEALHNNHYTKSLSPGK 330
DB 301 QQGNVFSCSVMEALHNNHYTKSLSPGK 330

RESULT 3
US-11-254-182-44
; Sequence 44, Application US/11254182
; Publication No. US20060088523A1
; GENERAL INFORMATION:
; APPLICANT: ANDYA, JAMES
; APPLICANT: GWEE, SHIANG C.
; APPLICANT: LIU, JUN
; APPLICANT: SHEN, YE
; TITLE OF INVENTION: ANTIBODY FORMULATIONS
; FILE REFERENCE: P2104R1
; CURRENT APPLICATION NUMBER: US/11/254,182
; CURRENT FILING DATE: 2005-10-19
; PRIOR APPLICATION NUMBER: US 60/620,413
; PRIOR FILING DATE: 2004-10-20
; NUMBER OF SEQ ID NOS: 74
; SEQ ID NO 44
; LENGTH: 453

US-11-219-563-132
; Sequence 132, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219,563
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Heavy chain variable and constant region of deJ591
US-11-219-563-132

Query Match          99.5%; Score 1756; DB 7; Length 464;
Best Local Similarity 99.4%; Pred. No. 2.2e-132;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 135 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 194
QY 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
DB 195 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELAGA 254
```


Db 203 GLYSLSVVVTPVSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCCPPCAPELLGG 262
Qy 121 PSVFLFPPPKDXTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 263 PSVFLFPPPKDXTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 322
Qy 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 323 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 382
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKSRW 300
Db 383 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKSRW 442
Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 443 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 472

RESULT 8
US-11-293-697-4284
; Sequence 4284, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4284
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4284

Query Match 99.5%; Score 1756; DB 7; Length 473;
Best Local Similarity 99.4%; Pred. No. 2.3e-132;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 60
Db 144 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 203
Qy 61 GLYSLSVVVTPVSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCCPPCAPELLAGA 120
Db 204 GLYSLSVVVTPVSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCCPPCAPELLGG 263
Qy 121 PSVFLFPPPKDXTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 264 PSVFLFPPPKDXTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 323
Qy 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 324 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 383
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKSRW 300
Db 384 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKSRW 443
Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 444 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 473

RESULT 9
US-11-293-697-4282
; Sequence 4282, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4282
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4282

Query Match 99.5%; Score 1756; DB 7; Length 474;
Best Local Similarity 99.4%; Pred. No. 2.3e-132;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 60
Db 145 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 204
Qy 61 GLYSLSVVVTPVSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCCPPCAPELLAGA 120
Db 205 GLYSLSVVVTPVSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCCPPCAPELLGG 264
Qy 121 PSVFLFPPPKDXTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 265 PSVFLFPPPKDXTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 324
Qy 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 325 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 384
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKSRW 300
Db 385 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKSRW 444
Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 445 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 474

RESULT 10
US-11-293-697-4288
; Sequence 4288, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4288
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4288

Query Match 99.5%; Score 1756; DB 7; Length 476;
Best Local Similarity 99.4%; Pred. No. 2.3e-132;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 60
Db 147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 206
Qy 61 GLYSLSVVVTPVSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCCPPCAPELLAGA 120

```
Db 207 GYLSLSSVVTPSSSLGTQYICNVNHPKSNTKVDKKVEPKSCDKTHTCCPCPAPELLGG 266
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 267 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 327 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLYSKLTVDKSRW 300
Db 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLYSKLTVDKSRW 446
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 447 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476

RESULT 11
US-11-293-697-4289
; Sequence 4289, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4289
; LENGTH: 477
; TYPE: PR1
; ORGANISM: Homo sapiens
US-11-293-697-4289

Query Match 99.5%; Score 1756; DB 7; Length 477;
Best Local Similarity 99.4%; Pred. No. 2.3e-132;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
Db 148 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 207
QY 61 GYLSLSSVVTPSSSLGTQYICNVNHPKSNTKVDKKVEPKSCDKTHTCCPCPAPELLAGA 120
Db 208 GYLSLSSVVTPSSSLGTQYICNVNHPKSNTKVDKKVEPKSCDKTHTCCPCPAPELLGG 267
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 268 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 327
QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 328 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 387
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLYSKLTVDKSRW 300
Db 388 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLYSKLTVDKSRW 447
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 448 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 477

RESULT 12
US-11-221-902-88
; Sequence 88, Application US/11221902
; Publication No. US20060088522A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGA
; FILE REFERENCE: 040000-0317285
; CURRENT APPLICATION NUMBER: US/11/221,902
; CURRENT FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 88
; LENGTH: 330
; TYPE: PR1
; ORGANISM: Homo sapiens
US-11-221-902-88

Query Match 99.4%; Score 1754; DB 7; Length 330;
Best Local Similarity 99.1%; Pred. No. 2.1e-132;
Matches 327; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
QY 61 GYLSLSSVVTPSSSLGTQYICNVNHPKSNTKVDKKVEPKSCDKTHTCCPCPAPELLAGA 120
Db 61 GYLSLSSVVTPSSSLGTQYICNVNHPKSNTKVDKKVEPKSCDKTHTCCPCPAPELLAGA 120
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 13
US-11-293-697-4285
; Sequence 4285, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4285
; LENGTH: 471
; TYPE: PR1
; ORGANISM: Homo sapiens
US-11-293-697-4285

Query Match 99.3%; Score 1752; DB 7; Length 471;
Best Local Similarity 99.1%; Pred. No. 4.7e-132;
Matches 327; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 60
Db 142 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 201
QY 61 GYLSLSSVVTPSSSLGTQYICNVNHPKSNTKVDKKVEPKSCDKTHTCCPCPAPELLAGA 120
```

Db 202 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCCPCPAPELLGG 261
Qy 121 PSVFLFPPKPKDXTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREQYN 180
Db 262 PSVFLFPPKPKDXTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREQYN 321
Qy 181 STYRVSVLTVLHQDLNKGKEYCKKVSNNKALPAPIEKTISKAKGPPREPQVYTLPPSRDE 240
Db 322 STYRVSVLTVLHQDLNKGKEYCKKVSNNKALPAPIEKTISKAKGPPREPQVYTLPPSRDE 381
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 382 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 441
Qy 301 QOQNVFSCVMHEALHNHYTQKSLSLSPG 330
Db 442 QOQNVFSCVMHEALHNHYTQKSLSLSPG 471

RESULT 14
US-11-183-218-56
; Sequence 56, Application US/11183218
; Publication No. US2006008906A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryne
; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
; TITLE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN
; FILE REFERENCE: 040853-01-5083-US02
; CURRENT APPLICATION NUMBER: US/11/183,218
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 10/410,945
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US02/32263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-183-218-56

Query Match 99.2%; Score 1751; DB 7; Length 448;
Best Local Similarity 99.4%; Pred. No. 5.3e-132;
Matches 327; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHVFPAVLQSS 60
Db 120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHVFPAVLQSS 179

Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCCPCPAPELLAGA 120
Db 180 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCCPCPAPELLGG 239
Qy 121 PSVFLFPPKPKDXTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREQYN 180
Db 240 PSVFLFPPKPKDXTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREQYN 299
Qy 181 STYRVSVLTVLHQDLNKGKEYCKKVSNNKALPAPIEKTISKAKGPPREPQVYTLPPSRDE 240
Db 300 STYRVSVLTVLHQDLNKGKEYCKKVSNNKALPAPIEKTISKAKGPPREPQVYTLPPSRDE 359
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 419
Qy 301 QOQNVFSCVMHEALHNHYTQKSLSLSPG 329
Db 420 QOQNVFSCVMHEALHNHYTQKSLSLSPG 448

RESULT 15
US-11-293-697-4292
; Sequence 4292, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4292
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4292

Query Match 99.2%; Score 1751; DB 7; Length 470;
Best Local Similarity 99.1%; Pred. No. 5.7e-132;
Matches 327; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHVFPAVLQSS 60
Db 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHVFPAVLQSS 200
Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCCPCPAPELLAGA 120
Db 201 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCCPCPAPELLGG 260
Qy 121 PSVFLFPPKPKDXTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREQYN 180
Db 261 PSVFLFPPKPKDXTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREQYN 320
Qy 181 STYRVSVLTVLHQDLNKGKEYCKKVSNNKALPAPIEKTISKAKGPPREPQVYTLPPSRDE 240
Db 321 STYRVSVLTVLHQDLNKGKEYCKKVSNNKALPAPIEKTISKAKGPPREPQVYTLPPSRDE 380
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 440
Qy 301 QOQNVFSCVMHEALHNHYTQKSLSLSPG 330
Db 441 QOQNVFSCVMHEALHNHYTQKSLSLSPG 470

Search completed: June 10, 2006, 12:39:10
Job time : 12.3964 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 12, 2006, 17:04:30 ; Search time 69.2929 Seconds
(without alignments)
706.020 Million cell updates/sec

Title: US-10-733-563-112

Perfect score: 553

Sequence: 1 RTVAAPSVFIPFPDEQLKS.....EVTHQGLSSPVTKSFNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : A_Geneseq_8.*

1: geneseqp1980s.*

2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

9: geneseqp2005s.*

10: geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553	100.0	107	2	Aaw40578 Human kap
2	553	100.0	107	2	Aay50152 Human kap
3	553	100.0	107	2	Aaw92425 Human kap
4	553	100.0	107	2	Aay08745 Human kap
5	553	100.0	107	3	Aab27000 Human kap
6	553	100.0	107	5	Aeg31883 Human kap
7	553	100.0	107	6	Abb98755 Human kap
8	553	100.0	107	6	Abx42732 Anti-tiss
9	553	100.0	107	6	Abx42734 Anti-tiss
10	553	100.0	107	6	Abx55835 Anti-Ang-
11	553	100.0	107	7	Adj94622 Human kap
12	553	100.0	107	8	Adf77161 Anti-VAP-
13	553	100.0	107	8	Adl35096 Human Igg
14	553	100.0	107	8	Adl35094 Human Igg
15	553	100.0	107	8	Adm41539 Anti-inte
16	553	100.0	107	8	Adx18336 Amino aci
17	553	100.0	107	8	Adn97487 Artificia
18	553	100.0	107	8	Adq89334 Human imm
19	553	100.0	107	8	Ads87911 Anti-IFN-
20	553	100.0	107	8	Ads94908 Anti-IFN-
21	553	100.0	107	8	Adt88871 Human Igg
22	553	100.0	107	8	Adt51583 Light cha
23	553	100.0	107	8	Adu68013 Mouse ant

24	553	100.0	107	9	Adw08870 IGF-IR an
25	553	100.0	107	9	Adw07454 Human kap
26	553	100.0	107	9	Adw24748 Variable
27	553	100.0	107	9	Adw24790 Variable
28	553	100.0	107	9	Adx98272 Human ant
29	553	100.0	107	9	Ady26693 Human ant
30	553	100.0	107	9	Ady74804 Human Iig
31	553	100.0	107	9	Adz08815 Mammalian
32	553	100.0	107	9	Adz08946 Amyloid a
33	553	100.0	107	9	Adz44472 Human imm
34	553	100.0	107	9	Aea25951 Human imm
35	553	100.0	107	9	Aea16547 Human MCP
36	553	100.0	107	9	Aea45321 Apolipopr
37	553	100.0	107	9	Aea45323 Apolipopr
38	553	100.0	107	9	Aea37411 Anti-huma
39	553	100.0	107	9	Aea37415 Anti-huma
40	553	100.0	107	9	Aeb09607 Human C k
41	553	100.0	107	9	Aeb72782 Anti-LfAl
42	553	100.0	107	9	Aec81787 Human imm
43	553	100.0	107	9	Aed01341 Light cha
44	553	100.0	107	9	Aed01379 Immunoglob
45	553	100.0	107	9	Aec94910 Anti-IL-1
46	553	100.0	107	9	Aed41914 Deimmuniz
47	553	100.0	107	9	Aed49132 Light cha
48	553	100.0	107	9	Aed28066 Human kap
49	553	100.0	107	9	Aed66964 Human kap
50	553	100.0	107	10	Aef16291 Humanized
51	553	100.0	107	10	Aef38694 Antibody
52	553	100.0	107	10	Aef57798 Anti-IL-1
53	553	100.0	107	10	Aef563498 Human imm
54	553	100.0	107	10	Aeg09130 Tie recep
55	553	100.0	108	8	Adl22765 Human ant
56	553	100.0	108	9	Adw15047 Human Fab
57	553	100.0	108	9	Aea52525 Human ant
58	553	100.0	109	8	Adj95916 Human kap
59	553	100.0	109	8	Aeq89338 Human imm
60	553	100.0	109	9	Aeb09611 Human C k
61	553	100.0	110	9	Aec22657 Ig lambda
62	553	100.0	117	7	AdD13779 Plasmid p
63	553	100.0	121	8	Adn98370 Human Igg
64	553	100.0	131	8	Aed85881 Ig kappa
65	553	100.0	134	8	Adj95970 Immunoglo
66	553	100.0	143	1	Aap93559 Sequence
67	553	100.0	155	9	Aeb27727 Humanized
68	553	100.0	193	4	Aam52145 Humanised
69	553	100.0	201	2	Aay29770 P-selecti
70	553	100.0	212	5	Abp51955 Humanised
71	553	100.0	212	6	Aao31100 Human A2-
72	553	100.0	212	10	Aef11766 Human SCF
73	553	100.0	212	10	Aef11804 SCF-bind
74	553	100.0	212	10	Aef11801 SCF-bind
75	553	100.0	212	10	Aef11803 SCF-bind
76	553	100.0	212	10	Aef11805 SCF-bind
77	553	100.0	212	10	Aef11806 SCF-bind
78	553	100.0	212	10	Aef11800 SCF-bind
79	553	100.0	212	10	Aef11802 SCF-bind
80	553	100.0	213	2	Aaw04301 Antibody
81	553	100.0	213	4	AAE10516 Humanised
82	553	100.0	213	4	AAE10526 Humanised
83	553	100.0	213	4	AAE10512 Humanised
84	553	100.0	213	4	AAE10514 Humanised
85	553	100.0	213	4	AAE10524 Humanised
86	553	100.0	213	4	AAE10518 Humanised
87	553	100.0	213	4	AAE10522 Humanised
88	553	100.0	213	4	AAE10510 Humanised
89	553	100.0	213	4	AAE10520 Humanised
90	553	100.0	213	4	AAE10520 Humanised
91	553	100.0	213	5	ABP66573 Ganglios
92	553	100.0	213	5	ABP66573 Human RSV
93	553	100.0	213	5	ABP66591 Human RSV
94	553	100.0	213	5	ABP66607 Human RSV
95	553	100.0	213	5	ABP66605 Human RSV
96	553	100.0	213	5	ABP66569 Human RSV
					ABP66585 Human RSV

97	553	100.0	213	5	ABP66597	Abp66597 Human RSV	170	553	100.0	213	7	ADE35969	Adc35969 SYNAGIS a
98	553	100.0	213	5	ABP66581	Abp66581 Human RSV	171	553	100.0	213	7	ADE35937	Adc35937 SYNAGIS a
99	553	100.0	213	5	ABP66589	Abp66589 Human RSV	172	553	100.0	213	7	ADE35945	Adc35945 SYNAGIS a
100	553	100.0	213	5	ABP66563	Abp66563 Human RSV	173	553	100.0	213	7	ADE35957	Adc35957 SYNAGIS a
101	553	100.0	213	5	ABP66575	Abp66575 Human RSV	174	553	100.0	213	7	ADE35943	Adc35943 SYNAGIS a
102	553	100.0	213	5	ABP66601	Abp66601 Human RSV	175	553	100.0	213	7	ADE35953	Adc35953 SYNAGIS a
103	553	100.0	213	5	ABP66571	Abp66571 Human RSV	176	553	100.0	213	7	ADE35955	Adc35955 SYNAGIS a
104	553	100.0	213	5	ABP66579	Abp66579 Human RSV	177	553	100.0	213	7	ADE35938	Adc35938 LM4-type
105	553	100.0	213	5	ABP66593	Abp66593 Human RSV	178	553	100.0	213	7	ADJ79837	Adj79837 LM3-type
106	553	100.0	213	5	ABP66611	Abp66611 Human RSV	179	553	100.0	213	7	ADJ79810	Adj79810 Humanized
107	553	100.0	213	5	ABP66595	Abp66595 Human RSV	180	553	100.0	213	7	ADJ79839	Adj79839 LM5-type
108	553	100.0	213	5	ABP66565	Abp66565 Human RSV	181	553	100.0	213	8	ADL15441	Adl15441 Humanised
109	553	100.0	213	5	ABP66567	Abp66567 Human RSV	182	553	100.0	213	8	ADL15445	Adl15445 Humanised
110	553	100.0	213	5	ABP66609	Abp66609 Human RSV	183	553	100.0	213	8	ADL92471	Adl92471 Antibody
111	553	100.0	213	5	ABP66583	Abp66583 Human RSV	184	553	100.0	213	8	ADO00849	Ado00849 Humanised
112	553	100.0	213	5	ABP66587	Abp66587 Human RSV	185	553	100.0	213	8	ADO00853	Ado00853 Humanised
113	553	100.0	213	5	ABP66599	Abp66599 Human RSV	186	553	100.0	213	8	ADP44641	Adp44641 Human ant
114	553	100.0	213	5	ABP66577	Abp66577 Human RSV	187	553	100.0	213	8	ADP88495	Adp88495 Humanised
115	553	100.0	213	5	AU72810	Au72810 TRA-8 lig	188	553	100.0	213	8	ADS18711	Ads18711 Protein s
116	553	100.0	213	5	AU72818	Au72818 DNA encod	189	553	100.0	213	8	ADS33303	Ads33303 Anti-CD20
117	553	100.0	213	5	AU72817	Au72817 DNA encod	190	553	100.0	213	8	ADT51702	Adt51702 Visilizum
118	553	100.0	213	5	AU72816	Au72816 DNA encod	191	553	100.0	213	8	ADT51685	Adt51685 Dacilizuma
119	553	100.0	213	6	ABU69426	Abu69426 Respirato	192	553	100.0	213	8	ADU68153	Adu68153 Novel var
120	553	100.0	213	6	ABU69472	Abu69472 Respirato	193	553	100.0	213	8	ADU80277	Adu80277 CD20 bind
121	553	100.0	213	6	ABU69442	Abu69442 Respirato	194	553	100.0	213	8	ADW20067	Adw20067 RSV antig
122	553	100.0	213	6	ABU69462	Abu69462 Respirato	195	553	100.0	213	9	ADW20069	Adw20069 RSV antig
123	553	100.0	213	6	ABU69432	Abu69432 Respirato	196	553	100.0	213	9	ADW20079	Adw20079 RSV antig
124	553	100.0	213	6	ABU69434	Abu69434 Respirato	197	553	100.0	213	9	ADW20099	Adw20099 RSV antig
125	553	100.0	213	6	ABU69436	Abu69436 Respirato	198	553	100.0	213	9	ADW20073	Adw20073 RSV antig
126	553	100.0	213	6	ABU69450	Abu69450 Respirato	199	553	100.0	213	9	ADW20081	Adw20081 RSV antig
127	553	100.0	213	6	ABU69460	Abu69460 Respirato	200	553	100.0	213	9	ADW20085	Adw20085 RSV antig
128	553	100.0	213	6	ABU69468	Abu69468 Respirato	201	553	100.0	213	9	ADW20075	Adw20075 RSV antig
129	553	100.0	213	6	ABU69474	Abu69474 Respirato	202	553	100.0	213	9	ADW20089	Adw20089 RSV antig
130	553	100.0	213	6	ABU69458	Abu69458 Respirato	203	553	100.0	213	9	ADW20095	Adw20095 RSV antig
131	553	100.0	213	6	ABU69464	Abu69464 Respirato	204	553	100.0	213	9	ADW20107	Adw20107 RSV antig
132	553	100.0	213	6	ABU69446	Abu69446 Respirato	205	553	100.0	213	9	ADW20109	Adw20109 RSV antig
133	553	100.0	213	6	ABU69470	Abu69470 Respirato	206	553	100.0	213	9	ADW20065	Adw20065 RSV antig
134	553	100.0	213	6	ABU69430	Abu69430 Respirato	207	553	100.0	213	9	ADW20087	Adw20087 RSV antig
135	553	100.0	213	6	ABU69438	Abu69438 Respirato	208	553	100.0	213	9	ADW20091	Adw20091 RSV antig
136	553	100.0	213	6	ABU69454	Abu69454 Respirato	209	553	100.0	213	9	ADW20063	Adw20063 RSV antig
137	553	100.0	213	6	ABU69456	Abu69456 Respirato	210	553	100.0	213	9	ADW20105	Adw20105 RSV antig
138	553	100.0	213	6	ABU69440	Abu69440 Respirato	211	553	100.0	213	9	ADW20077	Adw20077 RSV antig
139	553	100.0	213	6	ABU69444	Abu69444 Respirato	212	553	100.0	213	9	ADW20083	Adw20083 RSV antig
140	553	100.0	213	6	ABU69448	Abu69448 Respirato	213	553	100.0	213	9	ADW20093	Adw20093 RSV antig
141	553	100.0	213	6	ABU69428	Abu69428 Respirato	214	553	100.0	213	9	ADW20101	Adw20101 RSV antig
142	553	100.0	213	6	ABU69452	Abu69452 Respirato	215	553	100.0	213	9	ADW20097	Adw20097 RSV antig
143	553	100.0	213	6	AAO29886	Aao29886 LM5 fusio	216	553	100.0	213	9	ADW20071	Adw20071 RSV antig
144	553	100.0	213	6	AAO29878	Aao29878 LM2 fusio	217	553	100.0	213	9	ADW20111	Adw20111 RSV antig
145	553	100.0	213	6	AAO29884	Aao29884 LM3 fusio	218	553	100.0	213	9	ADW03409	Adw03409 Humanized
146	553	100.0	213	6	AAO29885	Aao29885 LM4 fusio	219	553	100.0	213	9	ADW77076	Adw77076 VEGF-spec
147	553	100.0	213	6	AAE35326	Aae35326 Humanised	220	553	100.0	213	9	ADX18542	Adx18542 VEGF-spec
148	553	100.0	213	6	AAE34878	Aae34878 B1W4/8 a	221	553	100.0	213	9	ADY50070	Ady50070 Endotheli
149	553	100.0	213	6	ABG75668	Abg75668 Synagis l	222	553	100.0	213	9	ADZ99429	Adz99429 Humanized
150	553	100.0	213	6	ABG75668	Abg75668 Synagis l	223	553	100.0	213	9	AEA60641	Aea60641 Human but
151	553	100.0	213	6	AAE33521	Aae33521 Human AQC	224	553	100.0	213	9	AEBO7087	Aeb07087 RSV-speci
152	553	100.0	213	6	AAE33445	Aae33445 KS antibo	225	553	100.0	213	9	AEBO7071	Aeb07071 RSV-speci
153	553	100.0	213	7	ABE35929	Abe35929 SYNAGIS a	226	553	100.0	213	9	AEBO7065	Aeb07065 RSV-speci
154	553	100.0	213	7	ABE35921	Abe35921 SYNAGIS a	227	553	100.0	213	9	AEBO7069	Aeb07069 RSV-speci
155	553	100.0	213	7	ABE35939	Abe35939 SYNAGIS a	228	553	100.0	213	9	AEBO7093	Aeb07093 RSV-speci
156	553	100.0	213	7	ABE35959	Abe35959 SYNAGIS a	229	553	100.0	213	9	AEBO7045	Aeb07045 RSV-speci
157	553	100.0	213	7	ABE35935	Abe35935 SYNAGIS a	230	553	100.0	213	9	AEBO7053	Aeb07053 RSV-speci
158	553	100.0	213	7	ABE35941	Abe35941 SYNAGIS a	231	553	100.0	213	9	AEBO7079	Aeb07079 RSV-speci
159	553	100.0	213	7	ABE35927	Abe35927 SYNAGIS a	232	553	100.0	213	9	AEBO7083	Aeb07083 RSV-speci
160	553	100.0	213	7	ABE35947	Abe35947 SYNAGIS a	233	553	100.0	213	9	AEBO7049	Aeb07049 RSV-speci
161	553	100.0	213	7	ABE35949	Abe35949 SYNAGIS a	234	553	100.0	213	9	AEBO7075	Aeb07075 RSV-speci
162	553	100.0	213	7	ABE35963	Abe35963 SYNAGIS a	235	553	100.0	213	9	AEBO7091	Aeb07091 RSV-speci
163	553	100.0	213	7	ABE35931	Abe35931 SYNAGIS a	236	553	100.0	213	9	AEBO7055	Aeb07055 RSV-speci
164	553	100.0	213	7	ABE35933	Abe35933 SYNAGIS a	237	553	100.0	213	9	AEBO7073	Aeb07073 RSV-speci
165	553	100.0	213	7	ABE35923	Abe35923 SYNAGIS a	238	553	100.0	213	9	AEBO7047	Aeb07047 RSV-speci
166	553	100.0	213	7	ABE35965	Abe35965 SYNAGIS a	239	553	100.0	213	9	AEBO7057	Aeb07057 RSV-speci
167	553	100.0	213	7	ABE35951	Abe35951 SYNAGIS a	240	553	100.0	213	9	AEBO7061	Aeb07061 RSV-speci
168	553	100.0	213	7	ABE35925	Abe35925 SYNAGIS a	241	553	100.0	213	9	AEBO7067	Aeb07067 RSV-speci
169	553	100.0	213	7	ABE35967	Abe35967 SYNAGIS a	242	553	100.0	213	9	AEBO7051	Aeb07051 RSV-speci

243	553	100.0	213	9	AEB07063	Aeb07063 RSV-speci	316	553	100.0	214	2	AAW34506	Aaw34506 Light cha
244	553	100.0	213	9	AEB07077	Aeb07077 RSV-speci	317	553	100.0	214	2	ADE51519	Ade51519 p-ANCA re
245	553	100.0	213	9	AEB07081	Aeb07081 RSV-speci	318	553	100.0	214	2	AAW49815	Aaw49815 Amino aci
246	553	100.0	213	9	AEB07089	Aeb07089 RSV-speci	319	553	100.0	214	2	AAW64671	Aaw64671 Human UC
247	553	100.0	213	9	AEB07059	Aeb07059 RSV-speci	320	553	100.0	214	2	AAW06842	Aay06842 Seq ID No
248	553	100.0	213	9	AEB17637	Aeb17637 Light cha	321	553	100.0	214	2	AAW08600	Aay08600 JP1112785
249	553	100.0	213	9	AEB29787	Aeb29787 Humanized	322	553	100.0	214	2	AAW08599	Aay08599 Anti-huma
250	553	100.0	213	9	AEB29791	Aeb29791 Humanized	323	553	100.0	214	2	AAW95615	Aaw95615 Humanized
251	553	100.0	213	9	AEB29782	Aeb29782 Humanized	324	553	100.0	214	2	AAW34039	Aay34039 NANUC-2 a
252	553	100.0	213	9	AEB29778	Aeb29778 Humanized	325	553	100.0	214	2	AAW30632	Aay30632 Recombina
253	553	100.0	213	9	AEB13533	Aeb13533 Mature ch	326	553	100.0	214	2	AAW08754	Aay08754 Human ant
254	553	100.0	213	9	AEC40038	Aec40038 Light cha	327	553	100.0	214	2	AAW30202	Aay30202 Light cha
255	553	100.0	213	9	AEC76842	Aec76842 SYNAGIS-d	328	553	100.0	214	2	AAW57337	Aay57337 UC PANCA
256	553	100.0	213	9	AEC76846	Aec76846 SYNAGIS-d	329	553	100.0	214	3	AAW93735	Aay93735 The kappa
257	553	100.0	213	9	AEC76884	Aec76884 SYNAGIS-d	330	553	100.0	214	3	AAW29407	Aab29407 Human mon
258	553	100.0	213	9	AEC76848	Aec76848 SYNAGIS-d	331	553	100.0	214	3	AEA11265	Aea11265 Humanized
259	553	100.0	213	9	AEC76852	Aec76852 SYNAGIS-d	332	553	100.0	214	3	AEA11267	Aea11267 Deamidate
260	553	100.0	213	9	AEC76886	Aec76886 SYNAGIS-d	333	553	100.0	214	4	ABW66777	Abw66777 rhuMAB CD
261	553	100.0	213	9	AEC76854	Aec76854 SYNAGIS-d	334	553	100.0	214	5	ABP66603	Abp66603 Human RSV
262	553	100.0	213	9	AEC76874	Aec76874 SYNAGIS-d	335	553	100.0	214	5	AAE19696	Aae19696 Antobody
263	553	100.0	213	9	AEC76850	Aec76850 SYNAGIS-d	336	553	100.0	214	5	AAO18399	Aao18399 Mature hu
264	553	100.0	213	9	AEC76856	Aec76856 SYNAGIS-d	337	553	100.0	214	5	ABG31889	Abg31889 Humanised
265	553	100.0	213	9	AEC76872	Aec76872 SYNAGIS-d	338	553	100.0	214	5	ABW47727	Abw47727 Light cha
266	553	100.0	213	9	AEC76860	Aec76860 SYNAGIS-d	339	553	100.0	214	5	ABB99223	Abb99223 Chimeric
267	553	100.0	213	9	AEC76862	Aec76862 SYNAGIS-d	340	553	100.0	214	6	AAE35890	Aae35890 Human 11.
268	553	100.0	213	9	AEC76878	Aec76878 SYNAGIS-d	341	553	100.0	214	6	ABU69466	Abu69466 Respirato
269	553	100.0	213	9	AEC76858	Aec76858 SYNAGIS-d	342	553	100.0	214	6	ABR55870	AbR55870 Human imm
270	553	100.0	213	9	AEC76870	Aec76870 SYNAGIS-d	343	553	100.0	214	6	ABG74711	Abg74711 Murine hu
271	553	100.0	213	9	AEC76888	Aec76888 SYNAGIS-d	344	553	100.0	214	7	ADB85319	AdB85319 Light cha
272	553	100.0	213	9	AEC76868	Aec76868 SYNAGIS-d	345	553	100.0	214	7	ADC26157	AdC26157 Anti-VEGF
273	553	100.0	213	9	AEC76876	Aec76876 SYNAGIS-d	346	553	100.0	214	7	ADC26154	AdC26154 Parent an
274	553	100.0	213	9	AEC76844	Aec76844 SYNAGIS-d	347	553	100.0	214	7	ADC26164	AdC26164 Humanised
275	553	100.0	213	9	AEC76864	Aec76864 SYNAGIS-d	348	553	100.0	214	7	ADC26166	AdC26166 Humanised
276	553	100.0	213	9	AEC76882	Aec76882 SYNAGIS-d	349	553	100.0	214	7	ADC26156	AdC26156 Anti-VEGF
277	553	100.0	213	9	AEC76840	Aec76840 SYNAGIS a	350	553	100.0	214	7	ADC73235	AdC73235 Protein s
278	553	100.0	213	9	AEC76866	Aec76866 SYNAGIS-d	351	553	100.0	214	7	ABR83150	AbR83150 Hu007 ant
279	553	100.0	213	9	AED19129	Aed19129 Humanized	352	553	100.0	214	7	ADE35961	AdE35961 SYNAGIS a
280	553	100.0	213	9	AED19167	Aed19167 Humanized	353	553	100.0	214	7	ADE01486	AdE01486 CDP870 li
281	553	100.0	213	9	AER01052	Aer01052 Anti-NGF	354	553	100.0	214	7	ADF11431	AdF11431 18B2 anti
282	553	100.0	213	9	AEB18959	Aeb18959 Humanized	355	553	100.0	214	7	ADF11423	AdF11423 2E11 anti
283	553	100.0	213	9	AEB18926	Aeb18926 Humanized	356	553	100.0	214	8	ADF11667	AdF11667 anti-HER2
284	553	100.0	213	9	AEB18956	Aeb18956 Humanized	357	553	100.0	214	8	ADF11669	AdF11669 anti-CD11
285	553	100.0	213	9	AEB18962	Aeb18962 Humanized	358	553	100.0	214	8	ADF73140	AdF73140 Humanized
286	553	100.0	213	9	AEB18944	Aeb18944 Humanized	359	553	100.0	214	8	ADF69630	AdF69630 Humanized
287	553	100.0	213	9	AEB18958	Aeb18958 Humanized	360	553	100.0	214	8	ADH34232	AdH34232 Anti-huma
288	553	100.0	213	9	AEB18953	Aeb18953 Humanized	361	553	100.0	214	8	ADH34591	AdH34591 Q23 light
289	553	100.0	213	9	AEB18963	Aeb18963 Humanized	362	553	100.0	214	8	ADH34510	AdH34510 Light cha
290	553	100.0	213	10	AEE28264	Aee28264 Humanized	363	553	100.0	214	8	ADJ11307	AdJ11307 BHA10 V1#
291	553	100.0	213	10	AEE28249	Aee28249 Humanized	364	553	100.0	214	8	ADK52358	AdK52358 Human ant
292	553	100.0	213	10	AEE26244	Aee26244 Humanized	365	553	100.0	214	8	ADL70802	AdL70802 Anti-TNPa
293	553	100.0	213	10	AEE64956	Aee64956 Mature 2H	366	553	100.0	214	8	ADL70799	AdL70799 Anti-TNPa
294	553	100.0	213	10	AEE64959	Aee64959 Mature 2H	367	553	100.0	214	8	ADK18342	AdK18342 Amino aci
295	553	100.0	213	10	AEE10477	Aee10477 Humanized	368	553	100.0	214	8	ADM31928	Adm31928 Humanised
296	553	100.0	213	10	AEE10480	Aee10480 Humanized	369	553	100.0	214	8	ADN49727	Adn49727 Human imm
297	553	100.0	213	10	AEE70763	Aee70763 Humanized	370	553	100.0	214	8	ADN98361	AdN98361 Human Igg
298	553	100.0	213	10	AEE70776	Aee70776 Humanized	371	553	100.0	214	8	ADQ31280	AdQ31280 Humanised
299	553	100.0	213	10	AEPF05019	Aepf05019 Humanized	372	553	100.0	214	8	ADQ31272	AdQ31272 Murine 11
300	553	100.0	213	10	AEPF05022	Aepf05022 Humanized	373	553	100.0	214	8	ADQ31278	AdQ31278 Humanised
301	553	100.0	213	10	AEPF27226	Aepf27226 Humanized	374	553	100.0	214	8	AQO07672	AqO07672 Amino aci
302	553	100.0	213	10	AEF16417	Aef16417 Humanized	375	553	100.0	214	8	AQO07415	AqO07415 Mature CB
303	553	100.0	213	10	AEF16400	Aef16400 Humanized	376	553	100.0	214	8	ADQ12198	AdQ12198 CBE11 pen
304	553	100.0	213	10	AEPF51205	Aepf51205 Human ant	377	553	100.0	214	8	ADR23360	AdR23360 Human CD7
305	553	100.0	213	10	AEPF64240	Aepf64240 Humanized	378	553	100.0	214	8	ADR23358	AdR23358 Human CD7
306	553	100.0	213	10	AEPF65387	Aepf65387 Anti-RhD	379	553	100.0	214	8	ADR23366	AdR23366 Human CD7
307	553	100.0	213	10	AEPF65406	Aepf65406 Anti-RhD	380	553	100.0	214	8	ADR23364	AdR23364 Human CD7
308	553	100.0	213	10	AEG04996	Aeg04996 Anti-CD20	381	553	100.0	214	8	ADS18705	AdS18705 Protein s
309	553	100.0	213	10	AEF95120	Aef95120 Anti-CD20	382	553	100.0	214	8	ADS18703	AdS18703 Protein s
310	553	100.0	214	2	AAR30776	Aar30776 H5216-158	383	553	100.0	214	8	ADT55440	AdT55440 Anti Ige
311	553	100.0	214	2	AAR43338	Aar43338 Completel	384	553	100.0	214	8	ADT51696	AdT51696 Fontollizu
312	553	100.0	214	2	AAW05828	Aaw05828 Humanised	385	553	100.0	214	8	ADU74403	AdU74403 Human imm
313	553	100.0	214	2	AAW45517	Aaw45517 NANUC-2 l	386	553	100.0	214	8	ADU86568	AdU86568 Immunoglo
314	553	100.0	214	2	AAW07615	Aaw07615 Ulcerativ	387	553	100.0	214	8	ADU86567	AdU86567 Immunoglo
315	553	100.0	214	2	AAW34504	Aaw34504 Light cha	388	553	100.0	214	8	ADU86523	AdU86523 Immunoglo

389	553	100.0	214	9	ADW201103	Adw201103 RSV antiag	462	553	100.0	214	10	AEF65375	Aef65375 Anti-Rhd
390	553	100.0	214	9	ADW77068	Adw77068 Light cha	463	553	100.0	214	10	AEF65419	Aef65419 Anti-Rhd
391	553	100.0	214	9	ADW44597	Adw44597 PRIMATE	464	553	100.0	214	10	AEF65392	Aef65392 Anti-Rhd
392	553	100.0	214	9	ADW11300	Adw11300 Human C-t	465	553	100.0	214	10	AEF65379	Aef65379 Anti-Rhd
393	553	100.0	214	9	ADW90321	Adw90321 Phage scF	466	553	100.0	214	10	AEF65377	Aef65377 Anti-Rhd
394	553	100.0	214	9	ADW18554	Adx18554 VEGF-spec	467	553	100.0	214	10	AEF65402	Aef65402 Anti-Rhd
395	553	100.0	214	9	ADW18564	Adx18564 VEGF-spec	468	553	100.0	214	10	AEF65400	Aef65400 Anti-Rhd
396	553	100.0	214	9	ADW18569	Adx18569 VEGF-spec	469	553	100.0	214	10	AEF65403	Aef65403 Tie recep
397	553	100.0	214	9	ADW18559	Adx18559 VEGF-spec	470	553	100.0	215	2	AAW07616	Aaw07616 Ulcerativ
398	553	100.0	214	9	ADW18555	Adx18555 VEGF-spec	471	553	100.0	215	2	ADE51521	Ade51521 p-ANCA re
399	553	100.0	214	9	ADW18555	Adx18555 VEGF-spec	472	553	100.0	215	4	AAW64673	Aaw64673 Human UC
400	553	100.0	214	9	ADW18562	Adx18562 VEGF-spec	473	553	100.0	215	4	RAU08379	Rau08379 Anti-OPCb
401	553	100.0	214	9	ADW18546	Adx18546 VEGF-spec	474	553	100.0	215	7	ADF11419	Adf11419 16E1 anti
402	553	100.0	214	9	ADW18568	Adx18568 VEGF-spec	475	553	100.0	215	7	ADF11419	Adf11419 22B3 anti
403	553	100.0	214	9	ADW18544	Adx18544 VEGF-spec	476	553	100.0	215	7	ADF11427	Adf11427 2D8 anti-
404	553	100.0	214	9	ADW18553	Adx18553 VEGF-spec	477	553	100.0	215	7	ADJ32146	Adj32146 Human int
405	553	100.0	214	9	ADW18557	Adx18557 VEGF-spec	478	553	100.0	215	8	ADQ311885	Adq311885 Antibody
406	553	100.0	214	9	ADW02220	Adx02220 SARS coro	479	553	100.0	215	8	ADQ311891	Adq311891 Antibody
407	553	100.0	214	9	ADW01873	Adx01873 SARS coro	480	553	100.0	215	8	ADR23356	Adr23356 Human CD7
408	553	100.0	214	9	ADW27044	Adx27044 Murine ht	481	553	100.0	215	8	ABM83746	Abm83746 Human dia
409	553	100.0	214	9	ADW80641	Adx80641 Trastuzum	482	553	100.0	215	8	ADS87927	Ads87927 Anti-IFN-
410	553	100.0	214	9	ADY50072	Ady50072 Endotheli	483	553	100.0	215	8	ADS87929	Ads87929 Anti-IFN-
411	553	100.0	214	9	ADY26729	Ady26729 Anti-NGF-	484	553	100.0	215	8	ADS87925	Ads87925 Anti-IFN-
412	553	100.0	214	9	ADY80251	Ady80251 Amino aci	485	553	100.0	215	8	ADS94926	Ads94926 Anti-IFN-
413	553	100.0	214	9	ADY70960	Ady70960 Human mon	486	553	100.0	215	8	ADS94922	Ads94922 Anti-IFN-
414	553	100.0	214	9	AEA36339	Aea36339 Human CBE	487	553	100.0	215	8	ADS94924	Ads94924 Anti-IFN-
415	553	100.0	214	9	AEA13853	Aea13853 VEGF rela	488	553	100.0	215	8	ADT51708	Adt51708 M200 anti
416	553	100.0	214	9	AEA13907	Aea13907 VEGF rela	489	553	100.0	215	8	ADT77644	Adt77644 Antibody
417	553	100.0	214	9	AEA13911	Aea13911 VEGF rela	490	553	100.0	215	8	ADU86570	Adu86570 Immunoglo
418	553	100.0	214	9	AEA13860	Aea13860 VEGF rela	491	553	100.0	215	8	ADY50068	Ady50068 Endotheli
419	553	100.0	214	9	AEA13947	Aea13947 VEGF rela	492	553	100.0	215	9	ADY50064	Ady50064 Endotheli
420	553	100.0	214	9	AEA13949	Aea13949 VEGF rela	493	553	100.0	215	9	AEBA48819	Aeb48819 Anti-onco
421	553	100.0	214	9	AEA13849	Aea13849 VEGF rela	494	553	100.0	215	9	ABE51163	Aeb51163 Chimeric
422	553	100.0	214	9	AEA13915	Aea13915 VEGF rela	495	553	100.0	215	9	ABE51169	Aeb51169 Chimeric
423	553	100.0	214	9	AEA14679	Aea14679 VEGF rela	496	553	100.0	215	9	ABE18932	Aeb18932 Humanized
424	553	100.0	214	9	AEA13913	Aea13913 VEGF rela	497	553	100.0	215	10	AEF12091	Aef12091 Anti-alpha
425	553	100.0	214	9	AEA13951	Aea13951 VEGF rela	498	553	100.0	215	10	AEF16423	Aef16423 Chimeric
426	553	100.0	214	9	AEA13909	Aea13909 VEGF rela	499	553	100.0	215	10	AEF65404	Aef65404 Anti-Rhd
427	553	100.0	214	9	AEA14262	Aea14262 VEGF rela	500	553	100.0	215	10	AEF65398	Aef65398 Anti-Rhd
428	553	100.0	214	9	AEA13861	Aea13861 VEGF rela	501	553	100.0	215	10	AEF65401	Aef65401 Anti-Rhd
429	553	100.0	214	9	AEA13912	Aea13912 VEGF rela	502	553	100.0	215	10	AEF65391	Aef65391 Anti-Rhd
430	553	100.0	214	9	AEA14264	Aea14264 VEGF rela	503	553	100.0	215	10	AEF65428	Aef65428 Anti-Rhd
431	553	100.0	214	9	AEA13917	Aea13917 VEGF rela	504	553	100.0	215	10	AEF65429	Aef65429 Anti-Rhd
432	553	100.0	214	9	AEA48169	Aea48169 Mouse ant	505	553	100.0	215	10	AEF65420	Aef65420 Anti-Rhd
433	553	100.0	214	9	AEA48166	Aea48166 Mouse ant	506	553	100.0	215	10	AEF65386	Aef65386 Anti-Rhd
434	553	100.0	214	9	ABE07085	Aeb07085 RSV-speci	507	553	100.0	215	10	AEF65414	Aef65414 Anti-Rhd
435	553	100.0	214	9	ABE56306	Aeb56306 Anti-IGF	508	553	100.0	215	10	AEF65378	Aef65378 Anti-Rhd
436	553	100.0	214	9	ABE46966	Aeb46966 CD1a spec	509	553	100.0	215	10	AEF65394	Aef65394 Anti-Rhd
437	553	100.0	214	9	ABE27968	Aeb27968 Humanized	510	553	100.0	215	10	AEF65415	Aef65415 Anti-Rhd
438	553	100.0	214	9	AEC16144	Aec16144 Human ant	511	553	100.0	215	10	AEF65425	Aef65425 Anti-Rhd
439	553	100.0	214	9	AEC76880	Aec76880 SYNAGIS-d	512	553	100.0	215	10	AEF65413	Aef65413 Anti-Rhd
440	553	100.0	214	9	AED20673	Aed20673 Trastuzum	513	553	100.0	215	10	AEF65385	Aef65385 Anti-Rhd
441	553	100.0	214	9	AED04291	Aed04291 Human ant	514	553	100.0	215	10	AEF65422	Aef65422 Anti-Rhd
442	553	100.0	214	9	AED04363	Aed04363 Human ant	515	553	100.0	215	10	AEF65388	Aef65388 Anti-Rhd
443	553	100.0	214	9	AED12732	Aed12732 Light cha	516	553	100.0	215	10	AEF65390	Aef65390 Anti-Rhd
444	553	100.0	214	9	AED66970	Aed66970 Humanized	517	553	100.0	215	10	AEF65397	Aef65397 Anti-Rhd
445	553	100.0	214	9	AED76655	Aed76655 Human Her	518	553	100.0	215	10	AEF65409	Aef65409 Anti-Rhd
446	553	100.0	214	10	AEF24412	Aef24412 Human 1-7	519	553	100.0	216	8	ADS87940	Ads87940 Anti-IFN-
447	553	100.0	214	10	AEF16411	Aef16411 Humanized	520	553	100.0	216	8	ADS94937	Ads94937 Anti-IFN-
448	553	100.0	214	10	AEF03139	Aef03139 Trastuzum	521	553	100.0	216	10	AEF65403	Aef65403 Anti-Rhd
449	553	100.0	214	10	AEF03141	Aef03141 Pertuzuma	522	553	100.0	216	10	AEF65412	Aef65412 Anti-Rhd
450	553	100.0	214	10	AEF27301	Aef27301 Humanized	523	553	100.0	216	10	AEF65376	Aef65376 Anti-Rhd
451	553	100.0	214	10	AEF27303	Aef27303 Humanized	524	553	100.0	216	10	AEF65381	Aef65381 Anti-Rhd
452	553	100.0	214	10	AEF41639	Aef41639 Humanized	525	553	100.0	216	10	AEF65374	Aef65374 Anti-Rhd
453	553	100.0	214	10	AEF80296	Aef80296 Antibody	526	553	100.0	216	10	AEF65380	Aef65380 Anti-Rhd
454	553	100.0	214	10	AEF80300	Aef80300 Antibody	527	553	100.0	216	10	AEF65393	Aef65393 Anti-Rhd
455	553	100.0	214	10	AEF65405	Aef65405 Anti-Rhd	528	553	100.0	216	10	AEF65423	Aef65423 Anti-Rhd
456	553	100.0	214	10	AEF65424	Aef65424 Anti-Rhd	529	553	100.0	216	10	AEF65423	Aef65423 Anti-Rhd
457	553	100.0	214	10	AEF65382	Aef65382 Anti-Rhd	530	553	100.0	217	9	ADY74780	Ady74780 Rat anti-
458	553	100.0	214	10	AEF65384	Aef65384 Anti-Rhd	531	553	100.0	217	10	AEF27311	Aef27311 Humanized
459	553	100.0	214	10	AEF65407	Aef65407 Anti-Rhd	532	553	100.0	217	10	AEF65411	Aef65411 Anti-Rhd
460	553	100.0	214	10	AEF65410	Aef65410 Anti-Rhd	533	553	100.0	217	10	AEF65383	Aef65383 Anti-Rhd
461	553	100.0	214	10	AEF65421	Aef65421 Anti-Rhd	534	553	100.0	218	2	AAR33312	Aar33312 Humanised

535	553	100.0	218	2	AAW13563	Aaw13563 Humanised	608	553	100.0	219	7	AAE39095	Aae39095 Protein #
536	553	100.0	218	2	AAW95660	Aaw95660 Mus muscu	609	553	100.0	219	7	ADE94065	Ades94065 Humanised
537	553	100.0	218	2	AAW95664	Aaw95664 Mus muscu	610	553	100.0	219	7	ADJ32152	Adj32152 Human int
538	553	100.0	218	2	AAW95662	Aaw95662 Mus muscu	611	553	100.0	219	7	ADJ32150	Adj32150 Human int
539	553	100.0	218	2	AAW95669	Aaw95669 Mus muscu	612	553	100.0	219	7	ADJ32140	Adj32140 Human int
540	553	100.0	218	2	AAW95658	Aaw95658 Mus muscu	613	553	100.0	219	7	ADJ32138	Adj32138 Human int
541	553	100.0	218	2	AAW50030	Aay50030 Human E27	614	553	100.0	219	8	ADH34589	Adh34589 011 light
542	553	100.0	218	3	AAW85200	Aay85200 Light cha	615	553	100.0	219	8	ADH34590	Adh34590 021 light
543	553	100.0	218	3	AAW807472	Aab07472 Amino aci	616	553	100.0	219	8	ADH34588	Adh34588 008 light
544	553	100.0	218	4	AAW47087	Aab47087 Anti-IGE	617	553	100.0	219	8	ADH35160	Adh35160 Humanised
545	553	100.0	218	4	AAW76947	Aab76947 Full vari	618	553	100.0	219	8	ADN07066	Adn07066 F(ab)-pha
546	553	100.0	218	4	AAW76949	Aab76949 Full leng	619	553	100.0	219	8	ADN61713	Adn61713 Humanised
547	553	100.0	218	4	AAW76951	Aab76951 Full leng	620	553	100.0	219	8	ADP84971	Adp84971 Chimeric
548	553	100.0	218	4	AAW76953	Aab76953 Variable	621	553	100.0	219	8	ADR19332	Adr19332 Chimeric
549	553	100.0	218	4	AAW76958	Aab76958 Variable	622	553	100.0	219	8	ADR19331	Adr19331 Chimeric
550	553	100.0	218	4	AAW74211	E27 anti-	623	553	100.0	219	9	ADW00688	Adw00688 Expressio
551	553	100.0	218	5	AAW49204	Aam49204 Humanised	624	553	100.0	219	9	ADW77072	Adw77072 Light cha
552	553	100.0	218	6	ABU62797	Abu62797 E27 anti-	625	553	100.0	219	10	ABE99308	Aee99308 Kappa lig
553	553	100.0	218	7	ABR82261	AbR82261 Chimeric	626	553	100.0	219	10	ABF18985	Aef18985 Humanized
554	553	100.0	218	7	ABR69597	Adf69597 Human ant	627	553	100.0	219	10	ABF18986	Aef18986 Humanized
555	553	100.0	218	8	ADP29038	Adf29038 Anti-IGE	628	553	100.0	219	10	AEF34625	Aef34625 Fab-4D5 C
556	553	100.0	218	8	ADP71899	Adf71899 Hu3G8VL-1	629	553	100.0	219	10	AEF65418	Aef65418 Anti-RD
557	553	100.0	218	8	ADP71903	Adf71903 Hu3G8VL-4	630	553	100.0	220	2	AAW07528	Aaw07528 Anti-HGF
558	553	100.0	218	8	ADP71920	Adf71920 Hu3G8VL-2	631	553	100.0	220	2	AAW50172	Aay50172 Antibody
559	553	100.0	218	8	ADN07034	Adn07034 Anti-IGE	632	553	100.0	220	2	ADK52298	Adk52298 Human ant
560	553	100.0	218	8	ADN07045	Adn07045 Anti-IGE	633	553	100.0	220	8	ADK52386	Adk52386 Human ant
561	553	100.0	218	8	ADN07036	Adn07036 Anti-IGE	634	553	100.0	220	8	ADK52314	Adk52314 Human ant
562	553	100.0	218	8	ADN07038	Adn07038 Anti-IGE	635	553	100.0	220	8	ADK52362	Adk52362 Human ant
563	553	100.0	218	8	ADN07040	Adn07040 Anti-IGE	636	553	100.0	220	8	ADK52334	Adk52334 Human ant
564	553	100.0	218	8	ADP84136	Adp84136 Anti-mono	637	553	100.0	220	8	ADO06858	Ado06858 Virucidal
565	553	100.0	218	8	ADP84130	Adp84130 Anti-mono	638	553	100.0	220	8	ADO06856	Ado06856 Virucidal
566	553	100.0	218	8	ADP88427	Adp88427 Antibody	639	553	100.0	220	8	ADP42960	Adp42960 Humanised
567	553	100.0	218	8	ADP88451	Adp88451 Antibody	640	553	100.0	220	9	ADW77054	Adw77054 Light cha
568	553	100.0	218	8	ADS31792	Chimeric	641	553	100.0	220	9	ADW77046	Adw77046 Light cha
569	553	100.0	218	8	ADP755439	Adt55439 Anti IGE	642	553	100.0	220	9	ADW44589	Adw44589 Antibody
570	553	100.0	218	8	ADP755438	Adt55438 Anti IGE	643	553	100.0	220	9	ABE43844	Aeb43844 Human Hui
571	553	100.0	218	8	ADW00660	Adw00660 Human ant	644	553	100.0	220	10	ABE99275	Aee99275 Light cha
572	553	100.0	218	9	ADW00667	Adw00667 Human ant	645	553	100.0	222	9	AEC92140	Aec92140 Chimeric
573	553	100.0	218	9	ADW00656	Adw00656 Human ant	646	553	100.0	222	9	AEC92144	Aec92144 DNA encod
574	553	100.0	218	9	ADW00662	Adw00662 Human ant	647	553	100.0	222	10	ABE99293	Aee99293 Anti-RON
575	553	100.0	218	9	ADW00691	Adw00691 Human ant	648	553	100.0	232	2	ABR80616	Aar80616 Anti-huma
576	553	100.0	218	9	ADW00692	Adw00692 Human ant	649	553	100.0	232	6	ABG76490	Abg76490 Light cha
577	553	100.0	218	9	ADW00658	Adw00658 Human ant	650	553	100.0	232	7	ADF64204	Adf64204 MN14LC pr
578	553	100.0	218	9	ADW79895	Adw79895 Anti-IGE	651	553	100.0	232	7	ADF60817	Adf60817 HMN-14 li
579	553	100.0	218	9	ADW79893	Adw79893 Anti-IGE	652	553	100.0	232	8	ADP79583	Adp79583 2H7.v16 L
580	553	100.0	218	9	ADW79897	Adw79897 Anti-IGE	653	553	100.0	232	8	ADW03398	Adw03398 Human ant
581	553	100.0	218	9	ADW79902	Adw79902 Anti-IGE	654	553	100.0	232	9	ADW21318	Adw21318 Mouse ant
582	553	100.0	218	9	ADW79891	Adw79891 Anti-IGE	655	553	100.0	232	9	ADW00804	Adw00804 Humanized
583	553	100.0	218	9	ADY74808	Ady74808 Rat anti-	656	553	100.0	232	9	ADY62624	Ady62624 Humanized
584	553	100.0	218	9	ADZ99438	Adz99438 Humanized	657	553	100.0	232	9	ADZ99447	Adz99447 12G8 anti
585	553	100.0	218	9	ABE13693	Aeb13693 Human ant	658	553	100.0	232	9	ABE18943	Aee18943 Humanized
586	553	100.0	218	9	ABE56304	Aeb56304 Anti-IGE	659	553	100.0	232	10	ABE26243	Aee26243 Humanized
587	553	100.0	218	9	ABE56305	Aeb56305 Anti-IGE	660	553	100.0	232	2	ABE22755	Aar22755 Reshaped
588	553	100.0	218	9	AED06841	Aed06841 Light cha	661	553	100.0	233	2	ABE22754	Aar22754 Reshaped
589	553	100.0	218	9	AED89915	Aed89915 Anti-IGE	662	553	100.0	233	2	AAW85690	Aaw85690 D5D10 lig
590	553	100.0	218	9	AED89926	Aed89926 Anti-IGE	663	553	100.0	233	2	AAW85690	Aaw85690 D5D10 lig
591	553	100.0	218	9	AED89917	Aed89917 Anti-IGE	664	553	100.0	233	3	AAW93704	Aay93704 The kappa
592	553	100.0	218	9	AED89921	Aed89921 Anti-IGE	665	553	100.0	233	3	AAW93731	Aay93731 The kappa
593	553	100.0	218	9	AED89919	Aed89919 Anti-IGE	666	553	100.0	233	4	ABE49242	AbE49242 Chimeric
594	553	100.0	218	10	ABF27196	Aef27196 Anti-CD4	667	553	100.0	233	6	ABE35886	Aae35886 Human 4.8
595	553	100.0	218	10	ABF27220	Aef27220 Anti-CD4	668	553	100.0	233	7	ABR61526	AbR61526 Humanised
596	553	100.0	218	10	ABF18405	Aef18405 HANA prot	669	553	100.0	233	7	ABR61528	AbR61528 Humanised
597	553	100.0	219	2	AAW29459	Aay29459 Recombina	670	553	100.0	233	7	ADL23195	Adl23195 Human ant
598	553	100.0	219	3	ABW77767	Aab77767 Humanised	671	553	100.0	233	8	ADP77160	Adp77160 Anti-VAP-
599	553	100.0	219	3	ABW30323	Aab30323 Humanised	672	553	100.0	233	8	ADM41575	Adm41575 Anti-inte
600	553	100.0	219	6	ABP58286	Abp58286 Humanised	673	553	100.0	233	8	ADL93656	Adl93656 Human CD4
601	553	100.0	219	6	ABR39464	AbR39464 Humanised	674	553	100.0	233	8	ADL93655	Adl93655 Human CD4
602	553	100.0	219	6	ABU08310	Abu08310 Humanised	675	553	100.0	233	8	ADR46823	Adr46823 Human ant
603	553	100.0	219	6	ABU13800	Abu13800 Humanised	676	553	100.0	233	8	ADU23620	Adu23620 Human Igg
604	553	100.0	219	6	ABU59513	Abu59513 Humanised	677	553	100.0	233	8	ADU68009	Adu68009 Mouse ant
605	553	100.0	219	6	ABR37992	AbR37992 Humanised	678	553	100.0	233	9	ABE45889	Aeb45889 Human mon
606	553	100.0	219	6	ABR80108	AbR80108 Light cha	679	553	100.0	233	9	ABE45851	Aeb45851 Human mon
607	553	100.0	219	6	ABP58272	Abp58272 Humanised	680	553	100.0	233	9	ABD04283	Aed04283 Human ant

681	553	100.0	233	9	AED04319	Aed04319 Human ant	754	553	100.0	235	8	ADQ28269	Adq28269 Complete
682	553	100.0	233	9	AED41910	Aed41910 Deimmuniz	755	553	100.0	235	8	ADR47464	Adr47464 gH3 encod
683	553	100.0	233	10	AEE86010	Aee86010 Anthrax t	756	553	100.0	235	9	ADV92498	Adv92498 Anti-CD20
684	553	100.0	234	10	AEF27305	Aef27305 Humanized	757	553	100.0	235	9	ADV98561	Adv98561 Novel chi
685	553	100.0	234	2	AAR13050	Aar13050 CD4-speci	758	553	100.0	235	9	ADW71862	Adw71862 OKT3vhck
686	553	100.0	234	2	AAR20058	Aar20058 Light cha	759	553	100.0	235	9	AEA41041	AEA41041 Anti-M-CS
687	553	100.0	234	2	AAR38162	Aar38162 Human imm	760	553	100.0	235	9	AEA41049	AEA41049 Anti-M-CS
688	553	100.0	234	2	AAW11638	Aaw11638 Human ant	761	553	100.0	235	9	AEA41059	AEA41059 Anti-M-CS
689	553	100.0	234	2	AAW10233	Aaw10233 TF8-SG9 C	762	553	100.0	235	9	AED04279	Aed04279 Human ant
690	553	100.0	234	3	AAV92239	Aay92239 Human bon	763	553	100.0	235	9	AED04315	Aed04315 Human ant
691	553	100.0	234	3	AAV93733	Aay93733 The kappa	764	553	100.0	235	9	AED04315	Aed04315 Human ant
692	553	100.0	234	3	AAV93708	Aay93708 The kappa	765	553	100.0	235	9	AED14792	Aed14792 Ab D anti
693	553	100.0	234	4	AAB36208	Aab36208 Human imm	766	553	100.0	235	9	AED54379	Aed54379 Anti-CD20
694	553	100.0	234	4	AAB36204	Aab36204 Human imm	767	553	100.0	235	10	AEE86006	Aee86006 Anthrax t
695	553	100.0	234	4	AAB36204	Aab36204 Human imm	767	553	100.0	235	10	AEE86006	Aee86006 Anthrax t
696	553	100.0	234	5	ABG65461	Abg65461 Human sec	768	553	100.0	236	1	AAP93910	Aap93910 Y22 light
697	553	100.0	234	5	AAO14066	Aao14066 Human alb	769	553	100.0	236	2	AAR42065	Aar42065 Human ant
698	553	100.0	234	6	AAE33588	Aae33588 Light cha	770	553	100.0	236	2	AAR77614	Aar77614 Humanised
699	553	100.0	234	6	ABU08018	Abu08018 Human mon	771	553	100.0	236	2	AAV34096	Aay34096 Partial a
700	553	100.0	234	6	ABP56809	Abp56809 Human kap	772	553	100.0	236	3	AAV96293	Aay96293 Human IGF
701	553	100.0	234	7	ADE28413	Ade28413 Human ant	773	553	100.0	236	3	AAV96297	Aay96297 Human IGF
702	553	100.0	234	7	ADE28473	Ade28473 Human ant	774	553	100.0	236	3	AAV96300	Aay96300 Human IGF
703	553	100.0	234	7	ADE28481	Ade28481 Human ant	775	553	100.0	236	4	AAU74299	Aau74299 Human gen
704	553	100.0	234	7	ADF65776	Adf65776 Human ant	776	553	100.0	236	5	AAU74299	Aau74299 Anti-huma
705	553	100.0	234	7	ADP65776	Adp65776 Human mon	777	553	100.0	236	5	AAU74301	Aau74301 Anti-huma
706	553	100.0	234	7	ADM47073	Adm47073 Mouse ant	778	553	100.0	236	5	AAU74301	Aau74301 Anti-huma
707	553	100.0	234	8	ADJ92516	Adj92516 Human SOJ	779	553	100.0	236	5	ABG63490	Abg63490 Human alb
708	553	100.0	234	8	ADL78728	Adl78728 Albumin f	780	553	100.0	236	5	ABP51696	Abp51696 SGL-1 lig
709	553	100.0	234	8	ADM72037	Adm72037 Chimeric	781	553	100.0	236	5	ABG77160	Abg77160 Germline
710	553	100.0	234	8	ABM84933	Abm84933 Human dia	782	553	100.0	236	5	ABG77163	Abg77163 Amino aci
711	553	100.0	234	8	ADS84470	Ads84470 Human ant	783	553	100.0	236	5	ABG77163	Abg77163 Amino aci
712	553	100.0	234	8	ADS84458	Ads84458 Human ant	784	553	100.0	236	5	ABG77164	Abg77164 Germline
713	553	100.0	234	8	ADS84476	Ads84476 Human ant	785	553	100.0	236	7	ADD93785	AdD93785 Monoclon
714	553	100.0	234	8	ADS84452	Ads84452 Human ant	786	553	100.0	236	7	ADM05596	Adm05596 Human pro
715	553	100.0	234	8	ADS84446	Ads84446 Human ant	787	553	100.0	236	8	ADL76755	AdL76755 Albumin f
716	553	100.0	234	8	ADS84464	Ads84464 Human ant	788	553	100.0	236	8	ADP07905	AdP07905 Human imm
717	553	100.0	234	8	ADR72766	Adr72766 Human ant	789	553	100.0	236	8	ADP44635	AdP44635 Murine an
718	553	100.0	234	8	ADR68618	Adr68618 Human mon	790	553	100.0	236	8	ADQ16649	AdQ16649 Immunoglo
719	553	100.0	234	8	ADR68588	Adr68588 Human ant	791	553	100.0	236	8	ADP79579	AdP79579 Chimeric
720	553	100.0	234	8	ADR68600	Adr68600 Human ant	792	553	100.0	236	8	ADR28582	Adr28582 Human ant
721	553	100.0	234	8	ADR68606	Adr68606 Human ant	793	553	100.0	236	8	ADR28581	Adr28581 Human ant
722	553	100.0	234	8	ADR68612	Adr68612 Human ant	794	553	100.0	236	8	ADR28586	Adr28586 Human ant
723	553	100.0	234	8	ADR68594	Adr68594 Human ant	795	553	100.0	236	8	ADR28585	Adr28585 Human ant
724	553	100.0	234	8	ADS14301	Ads14301 EGFR ligh	796	553	100.0	236	9	ADH86270	AdH86270 Anti-huma
725	553	100.0	234	9	AEA41027	Aea41027 Human ant	797	553	100.0	236	9	ADV44387	Adv44387 SGL-1 lig
726	553	100.0	234	9	AEA41019	Aea41019 Human ant	798	553	100.0	236	9	ADV92512	Adv92512 Anti-her2
727	553	100.0	234	9	AEA41023	Aea41023 Human ant	799	553	100.0	236	9	ADV98575	Adv98575 Novel chi
728	553	100.0	234	9	AEB48576	Aeb48576 Human kap	800	553	100.0	236	9	ADX57905	AdX57905 Human ger
729	553	100.0	234	9	AED04287	Aed04287 Human ant	801	553	100.0	236	9	ADX57906	AdX57906 Human pro
730	553	100.0	234	9	AED04327	Aed04327 Human ant	802	553	100.0	236	9	ADZ70600	AdZ70600 Human pro
731	553	100.0	234	10	AEF51018	Aef51018 Variable	803	553	100.0	236	9	ADZ57695	AdZ57695 Anti-cMet
732	553	100.0	234	10	AEF38714	Aef38714 Monoclon	804	553	100.0	236	9	ADZ57699	AdZ57699 Anti-cMet
733	553	100.0	235	2	AAR94558	Aar94558 Humanised	805	553	100.0	236	9	ADZ57703	AdZ57703 Anti-cMet
734	553	100.0	235	2	AAW06180	Aaw06180 Humanised	806	553	100.0	236	9	ADZ57707	AdZ57707 Anti-cMet
735	553	100.0	235	2	AAW11640	Aaw11640 Human ant	807	553	100.0	236	9	ADZ51040	AdZ51040 Amino aci
736	553	100.0	235	2	AAW11398	Aaw11398 Humanised	808	553	100.0	236	9	AEA41057	Aea41057 Human ant
737	553	100.0	235	2	AAW41392	Aaw41392 Chimeric	809	553	100.0	236	9	AEA41037	Aea41037 Human ant
738	553	100.0	235	2	AAW41410	Aaw41410 Humanised	810	553	100.0	236	9	AEA41031	Aea41031 Human ant
739	553	100.0	235	2	AAW41411	Aaw41411 Humanised	811	553	100.0	236	9	AEA41029	Aea41029 Human ant
740	553	100.0	235	2	AAW82740	Aaw82740 Plaemid p	812	553	100.0	236	9	AEA41045	Aea41045 Human ant
741	553	100.0	235	3	AAV93702	Aay93702 The kappa	813	553	100.0	236	9	AEA41053	Aea41053 Anti-M-CS
742	553	100.0	235	3	AAV93729	Aay93729 The kappa	814	553	100.0	236	9	AEA41055	Aea41055 Human ant
743	553	100.0	235	3	AAV08025	Aab08025 A dimeric	815	553	100.0	236	9	AEA60461	Aea60461 Mouse ant
744	553	100.0	235	4	AB90614	Ab90614 Human sec	816	553	100.0	236	9	ABE12860	Aeb12860 Anti-body
745	553	100.0	235	5	ABG65460	Abg65460 Human alb	817	553	100.0	236	9	ABE45893	Aeb45893 Human mon
746	553	100.0	235	5	AAE27925	Aae27925 Human C2B	818	553	100.0	236	9	ABE45847	Aeb45847 Human mon
747	553	100.0	235	6	AAE35884	Aae35884 Human 4.1	819	553	100.0	236	9	ABE45855	Aeb45855 Human mon
748	553	100.0	235	6	ABB82834	Abb82834 Anti-body	820	553	100.0	236	9	AEC88526	Aec88526 Human cDN
749	553	100.0	235	6	ABP71366	Abp71366 Anti-OPGL	821	553	100.0	236	9	AED14784	Aed14784 Ab B anti
750	553	100.0	235	6	ABP55322	Abp55322 Amino aci	822	553	100.0	236	9	AED14780	Aed14780 Ab A anti
751	553	100.0	235	7	ADD01357	AdD01357 Human imm	823	553	100.0	236	9	AED14796	Aed14796 Ab E and
752	553	100.0	235	8	ADL78727	AdL78727 Albumin f	824	553	100.0	236	9	AED19761	Aed19761 Chimeric
753	553	100.0	235	8	ADM41573	Adm41573 Anti-inte	825	553	100.0	236	9	AED54393	Aed54393 Anti-HER
			235	8	ADM41573	Adm41573 Anti-inte	826	553	100.0	236	10	AEE26239	Aee26239 Chimeric

827	553	100.0	236	10	AAE94840	Aee94840 Antibody	900	553	100.0	238	3	AAW90922	Humanised
828	553	100.0	236	10	AEF94869	Aee94869 Antibody	901	553	100.0	238	3	AAW90930	Humanised
829	553	100.0	236	10	AEF54367	Aef54367 Human lig	902	553	100.0	238	4	AAW72235	Humanised
830	553	100.0	236	10	AEF54345	Aef54345 Human ant	903	553	100.0	238	4	AAW72231	Humanised
831	553	100.0	236	10	AEF54346	Aef54346 Human lig	904	553	100.0	238	4	AAW72227	Humanised
832	553	100.0	236	10	AEF54349	Aef54349 Human ant	905	553	100.0	238	4	AAW72233	Humanised
833	553	100.0	236	10	AEF54350	Aef54350 Human lig	906	553	100.0	238	4	AAU07744	Humanised
834	553	100.0	236	10	AEF34921	Aef34921 Human ant	907	553	100.0	238	4	AAE03754	Chimeric
835	553	100.0	236	10	AEF34917	Aef34917 Human ant	908	553	100.0	238	5	ABB74937	Humanised
836	553	100.0	236	10	AEF34918	Aef34918 Human ger	909	553	100.0	238	5	ABB74938	Humanised
837	553	100.0	236	10	AEF34922	Aef34922 Human ger	910	553	100.0	238	5	ABB74939	Humanised
838	553	100.0	236	10	AEF73710	Aef73710 Human IL-	911	553	100.0	238	5	ABB74942	Humanised
839	553	100.0	237	2	AAE24047	AAe24047 Light cha	912	553	100.0	238	5	ABB74943	Humanised
840	553	100.0	237	2	AAW70703	Aaw70703 Protein e	913	553	100.0	238	5	ABB74944	Humanised
841	553	100.0	237	2	AAW95622	AAw95622 pS1130 ex	914	553	100.0	238	5	ABG70744	Mouse/hum
842	553	100.0	237	2	AAW30634	AAw30634 Recombina	915	553	100.0	238	5	ABG70744	Human CSE
843	553	100.0	237	2	AAW73873	AAw73873 Human ant	916	553	100.0	238	5	ABB74897	Humanised
844	553	100.0	237	3	AAW96289	AAy96289 Human IGF	917	553	100.0	238	5	ABB74899	Humanised
845	553	100.0	237	3	AAW96298	AAy96298 Human IGF	918	553	100.0	238	5	ABB74892	Humanised
846	553	100.0	237	3	AAW96301	AAy96301 Human IGF	919	553	100.0	238	5	ABB74893	Humanised
847	553	100.0	237	4	AAW66784	AAb66784 Protein e	920	553	100.0	238	5	ABB74891	Humanised
848	553	100.0	237	5	ABB81107	Abb81107 Anti-VEGF	921	553	100.0	238	5	ABB74896	Humanised
849	553	100.0	237	5	ABB81106	Abb81106 Anti-tiss	922	553	100.0	238	5	ABB74901	Humanised
850	553	100.0	237	5	ABP51952	ABp51952 Plasmid p	923	553	100.0	238	6	ABF58288	Humanised
851	553	100.0	237	6	ABP72745	ABp72745 Anti-CD18	924	553	100.0	238	6	ABR41582	Human DIT
852	553	100.0	237	6	ABF72747	ABf72747 Anti-tiss	925	553	100.0	238	6	ABR39842	Humanised
853	553	100.0	237	7	ABR61570	ABr61570 HIV-1 neu	926	553	100.0	238	6	ABR82839	Antibody
854	553	100.0	237	7	ADK69943	ADk69943 Immunoglo	927	553	100.0	238	6	ADA47330	TRX1 ligh
855	553	100.0	237	8	ADL93658	ADl93658 Human CD4	928	553	100.0	238	6	ADA47332	TRX1 ligh
856	553	100.0	237	8	ADL93657	ADl93657 Human CD4	929	553	100.0	238	7	ADL93652	Human CD4
857	553	100.0	237	8	ADL93651	ADl93651 Human CD4	930	553	100.0	238	8	ADL93653	Human CD4
858	553	100.0	237	8	ADL93651	ADl93651 Human CD4	931	553	100.0	238	8	ADL93653	Human CD4
859	553	100.0	237	8	ADL93651	ADl93651 Human CD4	932	553	100.0	238	8	ADL93650	Human CD4
860	553	100.0	237	8	ADL93651	ADl93651 Human CD4	933	553	100.0	238	8	ADL93650	Human CD4
861	553	100.0	237	8	ADL93651	ADl93651 Human CD4	934	553	100.0	238	8	ADL93650	Human CD4
862	553	100.0	237	8	ADL93651	ADl93651 Human CD4	935	553	100.0	238	8	ADL93652	Human CD4
863	553	100.0	237	8	ADL93651	ADl93651 Human CD4	936	553	100.0	238	8	ADL93653	Human CD4
864	553	100.0	237	8	ADL93651	ADl93651 Human CD4	937	553	100.0	238	8	ADL93653	Human CD4
865	553	100.0	237	8	ADL93651	ADl93651 Human CD4	938	553	100.0	238	8	ADL93650	Human CD4
866	553	100.0	237	8	ADL93651	ADl93651 Human CD4	939	553	100.0	238	8	ADL93650	Human CD4
867	553	100.0	237	8	ADL93651	ADl93651 Human CD4	940	553	100.0	238	8	ADL93650	Human CD4
868	553	100.0	237	8	ADL93651	ADl93651 Human CD4	941	553	100.0	238	8	ADL93650	Human CD4
869	553	100.0	237	8	ADL93651	ADl93651 Human CD4	942	553	100.0	238	8	ADL93650	Human CD4
870	553	100.0	237	8	ADL93651	ADl93651 Human CD4	943	553	100.0	238	8	ADL93650	Human CD4
871	553	100.0	237	8	ADL93651	ADl93651 Human CD4	944	553	100.0	238	8	ADL93650	Human CD4
872	553	100.0	237	9	ABE27976	ABe27976 E. coli S	945	553	100.0	238	8	ADS88804	Humanised
873	553	100.0	237	10	AEF47632	AEe47632 Humanized	946	553	100.0	238	8	ADS88785	Sequence
874	553	100.0	237	10	AEF17108	Aef17108 B. brevis	947	553	100.0	238	9	ADY30114	Human IGF
875	553	100.0	237	10	AEF17111	Aef17111 B. brevis	948	553	100.0	238	9	ADY91367	Anti-KID3
876	553	100.0	237	10	AEF18356	Aef18356 Middle wa	949	553	100.0	238	9	AEBO8041	Murine/hu
877	553	100.0	237	10	AEF18353	Aef18353 Middle wa	950	553	100.0	238	9	AEBO8041	Anti-NOGO
878	553	100.0	237	10	AEF18353	Aef18353 Middle wa	951	553	100.0	238	9	AEBO8041	Anti-NOGO
879	553	100.0	237	10	AEF41647	Aef41647 STII sign	952	553	100.0	238	9	AEBO8041	Anti-NOGO
880	553	100.0	238	2	AAW93554	AAr93554 Monoclonal	953	553	100.0	238	9	AEBO8041	Anti-NOGO
881	553	100.0	238	2	AAW14937	AAw14937 Murine an	954	553	100.0	238	9	AEBO8041	Anti-NOGO
882	553	100.0	238	2	AAW14936	AAw14936 2A2 Human	955	553	100.0	238	9	AEBO8041	Anti-NOGO
883	553	100.0	238	2	AAW14942	AAw14942 3F4 Human	956	553	100.0	238	9	AEBO8041	Anti-NOGO
884	553	100.0	238	2	AAW14931	AAw14931 Murine an	957	553	100.0	238	9	AEBO8041	Anti-NOGO
885	553	100.0	238	2	AAW83035	AAw83035 Anti-Fas	958	553	100.0	238	9	AEBO8041	Anti-NOGO
886	553	100.0	238	2	AAW83034	AAw83034 Anti-Fas	959	553	100.0	238	9	AEBO8041	Anti-NOGO
887	553	100.0	238	2	AAW83033	AAw83033 Anti-Fas	960	553	100.0	238	9	AEBO8041	Anti-NOGO
888	553	100.0	238	2	AAW83032	AAw83032 Anti-Fas	961	553	100.0	238	9	AEBO8041	Anti-NOGO
889	553	100.0	238	2	AAW83031	AAw83031 Anti-Fas	962	553	100.0	238	9	AEBO8041	Anti-NOGO
890	553	100.0	238	2	AAW83031	AAw83031 Anti-Fas	963	553	100.0	238	9	AEBO8041	Anti-NOGO
891	553	100.0	238	2	AAW83031	AAw83031 Anti-Fas	964	553	100.0	238	9	AEBO8041	Anti-NOGO
892	553	100.0	238	2	AAW83031	AAw83031 Anti-Fas	965	553	100.0	238	9	AEBO8041	Anti-NOGO
893	553	100.0	238	2	AAW83031	AAw83031 Anti-Fas	966	553	100.0	238	9	AEBO8041	Anti-NOGO
894	553	100.0	238	2	AAW83031	AAw83031 Anti-Fas	967	553	100.0	238	9	AEBO8041	Anti-NOGO
895	553	100.0	238	2	AAW83031	AAw83031 Anti-Fas	968	553	100.0	238	9	AEBO8041	Anti-NOGO
896	553	100.0	238	2	AAW83031	AAw83031 Anti-Fas	969	553	100.0	238	9	AEBO8041	Anti-NOGO
897	553	100.0	238	2	AAW83031	AAw83031 Anti-Fas	970	553	100.0	238	9	AEBO8041	Anti-NOGO
898	553	100.0	238	2	AAW83031	AAw83031 Anti-Fas	971	553	100.0	238	9	AEBO8041	Anti-NOGO
899	553	100.0	238	2	AAW83031	AAw83031 Anti-Fas	972	553	100.0	238	9	AEBO8041	Anti-NOGO

773 553 100.0 239 3 AAY82612 Human PTH
774 553 100.0 239 3 AAY82613 Human PTH
775 553 100.0 239 3 AAU77288 Aau77288 Protein #
776 553 100.0 239 3 AAB12914 Anti-huma
777 553 100.0 239 3 AAB12916 Anti-huma
778 553 100.0 239 3 AAB12913 Anti-huma
779 553 100.0 239 3 AAB12915 Anti-huma
780 553 100.0 239 5 AAU11540 Anti-huma
781 553 100.0 239 6 AAE37361 Monkey 7B
782 553 100.0 239 6 ABR48456 Human Cal
783 553 100.0 239 6 ABP58274 Humanised
784 553 100.0 239 7 ADE28405 Human ant
785 553 100.0 239 7 ADE28421 Human ant
786 553 100.0 239 7 ADE28465 Human ant
787 553 100.0 239 7 ADE28461 Human ant
788 553 100.0 239 7 ADE28521 Human ant
789 553 100.0 239 7 ADE28397 Human ant
790 553 100.0 239 7 ABG75316 Anti-CD22
791 553 100.0 239 7 ADM05343 Human pro
792 553 100.0 239 7 ADL23137 Mouse/hum
793 553 100.0 239 7 ADL23170 Mouse/hum
794 553 100.0 239 7 ADL23168 Mouse/hum
795 553 100.0 239 7 ADL23176 Mouse/hum
796 553 100.0 239 7 ADL23133 Mouse/hum
797 553 100.0 239 7 ADL23166 Mouse/hum
798 553 100.0 239 7 ADL23174 Mouse/hum
799 553 100.0 239 7 ADL23172 Mouse/hum
1000 553 100.0 239 7 ADL23139 Mouse/hum

ALIGNMENTS

RESULT 1
AAW40578
ID AAW40578 standard; protein; 107 AA.
XX
AC AAW40578;
XX
XX 21-JUL-1998 (first entry)
DE Human kappa CL domain protein fragment.
XX
DE Immunoglobulin G; IGG molecule; human; Fc region; LFA-1 receptor;
KW disorder; salvage receptor binding epitope; cell adherence interaction;
KW lymphocyte; T cell inflammatory response.
XX
OS Homo sapiens.
XX
XX US5739277-A.
PN
XX 14-APR-1998.
PD
XX 14-APR-1995; 95US-00422101.
PF
XX 14-APR-1995; 95US-00422101.
PR
XX (GETH) GENENTECH INC.
PA
XX Snedecor BR, Presta LG;
PI
XX WPI; 1998-250490/22.
DR
XX Polypeptide(s) that are not Fc fragments and have an increased half-life
PT - are useful for the treatment of LFA-1 mediated disorders.
XX
PS Disclosure; Fig 2; 38pp; English.
XX
CC This protein fragment is derived from a human immunoglobulin kappa CL
CC domain and is used to describe a novel method to produce polypeptides
CC which contain an epitope from the Fc region of an IGG molecule and a
CC mutated salvage receptor binding epitope. They are useful for the
CC treatment of LFA-1 mediated disorders. These are conditions caused by

CC cell adherence interactions involving the LFA-1 receptor on lymphocytes,
CC e.g. T cell inflammatory responses. The mutated salvage receptor sequence
CC in the polypeptides means that they have increased in vivo circulatory
CC half-lives when compared to normal Fc regions of IGG molecules
XX
SQ Sequence 107 AA;
Query Match 100.0%; Score 553; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYFREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RIVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYFREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYSLSSTLTLSKADYERKHYKVCETVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYSLSSTLTLSKADYERKHYKVCETVTHQGLSSPVTKSFNRGEC 107
RESULT 2
AAY50152
ID AAY50152 standard; protein; 107 AA.
XX
AC AAY50152;
XX
XX 31-JAN-2000 (first entry)
XX Human kappa light chain constant region.
XX
KW Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP;
KW humanisation; complementarity determining region; CDR; CDR grafting;
KW reshaped; reactive stroma; fibroblast; epithelial cancer; diagnosis;
KW immune response; framework sequence; constant region; variable region;
KW producibility; treatment; cancer; colorectal; lung; breast; head; neck;
KW ovarian; lung; bladder; pancreatic; metastasis; detection; wound healing;
KW skin inflammation; tumour; immunogenicity; light chain.
XX
OS Homo sapiens.
XX
XX EP953639-A1.
PN
XX 03-NOV-1999.
PD
XX 30-APR-1998; 98EP-00107925.
PF
XX 30-APR-1998; 98EP-00107925.
PR
XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA
XX Park JE, Garin-Chesa P, Bamberger U, Leger O, Saldanha J;
PI Rettig WJ;
XX
XX WPI; 1999-621833/54.
DR N-PSDB; AAZ32777.
XX
XX New antibody protein, useful for treating cancer and for imaging presence
PT of activated stromal fibroblasts in healing wound or inflamed skin.
XX
XX Disclosure; Fig 20; 143pp; English.
XX
CC This sequence represents a human kappa light chain, the cDNA of which was
CC used in the construction of a nucleotide encoding the light chain of a
CC human reshaped monoclonal antibody F19. F19 (AFCC Accession number HB
CC 8269) is a murine monoclonal antibody against fibroblast activation
CC protein alpha (FAP). FAP is a cell surface molecule of reactive stromal
CC fibroblasts, and its induction is a highly consistent molecular trait of
CC the reactive stroma of many types of epithelial cancer. Although F19 may
CC be useful in vitro, e.g., for diagnosis, its applications for in vivo use
CC in humans are problematic as it elicits a human anti-mouse response which
CC reduces the efficacy of the antibody in patients and impairs continued
CC administration. The novel human reshaped F19 was humanised by grafting
CC the murine complementarity determining regions (CDRs) of F19 onto human

CC variable region framework sequences, and then joining these "reshaped
CC human" variable regions to human constant regions. These modifications
CC also result in the improved producibility in eukaryotic cell culture
CC systems as compared to a chimeric antibody having the entire variable
CC regions of F19 joined to human constant regions. The human reshaped F19
CC antibody has low immunogenicity for humans and is useful for treating
CC cancers e.g., colorectal cancers, non-small cell lung cancers, breast
CC cancers, head and neck cancers, ovarian cancers, lung cancers, bladder
CC cancers, pancreatic cancers and metastatic cancers. It is also useful for
CC the detection of activated stromal fibroblasts in a healing wound,
CC inflamed skin or a tumour in a human patient
XX
SQ Sequence 107 AA;

Query Match 100.0%; Score 553; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSSTLTLSKADYEHKHYVACEVTHOGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSSTLTLSKADYEHKHYVACEVTHOGLSSPVTKSFNRGEC 107

RESULT 3
AAW92425
ID AAW92425 standard; peptide; 107 AA.
XX AC AAW92425;
XX 23-APR-1999 (first entry)
XX Human Kappa protein CL domain.
XX
KW Antibody; salvage receptor binding epitope; Fab; F(ab')2; immunoglobulin;
KW CH region; CL region; kidney; Fc region; CH1 domain; CH2 domain; IgG;
KW kappa protein; renal clearance rate; circulatory half-life.
XX
OS Homo sapiens.
XX US5869046-A.
XX 09-FEB-1999.
XX 14-APR-1995; 95US-00422092.
XX 14-APR-1995; 95US-00422092.
XX (GETH) GENENTECH INC.
XX Presta LG, Snedecor BR;
XX WPI; 1999-152694/13.
XX Production of antibody fragments with reduced renal clearance - by
PT introducing salvage receptor binding epitope into CH1 or CL region.
XX
PS Disclosure; Col 55-58; 38pp; English.
XX
CC This invention describes a method for preparing a variant Fab or F(ab')2
CC polypeptide having increased half-life in vivo, where the polypeptide
CC contains an Ig or Ig-like domain comprising a CH1 and/or CL region, is
CC cleared from the kidneys and does not contain an IgG Fc region. The
CC method involves altering the polypeptide within the CH1 or CL region to
CC incorporate a salvage receptor binding epitope taken from two loops of a
CC CH2 domain of an IgG Fc region. The polypeptides have a reduced renal
CC clearance rate and an increased circulatory half-life. This sequence
CC represents a human kappa protein CL domain used in the method of the
CC invention
XX

SQ Sequence 107 AA;

Query Match 100.0%; Score 553; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSSTLTLSKADYEHKHYVACEVTHOGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSSTLTLSKADYEHKHYVACEVTHOGLSSPVTKSFNRGEC 107

RESULT 4
AAW08745
ID AAW08745 standard; protein; 107 AA.
XX AC AAW08745;
XX 10-AUG-1999 (first entry)
XX Human Kappa-CL domain.
XX
KW IgG; immunoglobulin G; CH1 domain; human; anti-CD18; IgG1; IgG2; IgG3;
KW IgG4; Kappa-CL domain; lambda-CL domain; focal ischaemic stroke;
KW cerebroprotective; cerebral artery obstruction; blood flow; infarct;
KW CD18 extracellular domain; endothelium; CD11b/CD18 complex dissociation;
KW antibody.
XX
OS Homo sapiens.
XX US5914112-A.
XX 22-JUN-1999.
XX 22-JAN-1997; 97US-00788800.
XX 23-JAN-1996; 96US-0093038P.
XX (GETH) GENENTECH INC.
XX (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
XX Thomas GR, Bednar MM, Gross CE;
XX WPI; 1999-370483/31.
XX Anti-CD18 antibodies in stroke.
XX Disclosure; Fig 4A-B; 25pp; English.
XX
CC This invention describes a method for improving the clinical outcome in
CC focal ischaemic stroke by administering novel anti-CD18 antibody which
CC has cerebroprotective properties. The invention particularly describes a
CC method of treating focal ischaemic stroke caused by the obstruction of a
CC main cerebral artery which comprises administering an anti-CD18 antibody
CC to increase the blood flow or reduce the infarct size, where: (1) the
CC antibody binds to an extracellular domain of CD18 and inhibits or reduces
CC the ability of the cell expressing CD18 to bind to endothelium, (2) the
CC antibody binds CD18 with an affinity of less than 4 nm, or (3) the
CC antibody dissociates CD11b/CD18 complex. This sequence represents the
CC human Kappa-CL domain which is used to illustrate the method of the
CC invention
XX
SQ Sequence 107 AA;

Query Match 100.0%; Score 553; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSSTLTLSKADYEHKHYVACEVTHOGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSSTLTLSKADYEHKHYVACEVTHOGLSSPVTKSFNRGEC 107

```
Db 1 RTVAAPSVFIPPPSDEQLKSGTASVVCILNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
Qy 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 5
AAB27000
ID AAB27000 standard; protein; 107 AA.
XX
AC AAB27000;
XX
DT 25-JAN-2001 (first entry)
XX
DE Human kappa CL domain.
XX
KW Human; kappa CL domain; cerebral blood flow; infarct size;
KW focal ischaemic stroke; main cerebral artery;
KW tissue plasminogen activator; anti-CD18 antibody; stroke;
KW acute ischaemic stroke; thrombolytic therapy; thromboembolic stroke.
XX
OS Homo sapiens.
XX
PN US6121022-A.
XX
PD 19-SEP-2000.
XX
PF 14-APR-1995; 95US-00422112.
XX
PR 14-APR-1995; 95US-00422112.
XX
PA (GETH ) GENENTECH INC.
XX
PI Presta LG, Snedecor BR;
XX
DR WPI; 2000-610925/58.
XX
PT New nucleic acid encoding new modified polypeptides with increased
PT circulatory half-life useful for preventing/treating LFA-1-mediated
PT disorders, e.g. reducing inflammatory responses or inducing tolerance to
PT immunostimulants.
XX
PS Disclosure; Fig 2; 38pp; English.
XX
CC The present sequence was used in a method for improving the in vivo half-
CC life of polypeptides. The polypeptides comprise an Ig constant domain or
CC an Ig-like constant domain, and a salvage receptor binding epitope within
CC the Ig or Ig-like domain. The salvage receptor epitope is taken from two
CC loops of the CH2 domain of an Fc region of an Ig molecule. The modified
CC polypeptides are useful for preventing or treating LFA-1-mediated
CC disorders, e.g. Crohn's disease, psoriasis, meningitis, allergic
CC conditions (e.g. eczema), antigen-antibody complex mediated diseases, B-
CC cell lymphomas. They are also useful for wound repair, reducing
CC inflammatory responses and inducing tolerance to immunostimulants. They
CC may also be used in diagnostic assays. The nucleic acids and modified
CC polypeptides are useful for the passive immunisation of patients, as well
CC as for affinity purification of an antigen from recombinant cell culture
CC or natural sources
XX
SQ Sequence 107 AA;
Query Match 100.0%; Score 553; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCILNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIPPPSDEQLKSGTASVVCILNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
Qy 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
```

```
RESULT 6
ABG31883
ID ABG31883 standard; protein; 107 AA.
XX
AC ABG31883;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human kappa CL domain.
XX
KW Human; kappa CL domain; cerebral blood flow; infarct size;
KW focal ischaemic stroke; main cerebral artery;
KW tissue plasminogen activator; anti-CD18 antibody; stroke;
KW acute ischaemic stroke; thrombolytic therapy; thromboembolic stroke.
XX
OS Homo sapiens.
XX
PN US2002081294-A1.
XX
PD 27-JUN-2002.
XX
PF 20-DEC-2000; 2000US-00811384.
XX
PR 23-JAN-1996; 96US-0093038P.
XX
PR 22-JAN-1997; 97US-00788800.
XX
PR 17-FEB-1999; 99US-00251652.
XX
PA (GETH ) GENENTECH INC.
XX
PI Bednar MM, Gross CE, Thomas GR, Gross LJ;
XX
DR WPI; 2002-626528/67.
XX
PT Increasing cerebral blood flow and/or reducing infarct size in focal
PT ischemic stroke using anti-CD18 antibody and tissue plasminogen activator
PT is useful to improve clinical outcome in acute ischemic stroke.
XX
PS Disclosure; Fig 4; 27pp; English.
XX
CC The invention relates to a method of increasing cerebral blood flow and/
CC or reducing infarct size in focal ischaemic stroke caused by obstruction
CC of a main cerebral artery in a human, comprising co-administering tissue
CC plasminogen activator and anti-CD18 antibody about 3-5 hours after the
CC ischaemic stroke and to provide an alternative to thrombolytic therapy
CC for treating thromboembolic stroke, particularly where thrombolytic
CC therapy has been unsuccessful or is contra-indicated. The present
CC sequence represents the human kappa CL domain used in the method of the
CC invention
XX
SQ Sequence 107 AA;
Query Match 100.0%; Score 553; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCILNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIPPPSDEQLKSGTASVVCILNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
Qy 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 7
ABB98755
ID ABB98755 standard; protein; 107 AA.
XX
AC ABB98755;
XX
```

DT 23-JAN-2003 (first entry)
 XX Human kappa light constant chain.
 DE
 XX
 KW Human; cytostatic; antitumor; immunosuppressive; antiallergic;
 KW humanised; antibody; fibroblast activation protein alpha; FAPalpha;
 KW cancer; monoclonal antibody F19; colorectal cancer;
 KW non-small cell lung carcinoma; breast cancer; pancreatic cancer; tumour;
 KW systemic autoimmune disease; allergy; light chain; constant region.
 XX
 OS Homo sapiens.
 XX
 XX WO200283171-A2.
 PN
 XX
 XX 24-OCT-2002.
 PD
 XX
 XX 11-APR-2002; 2002WO-EP004041.
 PF
 XX
 XX 12-APR-2001; 2001US-0283868P.
 PR
 XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
 PA
 XX Amelsberg A, Scott A, Tanswell P;
 FI
 XX WPI; 2003-058609/05.
 DR N-PSDB; ABV74601.
 DR
 XX
 XX Use of a humanized antibody which specifically binds to fibroblast
 PT activation protein alpha for manufacturing a medicament for treating
 PT cancer.
 PT
 XX
 XX Claim 7; Page 55; 57pp; English.
 PS
 XX The present invention relates to the use of a humanised antibody (I),
 CC which specifically binds to fibroblast activation protein alpha (I),
 CC (FAPalpha), for manufacturing a medicament for treating cancer. (I) has
 CC the complementary determining region (CDR) of the monoclonal antibody
 CC F19, but has framework modifications resulting in improved producibility
 CC in host cells as compared to a chimeric antibody having the variable
 CC regions of F19 and foreign constant regions. To generate (I), a chimeric
 CC antibody was constructed having variable regions of the light and heavy
 CC chains of F19 and human light and heavy constant regions. (I) is useful
 CC for treating a patient suffering from a pathological condition
 CC characterised by expression of FAPalpha, such as colorectal cancer, non-
 CC small cell lung carcinoma, breast cancer, pancreatic cancer, tumours,
 CC systemic autoimmune diseases and allergies. The present sequence is human
 CC kappa light constant chain which was used to produce (I)
 XX
 SQ Sequence 107 AA;
 Query Match 100.0%; Score 553; DB 6; Length 107;
 Best Local Similarity 100.0%; Pred. No. 4.3e-48;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 QY 61 SKDSTYLSLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
 Db 61 SKDSTYLSLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
 RESULT 8
 ABR42732
 ID ABR42732 standard; protein; 107 AA.
 XX
 XX ABR42732;
 AC
 XX 26-AUG-2003 (first entry)
 DT
 XX Anti-tissue factor humanized antibody light chain constant region.

XX Tissue factor; humanization; antibody; anticoagulant; cytostatic;
 KW antiinflammatory; mouse; human; hOAT.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX WO2003037911-A2.
 PN
 XX 08-MAY-2003.
 PD
 XX 29-OCT-2002; 2002WO-US034727.
 PF
 XX 29-OCT-2001; 2001US-0343306P.
 PR 21-NOV-2001; 2001US-00990586.
 XX
 XX (SUNO-) SUNOL MOLECULAR CORP.
 PA
 XX Jiao J, Wong HC, Nieves EL, Mosquera LA;
 PI WPI; 2003-468399/44.
 DR
 XX New humanized antibody that binds specifically to human tissue factor,
 PT useful for in vivo diagnostic methods, or for inhibiting blood
 PT coagulation or blood clot formation, angiogenesis, tumor metastases or
 PT inflammation in a mammal.
 PT
 XX Example 10; Fig 14A; 110pp; English.
 PS
 XX The present sequence is the protein sequence of the light chain constant
 CC region of anti-human tissue factor (TF) humanized antibody hOAT
 CC (humanised ch36-IgG1). Humanized antibodies of the invention provide
 CC superior anticoagulant activity by binding native human TF with high
 CC affinity and specificity. The antibodies bind human TF, either alone or
 CC present in a TF:Factor VIIa complex, effectively preventing Factor X (or
 CC Factor IX) binding to TF or the complex, and thereby reducing blood
 CC coagulation. The humanized antibodies are useful for inhibiting blood
 CC coagulation or blood clot formation, angiogenesis, tumour metastases or
 CC inflammation in a mammal. They are also useful as drug carriers, as
 CC cytotoxic agents, for reducing TF levels in mammals, and for in vivo
 CC diagnosis
 CC
 SQ Sequence 107 AA;
 Query Match 100.0%; Score 553; DB 6; Length 107;
 Best Local Similarity 100.0%; Pred. No. 4.3e-48;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 QY 61 SKDSTYLSLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
 Db 61 SKDSTYLSLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
 RESULT 9
 ABR42734
 ID ABR42734 standard; protein; 107 AA.
 XX
 XX ABR42734;
 AC
 XX 26-AUG-2003 (first entry)
 DT
 XX Anti-tissue factor humanized antibody light chain constant region.
 DE
 XX Tissue factor; humanization; antibody; anticoagulant; cytostatic;
 KW antiinflammatory; mouse; human; hOAT.
 XX
 OS Mus sp.
 OS Homo sapiens.

XX PI Hansen H, Qu Z, Goldenberg DM;
XX WPI; 2003-697522/66.
DR N-PSDB; ADJ94621.
XX New humanized anti-CD20 monoclonal antibody (MAB) that retains
PT substantially the B-cell and B-cell lymphoma and leukemia cell targeting
PT of the murine anti-CD20 MAB, useful for treating B-cell lymphoma,
PT leukemia or an autoimmune diseases.
XX Example 1; Fig 7B; 106pp; English.
XX The invention comprises a humanised anti-CD20 (hCD20) monoclonal antibody
CC (MAB) or its antigen-binding fragment containing the complementarity
CC determining regions (CDRe) of at least one murine anti-CD20 Mab variable
CC region and the framework regions (FRs) of at least one human IIVIAB
CC variable region. The antibodies of the invention are useful for
CC diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune
CC disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The
CC present amino acid sequence represents a human kappa chain (CK) constant
CC region.
XX Sequence 107 AA;
SQ
Query Match 100.0%; Score 553; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYSLSSLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSSLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
RESULT 12
ADF77161
ID ADF77161 standard; protein; 107 AA.
XX ADF77161;
AC ADF77161;
XX 26-FEB-2004 (first entry)
DT Anti-VAP-1 monoclonal antibody L chain constant region.
XX complementarity determining region; CDR; mouse;
KW Vascular Adhesion Protein-1; VAP-1; antibody; heavy; light; chain;
KW chimeric; inflammatory disorder; rheumatoid arthritis;
KW inflammatory bowel disease; autoimmune disease; psoriasis;
KW immunoscintigraphic imaging.
XX Homo sapiens.
OS Homo sapiens.
XX WO2003093319-A1.
FN 13-NOV-2003.
PD 28-APR-2003; 2003WO-FI000330.
PF 29-APR-2002; 2002FI-00000807.
PR (BIOT-) BIOTIE THERAPIES CORP.
PA Jalkanen S, Salmi M, Laukkanen M, Clark MR;
XX WPI; 2004-022642/02.
XX New chimeric anti-Vascular Adhesion Protein-1 monoclonal antibodies and
PT encoding nucleic acid molecules, useful for diagnosing and treating
PT chronic inflammatory disorders, e.g. rheumatoid arthritis or psoriasis.

XX Claim 18; SEQ ID NO 22; 56pp; English.
XX This sequence represents the constant region of a human anti-Vascular
CC Adhesion Protein-1 (VAP-1) antibody light chain. This sequence may be
CC used in the production of a chimeric mouse-human anti-VAP-1 antibody. The
CC nucleic acid molecules, polypeptides or antibodies are useful in treating
CC VAP-1 mediated inflammatory disorders, such as rheumatoid arthritis,
CC inflammatory bowel disease, autoimmune diseases or psoriasis. The
CC chimeric VAP-1 antibody is further used for in vitro and in vivo
CC diagnostic applications, including in vivo immunoscintigraphic imaging of
CC inflammation sites. The chimeric MAB's of the invention have improved
CC kinetic properties compared to the corresponding murine antibodies.
XX Sequence 107 AA;
SQ
Query Match 100.0%; Score 553; DB 8; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYSLSSLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSSLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
RESULT 13
ADL35096
ID ADL35096 standard; protein; 107 AA.
XX ADL35096;
AC ADL35096;
XX 03-JUN-2004 (first entry)
DT Human IgG4 (hFAT) kappa light chain constant domain protein SeqID 99.
XX antibody; variable domain; framework region; FR; huFR;
KW immune system molecule; kappa; anti-tissue factor; hFAT; human.
XX Homo sapiens.
OS Homo sapiens.
XX WO2004020579-A2.
FN 11-MAR-2004.
PD 06-AUG-2003; 2003WO-US024637.
PF 29-AUG-2002; 2002US-00230880.
PR (SUNO-) SUNOL MOLECULAR CORP.
PA Wong HC, Stinson JR, Mosquera LA;
XX WPI; 2004-239169/22.
XX Producing humanized antibodies for diagnostic and therapeutic purposes
PT comprises optimizing similarity between individual antibody framework
PT regions to help identify human framework regions suitable for making the
PT antibodies.
XX Disclosure; SEQ ID NO 99; 137pp; English.
XX This invention relates to a novel method for producing a humanised
CC antibody variable (V) domain or its fragment by optimising sequence
CC similarity between individual antibody framework regions (FRs) in order
CC to identify suitable human FRs (huFRs). Specifically, it refers to novel
CC immune system molecules i.e. humanised monoclonal antibodies that exhibit
CC suitable binding affinity with reduced immunogenicity in humans. The
CC present invention describes a method of mutagenising DNA of non-human FRs
CC to encode humanised FRs having an amino acid sequence that is

CC substantially identical to the selected human FR previously identified
CC through sequence similarity searching. As such, this method provides
CC humanised light or heavy chain V domains of the sequence huFR1-CDRI-huFR2
CC -CDR2-huFR3-CDR3-huFR4, which can be used as therapeutic or diagnostic
CC products to treat and/ or diagnose diseases in humans and animals.
CC Furthermore, the method expands the number of best fit possibilities that
CC can be generated and provides a rational basis for assembling nearly all
CC humanised immune system molecules of interest. This polypeptide sequence
CC is the human IgG4 kappa light chain constant domain protein of the
CC invention.

XX Sequence 107 AA;
SQ Query Match 100.0%; Score 553; DB 8; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYLSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYLSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 14
ADL35094
ID ADL35094 standard; protein; 107 AA.
XX
AC ADL35094;
XX
DT 03-JUN-2004 (first entry)
DE Human IgG1 (hOAT) kappa light chain constant domain protein SeqID 97.
DE antibody; variable domain; framework region; FR; huFR;
KW immune system molecule; kappa; anti-tissue factor; hOAT; human.
XX Homo sapiens.
OS
XX WO2004020579-A2.
XX
XX 11-MAR-2004.
XX
XX 06-AUG-2003; 2003WO-US024637.
XX
XX 29-AUG-2002; 2002US-00230880.
XX
XX (SUNO-) SUNOL MOLECULAR CORP.
XX
XX Wong HC, Stinson JR, Mosquera LA;
XX WPI; 2004-239169/22.
XX
XX Producing humanized antibodies for diagnostic and therapeutic purposes
XX comprises optimizing similarity between individual antibody framework
XX regions to help identify human framework regions suitable for making the
XX antibodies.

XX Disclosure; SEQ ID NO 97; 137pp; English.
XX
XX This invention relates to a novel method for producing a humanised
XX antibody variable (V) domain or its fragment by optimising sequence
XX similarity between individual antibody framework regions (FRs) in order
XX to identify suitable human FRs (huFRs). Specifically, it refers to novel
XX immune system molecules i.e. humanised monoclonal antibodies that exhibit
XX suitable binding affinity with reduced immunogenicity in humans. The
XX present invention describes a method of mutagenising DNA of non-human FRs
XX to encode humanised FRs having an amino acid sequence that is
XX substantially identical to the selected human FR previously identified
XX through sequence similarity searching. As such, this method provides
XX humanised light or heavy chain V domains of the sequence huFR1-CDRI-huFR2

CC -CDR2-huFR3-CDR3-huFR4, which can be used as therapeutic or diagnostic
CC products to treat and/ or diagnose diseases in humans and animals.
CC Furthermore, the method expands the number of best fit possibilities that
CC can be generated and provides a rational basis for assembling nearly all
CC humanised immune system molecules of interest. This polypeptide sequence
CC is the human IgG1 kappa light chain constant domain protein of the
CC invention.

XX Sequence 107 AA;
SQ Query Match 100.0%; Score 553; DB 8; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYLSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYLSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 15
ADM41539
ID ADM41539 standard; protein; 107 AA.
XX
AC ADM41539;
XX
DT 03-JUN-2004 (first entry)
DE Anti-interleukin-1 receptor type 1 antibody kappa chain constant region.
DE Human; monoclonal antibody; antibody; interleukin-1; receptor;
KW antiasthmatic; antiinflammatory; dermatological; antiallergic;
KW prozoacide; antiarthritis; antidiabetic; osteopathic; vasotropic;
KW analgesic; antidiabetic; nephrotropic; antianaemic; nootropic;
KW anticonvulsant; dermatological; antigen; antiparkinsonian; antidiabetic;
KW cytostatic.
XX Homo sapiens.
OS
XX WO2004022718-A2.
XX
XX 18-MAR-2004.
XX
XX 05-SEP-2003; 2003WO-US027978.
XX
XX 06-SEP-2002; 2002US-0408719P.
XX
XX (AMGE-) AMGEN INC.
XX
XX Varnum B, Vezina C, Witte A, Qian X, Martin F, Huang H;
XX Elliott G;
XX
XX WPI; 2004-248462/23.
XX N-PSDB; ADM41538.
XX
XX Isolated human antibody that specifically binds interleukin-1 receptor
XX type 1 (IL-1R1) useful for treating IL-1 mediated diseases such as
XX rheumatoid arthritis, osteoarthritis and inflammatory conditions.
XX
XX Disclosure; SEQ ID NO 4; 179pp; English.
XX
XX The present sequence is that of a human anti-interleukin-1 receptor type
XX 1 (IL-1R1) monoclonal antibody (MAB) kappa chain constant region. Human
XX MABs to IL-1R1 were prepared using the HCo7 strain of transgenic mice,
XX which expresses human antibody genes. These mice were immunised with
XX purified recombinant IL-1R1, and splenocytes from immunised mice were
XX fused to a mouse myeloma cell line to generate hybridomas. Hybridomas
XX which secreted a MAB that bound with high avidity to IL-1R1 were
XX selected. The MABs inhibit IL-1 signalling by competing with IL-1beta and
XX IL-1alpha binding to IL-1R. These MABs, as well as single chain

CC antibodies single chain Fv antibodies, Fab antibodies, Fab' antibodies
 CC and (Fab')2 antibodies derived from them, are used in methods of treating
 CC IL-1 mediated diseases or for detecting the amount of IL-1 α in a sample.
 CC IL-1 mediated diseases include acute pancreatitis, amyotrophic lateral
 CC sclerosis, Alzheimer's disease, cachexia, anorexia, asthma,
 CC atherosclerosis, autoimmune vasculitis, chronic fatigue syndrome,
 CC Clostridium associated illnesses, coronary conditions, cancer including
 CC leukaemia and tumour metastasis, diabetes, endometriosis, fever,
 CC fibromyalgia, glomerulonephritis, graft versus host disease,
 CC osteoarthritis, rheumatoid arthritis, inflammatory eye disease,
 CC ischaemia, Kawasaki's disease, learning impairment, lung disease,
 CC multiple sclerosis, myopathy, osteoporosis, pain, Parkinson's disease,
 CC periodontal disease, pre-term labour, psoriasis, reperfusion injury,
 CC septic shock, side effects of radiation therapy, temporal mandibular
 CC joint disease, sleep disturbance, uveitis, or an inflammatory condition
 CC resulting from strain, sprain, cartilage damage, trauma, orthopaedic
 CC surgery, infection or other disease processes.
 XX
 SQ Sequence 107 AA;
 Query Match 100.0%; Score 553; DB 8; Length 107;
 Best Local Similarity 100.0%; Pred. No. 4.3e-48;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 QY 61 SKDSTYSLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 Db 61 SKDSTYSLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 RESULT 16
 ADK18336
 ID ADK18336 standard; protein; 107 AA.
 XX
 AC ADK18336;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Amino acid sequence of human kappa CL domain.
 XX
 KW Cerebral blood flow; infarct size; focal ischaemic stroke;
 KW cerebral artery; tissue plasminogen activator; tPA; anti-CD18 antibody;
 KW humanised H52 antibody; huH52 Fab; stroke; cerebroprotective; vasotropic;
 KW human; kappa; CL domain.
 XX
 OS Homo sapiens.
 XX
 PN US2004057951-A1.
 XX
 PD 25-MAR-2004.
 XX
 PF 31-MAR-2003; 2003US-00404286.
 XX
 PR 23-JAN-1996; 96US-0093038P.
 PR 22-JAN-1997; 97US-00788800.
 PR 17-FEB-1999; 99US-00251652.
 PR 20-DEC-2000; 2000US-00811384.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Bednar MM, Gross CE, Thomas GR, Gross L;
 PI WPI; 2004-257111/24.
 DR
 XX Increasing cerebral blood flow and/or reducing infarct size in focal
 PT ischemic stroke caused by obstruction of a main cerebral artery in a
 PT human comprises co-administering tissue plasminogen activator and anti-
 PT CD18 antibody.
 XX
 PS Disclosure; SEQ ID NO 5; 26pp; English.

XX The present invention relates to a method for increasing cerebral blood
 CC flow and/or reducing infarct size in focal ischaemic stroke caused by
 CC obstruction of a main cerebral artery in a mammal, particularly humans.
 CC The method comprises co-administering tissue plasminogen activator (tPA)
 CC and anti-CD18 antibody to the mammal, where neither the tPA nor the anti-
 CC CD18 antibody is administered to the mammal until about 3-5 hours after
 CC the onset of focal ischaemic stroke. The anti-CD18 antibody is a
 CC humanised H52 antibody (huH52 Fab). The anti-CD18 antibody binds to an
 CC extracellular domain of CD18 and inhibits or reduces the ability of a
 CC cell expressing CD18 to bind to endothelium. The anti-CD18 antibody binds
 CC CD18 with an affinity of 1-4 nm or less. The anti-CD18 antibody
 CC dissociates the CD11b/CD18 complex. The anti-CD18 antibody binds to the
 CC epitope bound by H52 antibody. The anti-CD18 antibody and the tPA are
 CC simultaneously administered to the mammal, or the anti-CD18 antibody is
 CC administered before the tPA is administered to the mammal. The method is
 CC useful in increasing cerebral blood flow and/or reducing infarct size in
 CC focal ischaemic stroke caused by obstruction of a main cerebral artery in
 CC a human. The antibodies are particularly useful for treating stroke.
 CC Unlike previous methods, the new method of treatment does not require
 CC prior administration of a thrombolytic agent to the mammal in order to
 CC remove an embolus/thrombus, and therefore increases cerebral blood flow
 CC and/or reduces infarct size. The present sequence represents a human
 CC kappa CL domain.
 XX
 SQ Sequence 107 AA;
 Query Match 100.0%; Score 553; DB 8; Length 107;
 Best Local Similarity 100.0%; Pred. No. 4.3e-48;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 QY 61 SKDSTYSLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 Db 61 SKDSTYSLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 RESULT 17
 ADN97487
 ID ADN97487 standard; protein; 107 AA.
 XX
 AC ADN97487;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Artificial protein construction protein #2.
 XX
 KW artificial proprotein; propeptide; protein engineering; antibody.
 XX
 OS Unidentified.
 XX
 PN WO2004031362-A2.
 XX
 PD 15-APR-2004.
 XX
 PF 03-OCT-2003; 2003WO-US031420.
 XX
 PR 03-OCT-2002; 2002US-0415940P.
 XX
 PA (LARG-) LARGE SCALE BIOLOGY CORP.
 XX
 XX Reini SJ, Edwards P;
 PI WPI; 2004-330170/30.
 DR N-PSDB; ADN97486.
 XX
 PT New artificial proprotein comprises three peptide sequences, useful for
 PT artificial multimeric protein engineering in eukaryotes.
 XX
 PS Example 15; SEQ ID NO 60; 244pp; English.

XX The invention relates to an artificial proprotein comprising three
CC peptide sequences: a first peptide sequence of interest, a propeptide
CC sequence attached to the C-terminus of the first peptide sequence of
CC interest, and a second peptide of interest attached to the C-terminus of
CC the propeptide sequence. The artificial proprotein and polynucleotides
CC are useful for sequence. The artificial proprotein and polynucleotides
CC are useful for sequence. The artificial proprotein and polynucleotides
CC and antibody fragments in eukaryotes. This sequence corresponds to a
CC protein used in the generation of the protein of the invention.

Qy	1	RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFY	PREAKVQMKVDNALQSGNSQSSVTEQD	60
Db	1	RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFY	PREAKVQMKVDNALQSGNSQSSVTEQD	60
Qy	61	SKDSTYLSSTLTLSKADYEHKHYACEVTHQGLSSPVT	KSFNRGEC	107
Db	61	SKDSTYLSSTLTLSKADYEHKHYACEVTHQGLSSPVT	KSFNRGEC	107

RESULT 18	
ADQ89334	
ID	ADQ89334 standard; protein; 107 AA.
XX	
AC	ADQ89334;
XX	
DT	21-OCT-2004 (first entry)
XX	
DE	Human immunoglobulin protein #45.
XX	
KW	Human; immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2;
KW	CCR2; inflammatory disease; autoimmune disorder; graft rejection;
KW	HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;
KW	anti-HIV; virucide; antiarteriosclerotic.

XX	OS	Homo sapiens.	
XX	XX	US2004151721-A1.	
XX	PN		
XX	XX	05-AUG-2004.	
XX	PD		
XX	XX		
XX	PF	10-DEC-2003; 2003US-00733563.	
XX	XX		
XX	PR	19-OCT-2001; 2001US-0350166P.	
XX	PR	26-JUN-2002; 2002US-0392364P.	
XX	PR	17-OCT-2002; 2002US-00272899.	
XX	XX		
XX	XX	(OKEE/) O'KEEFE T.	
XX	PA	(FONA/) FONATH P.	
XX	XX		
XX	PI	O'keefe T, Ponath P;	
XX	XX		
XX	DR	WPI; 2004-580175/56.	
XX	XX		
PT	PT	New humanized immunoglobulin	CC-chemokine receptor 2 (CCR2) antagonists,
PT	PT	useful for diagnosing and/or	treating inflammatory or autoimmune
PT	PT	diseases, and HIV infection.	

Claim 5; SEQ ID NO 112; 128pp; English.

CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV
CC infection and atherosclerosis. This sequence represents a human
CC immunoglobulin protein of the invention.

```

AA      SQ      Sequence 107 AA;
Query Match      100.0%; Score 553; DB 8; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy      1 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQD 60
      |||||
Db      1 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQD 60
      |||||
Qy      61 SKDSTYLSLTLLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
      |||||
Db      61 SKDSTYLSLTLLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
      |||||

```

RESULT 19	
ADS87911	
ID	ADS87911 standard; protein; 107 AA.
XX	
AC	ADS87911;
XX	
DT	18-NOV-2004 (first entry)
XX	
DE	Anti-IFN-gamma antibody light chain constant region SEQ ID NO:4.
XX	
KW	antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW	anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW	antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW	gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW	multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW	myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW	systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW	vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW	immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.

XX	Homo sapiens.
OS	
XX	WO2004034988-A2.
PN	
XX	29-APR-2004.
PD	
XX	14-OCT-2003; 2003WO-US032678.
PF	
XX	16-OCT-2002; 2002US-0419057P.
PR	
XX	17-JUN-2003; 2003US-0479241P.
XX	(AMGE-) AMGEN INC.
PA	
XX	
PI	Welcher A, Chute H, Li L, Huang H;
XX	
DR	WPI; 2004-348323/32.
DR	N-PSDB; ADS87910.
XX	
PT	New antibody that binds specifically to IFN-gamma and comprising a heavy
PT	chain CDR3, useful in preparing a composition for treating IFN-gamma
PT	mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT	atherosclerosis.
XX	
PS	Example 4; SEQ ID NO 4; 115pp; English.

The present invention describes an isolated antibody which binds specifically to interferon (IFN)-gamma and comprises a heavy chain complementarity determining region (CDR) 3 having a sequence comprising at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36 (ADS87943) in the same order and spacing, or an amino acid sequence of SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide encoding the antibody; (2) a method of treating an IFN-gamma mediated disease; and (3) a composition comprising a carrier and the antibody. The IFN-gamma binding antibody has anti-inflammatory, antiarthritis, anti-

CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
 CC antidiabetic activities, and can be used in gene therapy. The antibody is
 CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
 CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
 CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
 CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
 CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
 CC or haemolytic anaemia. The present sequence represents an immunoglobulin
 CC G1 (IgG1) anti-IFN-gamma light chain constant region, which is used in
 CC the exemplification of the present invention.

XX
 SQ Sequence 107 AA;

Query Match 100.0%; Score 553; DB 8; Length 107;
 Best Local Similarity 100.0%; Pred. No. 4.3e-48;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 DB 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 20
 ADS94908
 ID ADS94908 standard; protein; 107 AA.
 XX
 AC ADS94908;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Anti-IFN-gamma antibody light chain constant region SEQ ID NO:4.
 XX
 KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
 KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
 KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
 KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
 KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
 KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
 KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
 KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
 KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004035747-A2.
 XX
 PD 29-APR-2004.
 XX
 PF 16-OCT-2003; 2003WO-US032871.
 XX
 PR 16-OCT-2002; 2002US-0419057P.
 PR 17-JUN-2003; 2003US-0479241P.
 XX
 PA (AMGE-) AMGEN INC.
 PA (MEDA-) MEDAREX INC.
 XX
 XX Welcher AA, Chute HT, Li Y, Huang H;
 PI
 DR WPI; 2004-348443/32.
 DR N-PSDB; ADS94907.
 XX
 XX New human anti-interferon-gamma neutralising antibodies for treating
 PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
 PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
 PT rejection.
 XX
 XX Example 4; SEQ ID NO 4; 115pp; English.
 PS
 XX The present invention describes an isolated antibody which binds

CC specifically to interferon (IFN)-gamma and comprises a heavy chain
 CC complementarity determining region (CDR) 3 having a sequence comprising
 CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
 CC (ADS94940) in the same order and spacing, or an amino acid sequence of
 CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
 CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
 CC disease; and (3) a composition comprising a carrier and the antibody. The
 CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
 CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
 CC antidiabetic activities, and can be used in gene therapy. The antibody is
 CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
 CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
 CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
 CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
 CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
 CC or haemolytic anaemia. The present sequence represents an immunoglobulin
 CC G1 (IgG1) anti-IFN-gamma light chain constant region, which is used in
 CC the exemplification of the present invention.

XX
 SQ Sequence 107 AA;

Query Match 100.0%; Score 553; DB 8; Length 107;
 Best Local Similarity 100.0%; Pred. No. 4.3e-48;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 DB 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 21
 ADT88871
 ID ADT88871 standard; protein; 107 AA.
 XX
 AC ADT88871;
 XX
 DT 30-DEC-2004 (first entry)
 XX
 XX Human IgG1 antibody constant domain SEQ ID NO:10.
 DE
 KW antibody; IGF-IR; Insulin-like growth factor I receptor; cytostatic;
 KW antibody therapy; tumor; cancer; IgG1.
 XX
 OS Homo sapiens.
 XX
 PN WO2004087756-A2.
 XX
 PD 14-OCT-2004.
 XX
 PF 01-APR-2004; 2004WO-EP003442.
 XX
 PR 02-APR-2003; 2003US-0459837P.
 PR 15-APR-2003; 2003US-0463003P.
 XX
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 XX Graus Y, Kopetzki E, Kuenkele K, Mundigl O, Parren P, Rebers F;
 PI Schumacher R, Van De Winkel J, Van Vugt M;
 PI
 DR WPI; 2004-737667/72.
 DR N-PSDB; ADT88870.
 XX
 XX New antibody binding to insulin-like growth factor I receptor (IGF-IR)
 PT and inhibiting the binding of IGF-I and IGF-II to IGF-IR, useful for
 PT treating cancers of the colon, breast, prostate and lung.
 PT
 XX Disclosure; SEQ ID NO 10; 81pp; English.
 PS
 XX The invention relates to a novel antibody binding to insulin-like growth

CC factor I receptor (IGF-IR) and inhibiting the binding of IGF-I and IGF-II
 CC to IGF-IR. An antibody binding to insulin-like growth factor I receptor
 CC (IGF-IR) and inhibiting the binding of IGF-I and IGF-II to IGF-IR, where
 CC the antibody is of IgG1 isotype and shows a ratio of inhibition of the
 CC binding of IGF-I to IGF-IR to the inhibition of binding of IGF-II to IGF-
 CC IR of 1:3 to 3:1 and induces cell death of 20% or more cells of a
 CC preparation of IGF-IR expressing cells after 24 hours at a concentration
 CC of the antibody of 100 nM by ADCC, is new. An antibody of the invention
 CC has cytostatic activity, and may have a use in antibody therapy. The
 CC methods and compositions of the present invention are useful for the
 CC treatment of tumors and cancers of the colon, breast, prostate and lung
 CC using antibodies against human insulin-like growth factor I receptor (IGF
 CC -IR). The present sequence represents the constant domain of a human IgG1
 CC type antibody.

XX Sequence 107 AA;

Query Match 100.0%; Score 553; DB 8; Length 107;
 Best Local Similarity 100.0%; Pred. No. 4.3e-48;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 QY 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
 Db 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 22

ADTS1583
 ID ADTS1583 standard; protein; 107 AA.

XX ADTS1583;

XX 13-JAN-2005 (first entry)

XX Light chain constant region of human Hu1D10-IgG2M3.

XX Human; antibody; immunoglobulin G; IgG; light chain constant region; CL;
 KW FcRn binding affinity; serum half-life; dactilizumab; fontolizumab;
 KW visilizumab; M200; cancer; inflammatory disorder; asthma;
 KW autoimmune disease; viral infection; cytostatic; antiinflammatory;
 KW antischmatic; immunosuppressive; virucide.

XX Homo sapiens.

XX WO2004092219-A2.

XX 28-OCT-2004.

XX 09-APR-2004; 2004WO-US011213.

XX 10-APR-2003; 2003US-0462014P.

XX 03-JUN-2003; 2003US-0475762P.

XX 29-AUG-2003; 2003US-049048P.

XX 15-OCT-2003; 2003US-00687118.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Hinton PR, Taurushita N, Tso JY, Vasquez M;

XX WPI; 2004-758341/74.

XX New modified antibodies of class IgG that have altered binding affinities
 PT for FcRn or altered serum half-lives, useful for diagnosing or treating
 PT for e.g. cancer, inflammation, autoimmune diseases or viral infections.

PS Disclosure; SEQ ID NO 9; 157pp; English.

XX The present invention relates to a modified human antibody of class

CC immunoglobulin G (IgG) where at least one amino acid residue from the

CC heavy chain constant (CH) region selected from amino acid residues 250,
 CC 314 and 428 is different from that present in an unmodified class IgG
 CC antibody, and where the FcRn binding affinity and/or serum half-life of
 CC the modified antibody is altered relative to that of the unmodified
 CC antibody. The numbering of the residues in the heavy chain is that of the
 CC EU index. Also disclosed are methods of modifying an antibody of class
 CC IgG and producing the modified antibody cited, and a pharmaceutical
 CC composition comprising the above modified immunoglobulins, proteins and
 CC other bioactive molecules having altered half-lives. The unmodified or
 CC naturally occurring class IgG antibody is selected from dactilizumab,
 CC fontolizumab, visilizumab and M200. The amino acid residue 250 from the
 CC heavy chain constant region is glutamic acid or glutamine, or the amino
 CC acid residue 428 from the heavy chain constant region is phenylalanine or
 CC leucine. Alternatively, the amino acid residue 250 from the heavy chain
 CC constant region is glutamic acid and the amino acid residue 428 from the
 CC heavy chain constant region is phenylalanine, or the amino acid residue
 CC 250 from the heavy chain constant region is glutamine and the amino acid
 CC residue 428 from the heavy chain constant region is phenylalanine, or the
 CC amino acid residue 250 from the heavy chain constant region is glutamine
 CC and the amino acid residue 428 from the heavy chain constant region is
 CC leucine. The modified therapeutic antibody of class IgG has an in vivo
 CC elimination half-life of at least 1.3-fold longer than that of the
 CC corresponding unmodified class IgG antibody. The composition and methods
 CC of the invention are useful for various diagnostic and therapeutic
 CC purposes, especially in the treatment of cancer, inflammatory disorders
 CC (e.g. asthma), autoimmune diseases or viral infections. The present
 CC sequence represents a light chain constant (CL) region of a human IgG
 CC antibody.

XX Sequence 107 AA;

Query Match 100.0%; Score 553; DB 8; Length 107;

Best Local Similarity 100.0%; Pred. No. 4.3e-48;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107

Db 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 23

ADU68013

ID ADU68013 standard; protein; 107 AA.

XX AC ADU68013;

XX 10-FEB-2005 (first entry)

XX Mouse anti-PSMA antibody deJ591 light chain constant region.

XX antibody; antibody engineering; antibody therapy; prostate tumor;
 KW cytostatic; prostate specific membrane antigen; PSMA;
 KW light chain constant region; mutein.

OS Mus musculus.

OS Synthetic.

XX WO2004098535-A2.

XX 18-NOV-2004.

XX 03-MAR-2004; 2004WO-US006586.

XX 03-MAR-2003; 2003US-00379838.

XX 30-MAY-2003; 2003US-00449379.

XX (MILL-) MILLENNIUM PHARM INC.

XX Horvath CJ, Webb IJ;

XX WPI; 2004-805058/79.
DR N-PSDB; ADU68012.
XX
PT Use of an anti-prostate specific membrane antigen (anti-PSMA) antibody or
PT antigen-binding fragment for treating prostate cancer or monitoring a
PT patient receiving an anti-PSMA antibody to treat prostate cancer.
XX
PS Disclosure; SEQ ID NO 134; 284pp; English.
XX
CC The invention relates to the use of an anti-prostate specific membrane
CC antigen (anti-PSMA) antibody or antigen-binding fragment for treating
CC prostate cancer, monitoring a patient receiving an anti-PSMA antibody to
CC treat prostate cancer, or selecting a patient for treatment with an anti-
CC PSMA antibody. Also included are a method of treating prostate cancer in
CC a subject, a method of monitoring a patient receiving an anti-PSMA
CC antibody to treat prostate cancer and a method of selecting a patient for
CC treatment with an anti-PSMA antibody. Also disclosed are anti-PSMA
CC antibodies. The antibody or antigen-binding fragment is a human antibody
CC (or antigen-binding fragment), a modified antibody (or an antigen-binding
CC fragment). The modified antibody is selected from CDR-grafted antibody,
CC humanized antibody, deimmunized antibody, or antigen binding fragments.
CC The modified antibody or antigen-binding fragment has one or more CDRs
CC (complementarity determining region) from a mouse monoclonal antibody
CC selected from J591, J415, J533, or E99. The anti-PSMA antibody or antigen
CC binding fragment is useful for treating prostate cancer, monitoring a
CC patient receiving an anti-PSMA antibody to treat prostate cancer, or
CC selecting a patient for treatment with an anti-PSMA antibody. The present
CC sequence is a deimmunized light chain constant region from one of the
CC mouse monoclonal antibodies listed above.
XX
SQ Sequence 107 AA;

Query Match 100.0%; Score 553; DB 8; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYISLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYISLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 24
ADW08870
ID ADW08870 standard; protein; 107 AA.
XX
AC ADW08870;
XX
DT 07-APR-2005 (first entry)
XX
DE IGF-IR antibody 22 constant region domain, SEQ ID 8.
XX
XX Cytostatic; Antibody; antibody therapy; antibody production;
KW insulin-like growth factor I receptor; IGF-IR; constant region.
XX
XX Homo sapiens.
OS
XX US2005008642-A1.
FN
XX 13-JAN-2005.
PD
XX 08-JUL-2004; 2004US-00886838.
PF
XX 10-JUL-2003; 2003EP-00015526.
PR
XX (GRAU/) GRAUS Y.
PA (KOPETZKI) KOPETZKI E.
PA (KUENKELE) KUENKELE K.
PA (MUNDIGL) MUNDIGL O.

PA (PARR/) PARRIN P.
PA (REBE/) REBERS F.
PA (SCHU/) SCHUMACHER R.
PA (VMIN/) VAN DE WINKEL J.
XX (VUGT/) VUGT M V.
PI Graus Y, Kopetzki E, Kuenkele K, Mundigl O, Parren P, Rebers F;
PI Schumacher R, Van De Winkel J, Vugt MW;
XX WPI; 2005-099927/11.
DR N-PSDB; ADW08869.
XX
PT Novel antibody capable of inhibiting binding of insulin like growth
PT factor I (IGF-I) and IGF-II to IGF-I receptor, useful for treating
PT cancer.
XX
PS Disclosure; SEQ ID NO 8; 38pp; English.
XX
CC The present invention relates to antibodies 18 and 22, (A1) which bind to
CC insulin like growth factor I receptor (IGF-IR). The antibody is capable
CC of inhibiting the binding of IGF-I and IGF-II to IGF-IR, and is of the
CC IGI isotype. The antibodies induce cell death of 20% or more cells of a
CC preparation of IGF-IR expressing cells by antibody dependent cellular
CC toxicity (ADCC). (A1) are useful for making a pharmaceutical composition
CC which inhibits the binding of IGF-I and IGF-II to IGF-IR, which involves
CC combining (A1) with a carrier. (A1) is also useful for treating a patient
CC in need of an antitumor therapy, which involves administering (A1) alone
CC or in combination with a cytotoxic agent, its prodrug or cytotoxic
CC radiotherapy to the patient. The present sequence is the constant region
CC of antibody 22.
XX
SQ Sequence 107 AA;

Query Match 100.0%; Score 553; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYISLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYISLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 25
ADW07454
ID ADW07454 standard; protein; 107 AA.
XX
AC ADW07454;
XX
DT 07-APR-2005 (first entry)
XX
DE Human kappa light chain constant domain.
XX
XX Blood-clotting; light chain constant region; inflammation;
KW antiinflammatory; antibody; tissue factor; sepsis;
KW disseminated intravascular coagulation; anticoagulant;
KW hematological disease; thrombosis; lung injury; respiratory-gen.;
KW respiratory distress syndrome; immunosuppressive; Antibacterial;
KW Antiarthritic; Antianemic; anemia; rheumatoid arthritis;
KW glomerulonephritis; multiple sclerosis; psoriasis; sjogren's syndrome;
KW inflammatory bowel disease.
XX
OS Homo sapiens.
XX
XX WO2005004793-A2.
FN
XX 20-JAN-2005.
PD
XX 04-JUN-2004; 2004WO-US017900.
PF
XX

PR 19-JUN-2003; 2003US-0480254P.
PR 22-JAN-2004; 2004US-0538892P.
PA (SUNO-) SUNOL MOLECULAR CORP.
XX Jiao J, Wong HC, Egan JO;
PI WPI; 2005-091964/10.
XX
XX Preventing or treating sepsis or inflammation in mammals comprises
PT administering a humanized or chimeric antibody that binds to a human
PT tissue factor to form a complex in which factor X or IX binding to the
PT complex is inhibited.
XX
XX Example 1; Fig 5; 109pp; English.
PS
XX The invention relates to preventing or treating a sepsis or inflammatory
CC disease in a mammal comprising administering to the mammal a therapeutic
CC amount of at least one humanized antibody, chimeric antibody, or their
CC fragment that binds specifically to tissue factor (TF) to form a complex,
CC where factor X or IX binding to the complex is inhibited and the
CC administration prevents or treats the sepsis in the mammal. Also included
CC are a kit for performing the above method and reducing an inflammatory
CC cytokine production in a mammal. The inflammatory disease is associated
CC with arthritis (preferably rheumatoid arthritis), glomerulonephritis,
CC multiple sclerosis, psoriasis, Sjogren's syndrome, or inflammatory bowel
CC disease. The method also treats or prevents a sepsis-induced anemia or a
CC sepsis-related condition in a mammal, where the sepsis-related condition
CC is DIC, fibrin deposition, thrombosis, lung injury, or sepsis-associated
CC renal disorder. The lung injury is acute lung injury (ALI) or acute
CC respiratory distress syndrome (ARDS). The sepsis-associated renal
CC disorder is acute tubular necrosis. The methods and kit are useful for
CC preventing or treating sepsis or sepsis-related conditions (e.g. DIC or
CC anemia) or inflammatory diseases (e.g. arthritis). The humanized
CC antibodies are based on the chimeric antibody ch36 which comprises the
CC light and heavy chain variable regions (VL or VH) of an anti-TF antibody
CC fused to the human IgG4 heavy and kappa light constant regions. The CDRs
CC (complementarity determining region) and FRs (framework regions) are then
CC humanized. The present sequence represents the human light chain constant
CC region used to make the chimeric antibody.
XX
XX Sequence 107 AA;
Query Match 100.0%; Score 553; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48; Indels 0; Gaps 0;
Matches 107; Conservative 0; Mismatches 0;
QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYSLSSLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSSLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
RESULT 26
ID ADW24748
XX ADW24748 standard; protein; 107 AA.
XX AC ADW24748;
XX
DT 07-APR-2005 (first entry)
XX
XX Variable kappa light chain constant region version 1.
DE
XX cytostatic; gene therapy; antibody; light chain variable region;
KW diagnosis; pharmaceutical; tumor; cytostatic; neoplasm.
XX
XX Homo sapiens.
OS
XX WO2005005604-A2.
XX
XX

PD 20-JAN-2005.
XX
XX 21-JUN-2004; 2004WO-US019783.
XX
XX 30-JUN-2003; 2003US-0483654P.
XX
XX (CENZ) CENTOCOR INC.
XX
XX Lu J;
XX
XX WPI; 2005-092074/10.
DR
XX
XX New target Ig derived protein comprising a target binding sequence and a
PT portion of a heavy or light chain variable or constant region, useful in
PT preparing a composition for diagnosing or treating a target related
PT condition, e.g. tumor.
XX
XX Claim 4; SEQ ID NO 41; 321pp; English.
XX
XX The invention describes an isolated target immunoglobulin (Ig) derived
CC protein comprising a target binding sequence and a portion of a heavy or
CC light chain variable region or a portion of a heavy or light chain
CC constant region and optionally a substitution, insertion or deletion as
CC given in the specification. An isolated target Ig derived protein
CC comprises a target binding sequence and a portion of a heavy or light
CC chain variable region comprising 10-125 or 10-75 contiguous amino acids
CC of the sequence comprising 91-132 or 77-107 amino acids, respectively, or
CC its FR1, FR2, FR3 or FR4 fragment, or a portion of a heavy or light chain
CC constant region comprising 10-384 or 10-107 contiguous amino acids of the
CC sequence comprising 326-497 or 107 amino acids, respectively, or its FR1,
CC FR2, FR3, FR4, CH1, CH2, CH3, hinge1, hinge2, hinge3 or hinge4 fragment
CC and optionally a substitution, insertion or deletion as given in the
CC specification. Also described are: an isolated nucleic acid encoding an
CC isolated target Ig derived protein; a vector comprising the isolated
CC nucleic acid; a prokaryotic or eukaryotic host cell comprising the
CC isolated nucleic acid; a method for producing an isolated target Ig
CC derived protein; a composition comprising the isolated target Ig derived
CC protein and a carrier or diluent; an anti-idiotypic Ig derived protein
CC that specifically binds target Ig derived protein; a method for
CC diagnosing or treating a target related condition in a cell, tissue,
CC organ or animal; a medical device comprising target Ig derived protein
CC that is suitable for contacting or administering the target Ig derived
CC protein; an article of manufacture for human pharmaceutical or diagnostic
CC use, comprising packaging material and a container comprising a solution
CC or lyophilized form of target Ig derived protein; and a method for
CC producing an isolated mammalian target Ig derived protein. The target Ig
CC derived protein is useful in preparing a composition for diagnosing or
CC treating a target related condition in a cell, tissue, organ or animal,
CC e.g. tumor. This is the amino acid sequence of variable kappa light chain
CC constant region. Note: This sequence differs from the version given in
CC figure 41 in which the X residues have been expanded to represent the
CC whole CDR regions.
XX
XX Sequence 107 AA;
Query Match 100.0%; Score 553; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48; Indels 0; Gaps 0;
Matches 107; Conservative 0; Mismatches 0;
QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYSLSSLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSSLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
RESULT 27
ID ADW24790
XX ADW24790 standard; protein; 107 AA.
XX AC ADW24790;
XX

ADY26693
ID ADY26693 standard; protein; 107 AA.
AC ADY26693;
XX
XX 19-MAY-2005 (first entry)
DT
XX Human anti-NGF-antibody light chain SEQ ID NO 8.
DE
XX analgesic; gene therapy; antibody engineering; pharmaceutical; pain;
KW neurological disease; NGF; nerve growth factor; light chain.
XX
XX Homo sapiens.
OS
XX WO2005019266-A2.
FN
XX 03-MAR-2005.
PD
XX 15-JUL-2004; 2004WO-US022876.
PF
XX 15-JUL-2003; 2003US-0487431P.
PR
XX (AMGE-) AMGEN INC.
PA
XX Wild KD, Treanor JJS, Huang H, Inoue H, Zhang TJ, Martin F;
PI
XX WPI; 2005-202606/21.
DR N-PSDB; ADY26692.
XX
XX New human anti-nerve growth factor (NGF) neutralizing antibodies useful
PT for manufacturing a medicament for treating painful disorders (e.g. acute
PT pain) or conditions associated with increased expression or sensitivity
PT to NGF.
XX
XX Disclosure; SEQ ID NO 8; 190pp; English.
PS
XX The invention describes an isolated human antibody that interacts with or
CC binds specifically to human nerve growth factor (NGF) and neutralize the
CC function of NGF. Also described are: methods of treating a condition
CC caused by increased expression of NGF or increased sensitivity to NGF in
CC a patient; methods for detecting NGF in a biological sample; an NGF
CC specific binding agent comprising any of the 59 amino acid sequences
CC comprising, for e.g. 123, 107 or 14 amino acids, as mentioned in the
CC specification, and where the binding agent can bind to NGF; a
CC pharmaceutical composition comprising a pharmaceutical carrier and a
CC therapeutic amount of the antibody or binding agent cited above; or a
CC medicament for treating a painful disorder or condition associated with
CC increased expression of NGF or increased sensitivity to NGF, the
CC medicament comprising a pharmaceutical amount of a monoclonal antibody or
CC its immunologically functional immunoglobulin fragment, or pharmaceutical
CC salts of the monoclonal antibody or the fragment, where the monoclonal
CC antibody is at least one of the monoclonal antibody cited above, and a
CC pharmaceutical carrier, diluent or excipient; a nucleic acid molecule or
CC polynucleotide that encodes the above antibody or binding agent; an
CC isolated cell line that produces the above antibody or binding agent; an
CC expression vector comprising the above polynucleotide; and a host cell
CC comprising the nucleic acid or expression vector. The composition
CC (including the antibody) and methods are useful for manufacturing a
CC medicament for treating a painful disorder (e.g. acute pain, dental pain,
CC or pain from trauma or cancer), or a condition associated with increased
CC expression of NGF or increased sensitivity to NGF. This is the amino acid
CC sequence of a human NGF antibody light chain.
XX
XX Sequence 107 AA;
SQ
Query Match 100.0%; Score 553; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVEIFPPSDEQLKSGTASVTVCLINNFPYREAKVQMKVDNALQSGNSQESVTRQD 60
DB 1 RTVAAPSVEIFPPSDEQLKSGTASVTVCLINNFPYREAKVQMKVDNALQSGNSQESVTRQD 60

QY 61 SKDSTYSLSSTLTSLKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYSLSSTLTSLKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
XX
XX RESULT 30
ADY74804
ID ADY74804 standard; protein; 107 AA.
XX
XX AC ADY74804;
XX
XX 02-JUN-2005 (first entry)
DT
XX Human light chain constant region.
DE
XX Antibody; protein engineering; light chain; rheumatoid arthritis;
KW antiarthritic; antirheumatic; immune disorder; inflammation;
KW musculoskeletal disease; IL-1 receptor; antiinflammatory; osteopathic;
KW antibody therapy; osteoarthritis.
XX
XX OS Homo sapiens.
XX
XX WO2005023872-A1.
FN
XX 17-MAR-2005.
PD
XX 09-SEP-2004; 2004WO-EP010047.
PF
XX 10-SEP-2003; 2003US-0501681P.
PR
XX 23-DEC-2003; 2003EP-00029659.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA
XX Bartke I, Carr F, Chizzonite A, Eugui E, Fertig G, Hamilton A;
PI Lanzendoerfer M, Rueger P, Schumacher R, Truitt T;
XX
XX WPI; 2005-223354/23.
DR
XX Antibody binding to human interleukin-1 receptor (IL-1R) and inhibiting
PT the binding of human interleukin-1 (IL-1) to IL-1R, useful for
PT manufacturing a pharmaceutical composition for treating inflammatory
PT diseases, e.g. rheumatoid arthritis.
XX
XX Claim 4; SEQ ID NO 29; 83pp; English.
PS
XX The invention relates to an antibody binding to human interleukin-1
CC receptor (IL-1R) and inhibiting the binding of human IL-1 to IL-1R, for
CC the inhibition of IL-1 mediated secretion of IL-8 and IL-6 in human
CC fibroblast cells like MRC5 (ATCC CCL 171). Also included are a
CC pharmaceutical composition comprising the antibody in a pharmaceutical
CC amount, hybridoma cell lines MAKn-IL-1R12D8 (DSM ACC 2601), a method for
CC the manufacture of a pharmaceutical composition comprising an amount of
CC the antibody, a nucleic acid encoding a polypeptide capable of assembling
CC together with the respectively other antibody chain below, (where the
CC polypeptide is either an antibody heavy chain comprising as CDRs CDR1 (aa
CC 45-54), CDR2 (aa 69-84), and CDR3 (aa 117-123) of ADY74776 or an antibody
CC light chain comprising as CDRs CDR1 (aa 43-57), CDR2 (aa 73-79), and CDR3
CC (aa 112-120) of ADY74777, an expression vector comprising the nucleic
CC acid capable of expressing the nucleic acid in a prokaryotic or
CC eukaryotic host cell, a prokaryotic or eukaryotic host cell comprising
CC the vector, production of a polypeptide binding to IL-1R (and inhibiting
CC the binding of IL-1 to IL-1R) and manufacturing the antibody. The
CC antibody is chimeric, humanized or T-cell epitope deleted. The antibody
CC is useful for the manufacture of a pharmaceutical composition for
CC treatment of a patient in need of an anti-inflammatory therapy. It is
CC useful for the treatment of inflammatory diseases including rheumatoid
CC arthritis and osteoarthritis. The present sequence represents the human
CC light chain constant region used to make chimeric antibodies with the rat
CC anti-IL1R antibody.
XX
XX Sequence 107 AA;
SQ
Query Match 100.0%; Score 553; DB 9; Length 107;

CC	isolated nucleic acid vector comprising an isolated nucleic acid encoding an amyloid antibody, (v) a prokaryotic or eukaryotic host cell comprising an isolated nucleic acid encoding an amyloid antibody, (vi) a method of producing at least one amyloid antibody, (vii) a composition comprising at least one of any of the isolated mammalian amyloid antibodies mentioned, and at least one pharmaceutical carrier or diluent, (viii) an anti-idiotypic antibody or fragment that specifically binds at least one of the amyloid antibodies mentioned, (ix) a method of diagnosing or treating an amyloid related condition in a cell, tissue, organ or animal, comprising contacting or administering a composition comprising at least one of the antibodies mentioned, with, or to, the cell, tissue, organ or animal, (x) a medical device comprising at least one amyloid antibody mentioned, where the device is suitable for contacting or administering at least one amyloid antibody, (xi) an article of manufacture for human pharmaceutical or diagnostic use, comprising packaging material and a container comprising a solution or a lyophilized form of at least one of the amyloid antibodies mentioned, and (xii) a method of producing at least one of the isolated mammalian amyloid antibodies, comprising providing a host cell or transgenic animal or transgenic plant or plant cell capable of expressing the antibody in recoverable amounts. The methods and compositions of the present invention are useful for producing therapeutic compositions and devices for treating amyloid-associated disorders, such as Alzheimer's disease, cancer, allergies, autoimmune disease, Parkinson's disease, AIDS, multiple sclerosis, migraine, dementia and infections. This sequence represents a light chain constant region useful in the antibody of the invention.
CC	Sequence 107 AA;
SQ	
CC	Query Match 100.0%; Score 553; DB 9; Length 107;
CC	Best Local Similarity 100.0%; Pred. No. 4.3e-48;
CC	Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB	1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY	61 SKDSTYLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
DB	61 SKDSTYLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
RESULT 32	
ADZ08946	
ID	ADZ08946 standard; protein; 107 AA.
XX	
AC	ADZ08946;
XX	
DT	16-JUN-2005 (first entry)
XX	
DE	Amyloid antibody, light chain constant region prototype, Igkappa.
XX	
KW	amyloid; antibody engineering; antibody production;
KW	amyloid-associated disorder; Alzheimer's disease; cancer; allergy;
KW	autoimmune disease; Parkinson's disease;
KW	acquired immune deficiency syndrome; multiple sclerosis; migraine;
KW	dementia; infection; neurotropic; neuroprotective; cytosstatic;
KW	antiallergic; immunosuppressive; antiparkinsonian; antimigraine;
KW	antimicrobial; anti-HIV; light chain constant region.
XX	
OS	Mammalia.
OS	Synthetic.
XX	
PN	WO2005028511-A2.
XX	
PD	31-MAR-2005.
XX	
PF	26-MAR-2004; 2004WO-US009522.
XX	
PR	28-MAR-2003; 2003US-0458469P.
PR	28-MAR-2003; 2003US-0458474P.
PR	28-MAR-2003; 2003US-0458509P.
PR	28-MAR-2003; 2003US-0458510P.
PA	(CENZ) CENTOCOR INC.
PA	(MERC/) MERCKEN M.
PA	(BENS/) BENSON J M.
XX	
FI	Mercken M, Benson JM;
XX	
DR	WPI; 2005-242565/25.
XX	
PT	New isolated mammalian anti-amyloid antibodies useful for treating
PT	amyloid-associated disorders, such as Alzheimer's disease, cancer,
PT	allergies, autoimmune disease, Parkinson's disease, multiple sclerosis,
PT	migraine and dementia.
XX	
PS	Disclosure; SEQ ID NO 40; 306pp; English.
XX	
CC	The invention relates to at least one isolated mammalian amyloid antibody
CC	comprising at least one variable region comprising at least one heavy
CC	chain and at least one light chain, of a fully defined sequence of SEQ ID
CC	NOS: 48, 49, 59, 60, 69, 70, 79 and 80, respectively. Also described are:
CC	(i) at least one isolated mammalian amyloid antibody that binds to the
CC	same region of an amyloid polypeptide as an antibody comprising at least
CC	one heavy chain or light chain complementarity determining region (CDR)
CC	having the amino acid sequence of at least one of SEQ ID NO: 73-78, (ii)
CC	at least one isolated mammalian amyloid antibody, comprising at least one
CC	human CDR, where the antibody specifically binds at least one epitope
CC	selected from amino acids 2-7, 3-8, 33-42, or 34-40 of a fully defined
CC	sequence of 42 amino acids (SEQ ID NO: 50), (iii) an isolated nucleic
CC	acid encoding at least one of any of the isolated mammalian amyloid
CC	antibodies mentioned and having at least one human CDR of a fully defined
CC	sequence of SEQ ID NO: 51, 52, 61, 62, 71, 72, 81 and 82, (iv) an

XX (CENZ) CENTOCOR INC.
PA (MERC/) MERCKEN M.
PA (BENS/) BENSON J M.
XX
PI Mercken M, Benson JM;
XX
XX WPI; 2005-242565/25.
XX
XX New isolated mammalian anti-amyloid antibodies useful for treating
PT amyloid-associated disorders, such as Alzheimer's disease, cancer,
PT allergies, autoimmune disease, Parkinson's disease, multiple sclerosis,
PT migraine and dementia.
XX
XX Disclosure; Fig 40; 306pp; English.
XX
XX The invention relates to at least one isolated mammalian amyloid antibody
CC comprising at least one variable region comprising at least one heavy
CC chain and at least one light chain, of a fully defined sequence of SEQ ID
CC NOS: 48, 49, 59, 60, 69, 70, 79 and 80, respectively. Also described are:
CC (i) at least one isolated mammalian amyloid antibody that binds to the
CC same region of an amyloid polypeptide as an antibody comprising at least
CC one heavy chain or light chain complementarity determining region (CDR)
CC having the amino acid sequence of at least one of SEQ ID NO: 73-78, (ii)
CC at least one isolated mammalian amyloid antibody, comprising at least one
CC human CDR, where the antibody specifically binds at least one epitope
CC selected from amino acids 2-7, 3-8, 33-42, or 34-40 of a fully defined
CC sequence of 42 amino acids (SEQ ID NO: 50), (iii) an isolated nucleic
CC acid encoding at least one of any of the isolated mammalian amyloid
CC antibodies mentioned and having at least one human CDR of a fully defined
CC sequence of SEQ ID NO: 51, 52, 61, 62, 71, 72, 81 and 82, (iv) an
CC isolated nucleic acid vector comprising an isolated nucleic acid encoding
CC an amyloid antibody, (v) a prokaryotic or eukaryotic host cell comprising
CC an isolated nucleic acid encoding an amyloid antibody, (vi) a method of
CC producing at least one amyloid antibody, (vii) a composition comprising
CC at least one of any of the isolated mammalian amyloid antibodies
CC mentioned, and at least one pharmaceutical carrier or diluent, (viii) an
CC anti-idiotypic antibody or fragment that specifically binds at least one
CC of the amyloid antibodies mentioned, (ix) a method of diagnosing or
CC treating an amyloid related condition in a cell, tissue, organ or animal,
CC comprising contacting or administering a composition comprising at least
CC one of the antibodies mentioned, with, or to, the cell, tissue, organ or
CC animal, (x) a medical device comprising at least one amyloid antibody
CC mentioned, where the device is suitable for contacting or administering
CC at least one amyloid antibody, (xi) an article of manufacture for human
CC pharmaceutical or diagnostic use, comprising packaging material and a
CC container comprising a solution or a lyophilized form of at least one of
CC the amyloid antibodies mentioned, and (xii) a method of producing at
CC least one of the isolated mammalian amyloid antibodies, comprising
CC providing a host cell or transgenic animal or transgenic plant or plant
CC cell capable of expressing the antibody in recoverable amounts. The
CC methods and compositions of the present invention are useful for
CC producing therapeutic compositions and devices for treating amyloid-
CC associated disorders, such as Alzheimer's disease, cancer, allergies,
CC autoimmune disease, Parkinson's disease, AIDS, multiple sclerosis,
CC migraine, dementia and infections. This sequence represents a light chain
CC constant region prototype useful in the antibody of the invention.
XX
SQ Sequence 107 AA;

Query Match 100.0%; Score 553; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSSLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSSLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 33
ADZ44472
ID ADZ44472 standard; protein; 107 AA.
XX
XX AC ADZ44472;
XX
XX DT 30-JUN-2005 (first entry)
XX
XX DE Human immunoglobulin light chain constant region - SEQ ID 71.
XX
XX KW hematological disease; bone disease; arthropathy; cardiovascular disease;
KW cardiovascular-gen.; dermatological disorders; dermatological;
KW endocrine disease; metabolic disorder; gastrointestinal disease;
KW gastrointestinal-gen.; gynecological disorder; psychiatric disorder;
KW light chain constant region; antibody.
XX
XX OS Homo sapiens.
XX
XX PN WO2005032460-A2.
XX
XX PD 14-APR-2005.
XX
XX PF 03-SEP-2004; 2004WO-US028976.
XX
XX PR 30-SEP-2003; 2003US-0507349P.
XX
XX PA (CENZ) CENTOCOR INC.
XX
XX PI Heavner G, Knight DM, Scallion B, Ghrayeb J, Nesspor TC, Huang C;
XX WPI; 2005-285320/29.
XX
XX PT New erythropoietin (EPO) hinge core mimetibody polypeptide and encoding
PT nucleic acid molecule useful for diagnosing, preventing or treating EPO-
PT related conditions, e.g. hematological, cardiovascular or oncological
PT disorders.
XX
PS Disclosure; SEQ ID NO 71; 167pp; English.
XX
CC The invention comprises the amino acid sequences of erythropoietin (EPO)
CC mimetic hinge core mimetibody polypeptides. The EPO hinge core mimetibody
CC polypeptides of the invention are useful for diagnosing, treating or
CC preventing EPO ligand-related conditions, such as: hematological
CC disorders, bone or joint disorders, cardiovascular disorders,
CC dermatological disorders, endocrine or metabolic disorders,
CC gastrointestinal disorders, gynecological disorders, oncological
CC disorders and psychiatric disorders. The present amino acid sequence
CC represents a human immunoglobulin light chain constant region.
XX
SQ Sequence 107 AA;

Query Match 100.0%; Score 553; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSSLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSSLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 34
AEA25951
ID AEA25951 standard; protein; 107 AA.
XX
XX AC AEA25951;
XX
XX DT 28-JUL-2005 (first entry)
XX
XX DE Human immunoglobulin constant region, SEQ ID No:34.

XX antibody; antibody production; immunoglobulin; transformation;
KW expression; heavy chain constant region; light chain constant region.
XX Homo sapiens.
XX WO2005047335-A1.
XX 26-MAY-2005.
XX 13-NOV-2004; 2004WO-KR002943.
XX 13-NOV-2003; 2003KR-00080299.
XX (HANN-) HANMI PHARM CO LTD.
XX Jung SY, Kim JS, Park YJ, Choi K, Kwon SC, Lee GS;
XX WPI; 2005-372351/38.
XX Producing an immunoglobulin constant region by transforming a prokaryotic
PT cell with a vector encoding an E. coli-derived signal sequence and an
PT immunoglobulin constant region.
XX Claim 9; SEQ ID NO 34; 92pp; English.
XX The invention relates to a method of producing an immunoglobulin constant
CC region on a large scale. The method comprises transforming a prokaryotic
CC cell with a recombinant expression vector including a nucleotide sequence
CC encoding an E. coli-derived signal sequence and a nucleotide sequence
CC encoding an immunoglobulin constant region, culturing a resulting
CC transformant, and isolating and purifying the immunoglobulin constant
CC region expressed by the transformant. Also described is an immunoglobulin
CC constant region prepared by the method above. The immunoglobulin constant
CC region is a constant region from IgG, IgA, IgM, IgE, IgD, or their
CC combinations and hybrids. The IgG is a constant region from IgG1, IgG2,
CC IgG3, IgG4, or their combinations and hybrids, preferably an IgG4
CC constant region, i.e. a human aglycosylated IgG4 constant region. The
CC immunoglobulin constant region is composed of one to four domains, e.g.
CC CH1, CH2, CH3, and CH4 domains, where the immunoglobulin constant region
CC further comprises a hinge region. The recombinant expression vector
CC comprises a nucleotide sequence encoding a heavy chain constant region
CC and a nucleotide sequence encoding a light chain constant region. The
CC immunoglobulin constant region has a sequence of 109-330 amino acids (SEQ
CC ID NOS: 21-25, 27, 29, 30, 34 or 35). The E. coli-derived signal sequence
CC is a signal sequence, e.g. alkaline phosphatase, penicillinase, Ipp, heat
CC -stable enterotoxin II, LamB, PhoE, PelB, OmpA or maltose binding
CC protein, where the heat-stable enterotoxin II signal peptide comprises
CC any of the 11 sequences of given in the specification (SEQ ID NOS: 36-
CC 46). The method of the invention is useful for the mass production of an
CC immunoglobulin constant region. This sequence represents a human
CC immunoglobulin constant region that can be produced by the method of the
XX invention.
XX Sequence 107 AA;
Query Match 100.0%; Score 553; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Qy 61 SKDSTYSLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107
RESULT 35
ID AEA16547 standard; protein; 107 AA.
XX

AC AEA16547;
XX 28-JUL-2005 (first entry)
XX Human MCP-1 immunoglobulin heavy chain constant region, Ig-kappa-c.
XX monocyte chemoattractant protein-1; MCP-1; immunoglobulin;
KW immunosuppressive; immunostimulant; cardiovascular-Gen.; antimicrobial;
KW cytostatic; neuroprotective; vulnery; antirheumatic; Muscle relaxant;
KW analgesic; anesthetic; antipsoriatic; antithyroid; antidiarrheic;
KW antitussive; antiemetic; antiulcer; laxative; anticoagulant; metabolic;
KW cytostatic; antidepressant; antimanic; neuroleptic; tranquilizer;
KW hypnotic; CNS-Gen.; antiasthmatic; auditory; immune disorder;
KW cardiovascular disease; infectious disease; malignant disease;
KW neurological disease; wound healing; trauma.
XX Homo sapiens.
XX WO2005044200-A2.
XX 19-MAY-2005.
XX 05-NOV-2004; 2004WO-US037024.
XX 05-NOV-2003; 2003US-0517370P.
XX (CENZ) CENTOCOR INC.
XX Yan L, Nakada MT, Das A;
XX WPI; 2005-356202/36.
XX Treating at least one human monocyte chemoattractant protein-1 (MCP-1)
PT related pathology, e.g. immune, neurologic, or cardiovascular diseases,
PT comprises administering at least one MCP-1 immunoglobulin-derived protein
PT to the animal.
XX Disclosure; SEQ ID NO 40; 96pp; English.
XX The invention relates to a novel method for treating at least one human
CC monocyte chemoattractant protein-1 (MCP-1) related pathology. The method
CC comprises contacting or administering a therapeutically effective amount
CC of at least one MCP-1 immunoglobulin (Ig) derived protein to the cells,
CC tissue or animal, where the MCP-1 Ig derived protein inhibits a
CC biological activity of MCP-1, in vivo, in vitro or in situ. The method
CC and MCP-1 composition have the following activities: immunosuppressive,
CC immunostimulant, cardiovascular-Gen., antimicrobial, cytostatic,
CC neuroprotective, vulnery, antirheumatic, muscle-relaxant, analgesic,
CC anesthetic, sedative, antipsoriatic, antithyroid, antidiarrheic,
CC antitussive, antiemetic, antiulcer, laxative, anticoagulant, metabolic,
CC cytostatic, antidepressant, antimanic, neuroleptic, tranquilizer,
CC hypnotic, CNS-Gen., antiasthmatic, and auditory. The method and
CC composition are useful for treating at least one human MCP-1 related
CC pathology, such as an immune related disease, a cardiovascular disease,
CC an infectious disease, a malignant disease, a neurological disease, or
CC any wound or trauma. This sequence represents a human monocyte
CC chemoattractant protein-1 immunoglobulin derived protein of the
CC invention.
XX Sequence 107 AA;
Query Match 100.0%; Score 553; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Qy 61 SKDSTYSLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107

```
RESULT 36
AEA45321
ID AEA45321 standard; protein; 107 AA.
XX
AC AEA45321;
XX
DT 11-AUG-2005 (first entry)
XX
DE Apolipoprotein E C-terminal domain related sequence, SEQ ID 519.
XX
KW Neuroprotective; Nootropic; Antidiabetic; Endocrine-Gen.; Nephrotropic;
KW Antiparkinsonian; Anticonvulsant; Respiratory-Gen; Apolipoprotein E;
KW Alzheimers disease; amyloidosis; Parkinsons disease; Huntingtons chorea;
KW Kuru; Dementia; non-insulin dependent diabetes; Down syndrome;
KW Spongiform encephalopathy; Creutzfeldt Jakob disease;
KW motor neurone disease; chronic obstructive pulmonary disease.
XX
OS Homo sapiens.
XX
PN GB2408508-A.
XX
PD 01-JUN-2005.
XX
PF 26-NOV-2004; 2004GB-00026043.
XX
PR 28-NOV-2003; 2003US-0525174P.
XX
PA (ASTR ) ASTRAZENECA AB.
XX
PI (DYAX-) DYAX CORP.
XX
PI Nordstedt C, Goldschmidt T, Henderikx M, Hoet R, Hoogenboom H;
PI Hufton S, Andersson CV, Lindquist J, Sunnemark D, Leonov S;
XX
DR WPI; 2005-408785/42.
XX
PT New human antibody or antibody fragment which binds to a sequence of the
PT C-terminal domain of Apolipoprotein E (ApoE-CTD), useful for
PT manufacturing a medicament for treating or preventing an amyloid disorder
PT e.g. Alzheimers disease.
XX
PS Claim 36; SEQ ID NO 519; 392pp; English.
XX
CC The present invention relates to a human antibody or antibody fragment,
CC which binds to the C-terminal domain of Apolipoprotein E (ApoE-CTD;
CC AEA44803) and also to human plaques. The antibody or its fragment is
CC useful for manufacturing a medicament for treating or preventing an
CC amyloid disorder such as Alzheimers disease, primary systemic
CC amyloidosis, secondary systemic amyloidosis, senile systemic amyloidosis,
CC familial amyloid polynuropathy I, familial amyloid polynuropathy III,
CC familial non-neuropathic amyloidosis, hereditary cerebral amyloid
CC angiopathy, Familial British Dementia, Hemodialysis-related amyloidosis,
CC amyloidosis, injection localized amyloidosis, Medullary carcinoma of the
CC thyroid, Atrial amyloidosis, Familial Danish dementia (PDD), Downs
CC syndrome, Spongiform encephalopathies, Sporadic Creutzfeldt-Jakob
CC disease, Gerstmann-Straussler-Scheinker Disease (GSS), Kuru, Parkinsons
CC disease, Huntingtons disease, Familial amyotrophic lateral sclerosis, and
CC chronic obstructive pulmonary disease. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 107 AA;
XX
Query Match 100.0%; Score 553; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTRQD 60
DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTRQD 60
QY 61 SKDSTYSLSSTLTLSKADYERKHYACEVTHQGLSSPVTKSFNRGEC 107
```

Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Qy 61 SKDSTYSLSTLTLSKADYERKHVYACEVTHOGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYERKHVYACEVTHOGLSSPVTKSFNRGEC 107
RESULT 38
AEA37411
ID AEA37411 standard; protein; 107 AA.
XX AEA37411;
AC AEA37411;
DT 25-AUG-2005 (first entry)
XX Anti-human CD40 antibody 3.1.1 light chain constant region.
DE antibody engineering; cytostatic; vaccine; cancer; CD40; antibody;
KW light chain constant region.
XX Homo sapiens.
OS US2005136055-A1.
PN 23-JUN-2005.
PD 02-DEC-2004; 2004US-00001980.
PF 22-DEC-2003; 2003US-0531639P.
PR 22-DEC-2003; 2003US-0531639P.
XX (PFIZ) PFIZER INC.
PA Gladue RP, Cusmano JD, Bedian V;
XX WPI; 2005-444081/45.
XX Treating cancer in a patient by administering a CD40 agonist antibody or
PT its fragment according to an intermittent dosing regimen of at least two
PT cycles, each cycle comprising a dosing period during and a resting
PT period.
XX Disclosure; SEQ ID NO 4; 18pp; English.
PS The invention relates to a method of treating cancer in a patient by
XX administering a CD40 agonist antibody or its fragment according to an
XX intermittent dosing regimen of at least two cycles, each cycle
XX comprising: (a) a dosing period during which a therapeutically effective
XX amount of the CD40 agonist antibody is administered to the patient and,
XX thereafter; (b) a resting period. The CD40 agonist antibody or its
XX fragment is useful in the manufacture of a medicament for treating cancer
XX in a patient. This sequence corresponds to the constant region of the
XX light chain from the antibody 3.1.1 used in the method of the invention.
XX Sequence 107 AA;
Qy Query Match 100.0%; Score 553; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Qy 61 SKDSTYSLSTLTLSKADYERKHVYACEVTHOGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYERKHVYACEVTHOGLSSPVTKSFNRGEC 107
RESULT 39
AEA37415
ID AEA37415 standard; protein; 107 AA.
XX AEA37415;
AC AEA37415;
DT 25-AUG-2005 (first entry)
XX Anti-human CD40 antibody 21.4.1 light chain constant region.
DE antibody engineering; cytostatic; vaccine; cancer; CD40; antibody;
KW light chain constant region.
XX Homo sapiens.
OS US2005136055-A1.
PN 23-JUN-2005.
PD 02-DEC-2004; 2004US-00001980.
PF 22-DEC-2003; 2003US-0531639P.
PR 22-DEC-2003; 2003US-0531639P.
XX (PFIZ) PFIZER INC.
PA Gladue RP, Cusmano JD, Bedian V;
XX WPI; 2005-444081/45.
XX Treating cancer in a patient by administering a CD40 agonist antibody or
PT its fragment according to an intermittent dosing regimen of at least two
PT cycles, each cycle comprising a dosing period during and a resting
PT period.
XX Disclosure; SEQ ID NO 8; 18pp; English.
PS The invention relates to a method of treating cancer in a patient by
XX administering a CD40 agonist antibody or its fragment according to an
XX intermittent dosing regimen of at least two cycles, each cycle
XX comprising: (a) a dosing period during which a therapeutically effective
XX amount of the CD40 agonist antibody is administered to the patient and,
XX thereafter; (b) a resting period. The CD40 agonist antibody or its
XX fragment is useful in the manufacture of a medicament for treating cancer
XX in a patient. This sequence corresponds to the constant region of the
XX light chain from the antibody 21.4.1 used in the method of the invention.
XX Sequence 107 AA;
Qy Query Match 100.0%; Score 553; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Qy 61 SKDSTYSLSTLTLSKADYERKHVYACEVTHOGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYERKHVYACEVTHOGLSSPVTKSFNRGEC 107
RESULT 40
AEA37415
ID AEA37415 standard; protein; 107 AA.
XX AEA37415;
AC AEA37415;
DT 08-SEP-2005 (first entry)
XX Human C kappa constant region SEQ ID NO 112.
DE antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;
KW antibody engineering; therapeutic; diagnosis; inflammation;
KW autoimmune disease; immune disorder; graft rejection; HIV infection;
KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;
XX heavy chain constant region.
OS Homo sapiens.

```
XX WO2005060368-A2.
XX
XX 07-JUL-2005.
XX
XX 10-DEC-2003; 2003WO-US039599.
XX
XX 10-DEC-2003; 2003WO-US039599.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Okeefe T, Ponath P;
XX
XX WPI; 2005-488561/49.
XX
XX N-PSDB; AEB09608.
XX
XX New humanized immunoglobulin or its antigen binding portion having
XX binding specificity for CC-chemokine receptor 2 and having a heavy chain
XX and light chain, for treating inflammatory diseases, HIV, and autoimmune
XX diseases.
XX
XX Claim 1; SEQ ID NO 112; 192pp; English.
XX
XX The invention describes a humanized immunoglobulin (I) or its antigen
XX binding portion having binding specificity for CC-chemokine receptor 2
XX (CCR2) and having a heavy chain and a light chain, where the heavy chain
XX comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)
XX sequence, given in specification or its portion, and the light chain
XX comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given
XX in specification. Also described are: a humanized immunoglobulin heavy
XX chain, or its antigen binding fragment, having binding specificity for
XX CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the
XX amino acid of (SEQ ID NO: 110), or its portion; and a humanized
XX immunoglobulin light chain, or its antigen binding fragment, having
XX binding specificity for CCR2 and comprising the amino acid sequence of
XX (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)
XX sequence, given in specification. The following are disclosed: isolated
XX nucleic acid molecules comprising nucleic acid sequence encoding (1); a
XX construct comprising nucleic acid molecule encoding (1); and host cell
XX comprising the nucleic acid molecule. (1) is useful as a therapeutic
XX agent for controlling lymphocyte homing the mucosal lymphoid tissue thus
XX reducing inflammatory response, for use in the treatment of diseases
XX associated with leukocyte infiltration of tissue, e.g. in the treatment
XX of inflammatory diseases, autoimmune diseases, graft rejection, HIV
XX infection and monocyte-mediated disorders such as atherosclerosis. (1) is
XX useful for detecting and/or measuring the level of CCR2 in a sample (e.g.
XX tissues or body fluids such as inflammatory exudates, blood, serum, bowel
XX fluid), and for modulating binding function and/or leukocyte trafficking
XX modulated by CCR2. This is the amino acid sequence of human C kappa
XX constant region used in the creation of a humanized anti-CCR2-antibody.
XX
XX Sequence 107 AA;
XX
XX Query Match 100.0%; Score 553; DB 9; Length 107;
XX Best Local Similarity 100.0%; Pred. No. 4.3e-48;
XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
XX |||||
XX 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
XX |||||
XX 61 SKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
XX |||||
XX 61 SKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
XX |||||
XX
XX RESULT 41
XX AEB72782
XX ID AEB72782 standard; protein; 107 AA.
XX
XX AC AEB72782;
XX
XX 06-OCT-2005 (first entry)
XX
XX
```

```
XX Anti-LtAlpha antibody light chain constant region Igekappac.
XX
XX antibody; Anorectic; Immunosuppressive; Cardiovascular-Gen; Cytostatic;
XX Neuroprotective; Vaccine; lymphotoxin alpha; obesity; immune disorder;
XX cardiovascular disease; infection; neurological disease.
XX
XX Synthetic.
XX
XX WO2005067477-A2.
XX
XX 28-JUL-2005.
XX
XX 30-NOV-2004; 2004WO-US040018.
XX
XX 08-DEC-2003; 2003US-0527794P.
XX
XX (CENZ ) CENTOCOR INC.
XX
XX Giles-Komar J, Scallon BJ, Cai A;
XX
XX WPI; 2005-522703/53.
XX
XX New anti-human lymphotoxin alpha antibody, useful for diagnosing or
XX treating immune, cardiovascular, infectious disease, malignant, or
XX neurological disease, or obesity.
XX
XX Disclosure; SEQ ID NO 40; 114pp; English.
XX
XX This sequence represents a mammalian anti-lymphotoxin alpha (LtAlfa)
XX antibody light chain constant region. The antibody preferably comprises
XX at least one variable region AEB72785AEB72787 at least one light chain
XX complementarity determining region (CDR) AEB72797AEB72798AEB72799 and at
XX least one heavy chain CDR AEB72800AEB72801AEB72802. The antibody binds
XX LtAlfa with an affinity of 10-9 to 10-2 M. The antibody substantially
XX neutralizes at least one activity of at least one LtAlfa protein. The
XX antibody and compositions, medical devices, and methods for its
XX production, are useful for diagnosing or treating a LtAlfa related
XX condition, e.g. obesity, an immune related disease, a cardiovascular
XX disease, an infectious disease, a malignant disease, or a neurological
XX disease.
XX
XX Sequence 107 AA;
XX
XX Query Match 100.0%; Score 553; DB 9; Length 107;
XX Best Local Similarity 100.0%; Pred. No. 4.3e-48;
XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
XX |||||
XX 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
XX |||||
XX 61 SKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
XX |||||
XX 61 SKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
XX |||||
XX
XX RESULT 42
XX AEC81787
XX ID AEC81787 standard; protein; 107 AA.
XX
XX AC AEC81787;
XX
XX 01-DEC-2005 (first entry)
XX
XX Human immunoglobulin light chain constant region kappa.
XX
XX Fusion protein; protein production; immunoglobulin; antibody;
XX light chain constant region.
XX
XX Homo sapiens.
XX
XX WO2005087810-A2.
XX
```

XX PD 22-SEP-2005.
XX PF 08-MAR-2005; 2005WO-US007590.
XX PR 08-MAR-2004; 2004US-0551174P.
XX PA (ZYMO) ZYMOGENETICS INC.
XX PI Moore MD, Fox BA;
XX WPI; 2005-630945/64.
XX DR New dimeric protein comprising a first polypeptide fusion disulfide
XX PT bonded to a second polypeptide fusion, useful as cytokine antagonist for
XX PT treating cancers, or as growth factor agonist for promoting tissue
XX PT growth.
XX PS Disclosure; SEQ ID NO 61; 85pp; English.
XX
XX The present invention relates to dimeric fusion proteins and methods of
XX making them. A claimed dimeric protein comprises a first polypeptide
XX fusion disulfide bonded to a second polypeptide fusion. The first
XX polypeptide fusion has the formula P1-L1-D1-(P2)n, where: P1 is a first
XX non-immunoglobulin polypeptide; L1 is a first polypeptide linker of 18-32
XX amino acid residues where x of these residues are Cys residues; D1 is a
XX first dimerizing domain selected from an immunoglobulin CH1 domain, a T-
XX cell receptor C alpha domain, a T-cell receptor C beta domain, a major
XX histocompatibility complex (MHC) class I alpha 3 domain, beta2-
XX microglobulin, a MHC class II alpha 2 domain, and a MHC class II beta 2
XX domain; P2 is a linking polypeptide of 1-29 amino acid residues where at
XX least one residue is Cys; and n is 0 or 1. The second polypeptide fusion
XX has the formula P3-L2-D2, where: P3 is a second non-immunoglobulin
XX polypeptide; L2 is a second polypeptide linker of 18-32 amino acid
XX residues, where y of these residues are Cys residues; and D2 is a second
XX dimerizing domain selected from an immunoglobulin light chain constant
XX domain, a T-cell receptor C alpha domain, a T-cell receptor C beta
XX domain, a MHC class I alpha 3 domain, beta2-microglobulin, a MHC class II
XX alpha 2 domain and a MHC class II beta 2 domain. In the dimeric protein,
XX each of x and y is an integer of 1-8, and x=y. Also claimed are dimeric
XX proteins in which: P1 and P3 are different; n=1; x=2 and y=2; each of P1
XX and P3 is an extracellular domain of a cell surface receptor, including a
XX human cell surface receptor; each of P1 and P3 is not a member of the
XX immunoglobulin superfamily; and each of P1 and P3 is individually
XX selected from interleukin-17 receptor, interleukin-20 receptor A or B,
XX interleukin-21 receptor, interleukin-28 receptor A, interleukin-31
XX receptor A, CCR2-4 or gammaC. In a further claimed polypeptide fusion, D1
XX is an immunoglobulin CH1 domain, and D2 is an immunoglobulin kappa light
XX chain constant domain or immunoglobulin lambda light chain constant
XX domain. In a further claimed dimeric protein: (a) one of P1 and P3 is a
XX zcytor7 extracellular domain and the other of P1 and P3 is a DIRS1
XX extracellular domain; (b) one of P1 and P3 is a zcytor11 extracellular
XX domain and the other of P1 and P3 is a DIRS1 extracellular domain; (c)
XX one of P1 and P3 is a zalphall extracellular domain and the other of P1
XX and P3 is an interleukin-2 receptor gamma common extracellular domain; or
XX (d) one of P1 and P3 is a PDGF alpha receptor extracellular domain and the
XX other of P1 and P3 is a PDGF beta receptor extracellular domain. Also
XX claimed are polypeptide fusions of formula P1-L1-(P2)n and P3-L-D2,
XX polynucleotides encoding each polypeptide fusion, expression vectors,
XX cultured cells, and a method of making the dimeric proteins of the
XX invention by culturing cells comprising first and second expression units
XX such that the encoded polypeptide fusions are produced as a dimeric
XX protein. A dimeric protein consisting of 2 polypeptide chains joined via
XX at least one disulfide bond, where each polypeptide chain is a
XX polypeptide fusion of formula P3-L-D2, and a method of making this
XX dimeric protein, are also claimed. The dimeric proteins of the invention
XX can be used for diagnosis, therapy, or research to provide one or more
XX activities associated with the first and second non-immunoglobulin
XX polypeptides. Such activities include receptor binding, receptor
XX activation and ligand binding. Therapeutic uses include use as cytokine
XX antagonists for treatment of cancers or immunological disorders, growth
XX factor agonists to promote tissue growth or healing or to promote
XX development of vasculature or other tissue. Diagnostic uses include use

CC as targeting agents for radioisotopes or other labels. The present
CC sequence is that of a human immunoglobulin light chain kappa constant
CC region, which can be used in fusion proteins of the invention.
XX
XX Sequence 107 AA;
SQ
Query Match 100.0%; Score 553; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEOD 60
DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEOD 60
QY 61 SKDSTYLSLSLTITLSKADYEHKVKYACVETHTQGLSSPVTKSPNRRGEC 107
DB 61 SKDSTYLSLSLTITLSKADYEHKVKYACVETHTQGLSSPVTKSPNRRGEC 107
RESULT 43
AED01341
ID AED01341 standard; protein; 107 AA.
XX
XX AED01341;
XX
XX 01-DEC-2005 (first entry)
XX
XX Light chain constant region C kappa.
XX
XX immunomodulatory; antimicrobial; antiinflammatory; neuroprotective;
XX cytostatic; immunogenicity; antibody therapy; antibody engineering;
XX diagnostic; therapeutic; autoimmune disease; immunosuppressive;
XX immune disorder; infection; inflammation; neurological disease; neoplasia;
XX cancer; light chain constant region.
XX
XX Homo sapiens.
XX
XX WO2005092325-A2.
XX
XX 06-OCT-2005.
XX
XX 24-MAR-2005; 2005WO-US010199.
XX
XX 24-MAR-2004; 2004US-0556353P.
XX 21-MAY-2004; 2004US-0573302P.
XX 01-JUL-2004; 2004US-0585328P.
XX 09-JUL-2004; 2004US-0586837P.
XX 06-AUG-2004; 2004US-0599741P.
XX 02-SEP-2004; 2004US-0607398P.
XX 29-SEP-2004; 2004US-0614944P.
XX 14-OCT-2004; 2004US-0619409P.
XX
XX (XENC-) XENCOR INC.
XX
XX Lazar GA, Karki SB;
XX
XX WPI; 2005-684098/70.
XX
XX New antibody variant comprising an amino acid modification outside the Fc
XX region, for treating antibody-related disorders e.g. autoimmune,
XX immunological, infectious, and neurological diseases.
XX
XX Example; Fig 3c; 92pp; English.
XX
XX The invention describes an antibody variant (I) comprising an amino acid
XX modification outside the Fc region, where the modification improves
XX affinity of (I) for one or more effector ligands relative to the parent
XX antibody. Also disclosed are: a method for engineering optimizing (I);
XX isolated nucleic acids encoding (I); vectors comprising the nucleic
XX acids, optionally, operably linked to control sequences; host cells
XX comprising the vector; methods for producing and optionally recovering
XX (I); and composition comprising (I) and carrier or diluent. (I) is useful
XX as a therapeutic, diagnostic or research reagent. (I) is useful for

CC treating an antibody-related disorder chosen from autoimmune diseases,
 CC immunological diseases, infectious diseases, inflammatory diseases,
 CC neurological diseases, and oncological and neoplastic diseases including
 CC cancer (e.g. carcinoma, lymphoma, blastoma, sarcoma, leukemia,
 CC neuroendocrine tumors and melanoma). (I) Has improved affinity for
 CC effector ligands relative to parent antibody. (I) Has enhanced stability,
 CC solubility, function and clinical use, and reduced immunogenicity in
 CC humans. This is the amino acid sequence of an immunoglobulin light chain
 CC constant region.

XX Sequence 107 AA;

Query Match 100.0%; Score 553; DB 9; Length 107;
 Best Local Similarity 100.0%; Pred. No. 4.3e-48;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYFPREAKVQWKVDNALQSGNSQESVTRQD 60
 Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYFPREAKVQWKVDNALQSGNSQESVTRQD 60
 QY 61 SKDSTYLSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 Db 61 SKDSTYLSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 44

ID AED01379 standard; protein; 107 AA.

AC AED01379;

XX 01-DEC-2005 (first entry)

XX Immunoglobulin kappa light chain constant region.

XX immunomodulatory; antimicrobial; antiinflammatory; neuroprotective;
 KW cytostatic; immunogenicity; antibody therapy; antibody engineering;
 KW diagnostic; therapeutic; autoimmune disease; immunosuppressive;
 KW immune disorder; infection; inflammation; neurological disease; neoplasm;
 KW cancer; light chain constant region; immunoglobulin.

XX Homo sapiens.

PN WO2005092925-A2.

XX 06-OCT-2005.

XX 24-MAR-2005; 2005WO-US010199.

XX 24-MAR-2004; 2004US-0556353P.

PR 21-MAY-2004; 2004US-0573302P.

PR 01-JUL-2004; 2004US-0585328P.

PR 09-JUL-2004; 2004US-0586837P.

PR 06-AUG-2004; 2004US-0599741P.

PR 02-SEP-2004; 2004US-0607398P.

PR 29-SEP-2004; 2004US-061494P.

PR 14-OCT-2004; 2004US-0619403P.

XX (XENC-) XENCOR INC.

XX Lazar GA, Karki SB;

XX WPI; 2005-684098/70.

XX New antibody variant comprising an amino acid modification outside the Fc
 PT region, for treating antibody-related disorders e.g. autoimmune,
 PT immunological, infectious, and neurological diseases.

XX Example 3; Fig 15b-c; 92pp; English.

XX The invention describes an antibody variant (I) comprising an amino acid
 CC modification outside the Fc region, where the modification improves
 CC affinity of (I) for one or more effector ligands relative to the parent

CC antibody. Also disclosed are: a method for engineering optimizing (I);
 CC isolated nucleic acids encoding (I); vectors comprising the nucleic
 CC acids, optionally, operably linked to control sequences; host cells
 CC comprising the vector; methods for producing and optionally recovering
 CC (I); and composition comprising (I) and carrier or diluent. (I) is useful
 CC as a therapeutic, diagnostic or research reagent. (I) is useful for
 CC treating an antibody-related disorder chosen from autoimmune diseases,
 CC immunological diseases, infectious diseases, inflammatory diseases,
 CC neurological diseases, and oncological and neoplastic diseases including
 CC cancer (e.g. carcinoma, lymphoma, blastoma, sarcoma, leukemia,
 CC neuroendocrine tumors and melanoma). (I) Has improved affinity for
 CC effector ligands relative to parent antibody. (I) Has enhanced stability,
 CC solubility, function and clinical use, and reduced immunogenicity in
 CC humans. This is the amino acid sequence of an immunoglobulin light chain
 CC constant region.

XX Sequence 107 AA;

Query Match 100.0%; Score 553; DB 9; Length 107;
 Best Local Similarity 100.0%; Pred. No. 4.3e-48;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYFPREAKVQWKVDNALQSGNSQESVTRQD 60

Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYFPREAKVQWKVDNALQSGNSQESVTRQD 60

QY 61 SKDSTYLSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107

Db 61 SKDSTYLSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 45

ID AEC94910 standard; protein; 107 AA.

XX AEC94910;

XX 01-DEC-2005 (first entry)

XX Anti-IL-13-antibody light chain constant region Ig kappa c.

XX immunomodulator; cardiovascular-gen.; antimicrobial; cytostatic;
 KW neuroprotective; vulnery; therapeutic; immune modulation;
 KW immune disorder; cardiovascular disease; infection; neoplasm;
 KW neurological disease; trauma; light chain constant region.

XX Homo sapiens.

OS Synthetic.

XX WO2005091853-A2.

XX 06-OCT-2005.

XX 18-FEB-2005; 2005WO-US005249.

XX 27-FEB-2004; 2004US-0548658P.

XX (CENZ) CENTOCOR INC.

XX Heavner GA, Li L, Oneil K;

XX WPI; 2005-664875/68.

XX Treating human IL-13 related pathology comprises use of least one IL-13
 PT immunoglobulin derived protein comprising 3 or more of 7 defined
 PT characteristics such as apparent Kd for human IL-13 wt or specific mutant
 PT less than or equal to 0.5 nM.

XX Disclosure; SEQ ID NO 40; 98pp; English.

XX The invention describes a method of treating a human IL-13 related

CC pathology comprising contacting or administering at least one IL-13
 CC immunoglobulin (Ig) derived protein to the cells, tissue or animal, where

CC the IL-13 Ig derived protein inhibits at least one biological activity of
 CC the IL-13, in vivo, in vitro or in situ and comprises at least 3 of 7
 CC specific characteristics such as apparent kd for human IL-13 wt or
 CC specific mutant less than or equal to 0.5 nM (as determined by BIA core).
 CC Also described is an anti-IL-13 composition, comprising a therapeutically
 CC effective amount of the at least one IL-13 Ig derived protein. The method
 CC and composition are useful for treating at least one human IL-13 related
 CC pathology, e.g. immune-related disease, a cardiovascular disease, an
 CC infectious disease, a malignant disease, a neurologic disease, or any
 CC wound or trauma. This is the amino acid sequence of an anti-IL-13-
 CC antibody light chain constant region.

XX Sequence 107 AA;

Query Match 100.0%; Score 553; DB 9; Length 107;
 Best Local Similarity 100.0%; Pred. No. 4.3e-48;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 107
 DB 61 SKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 107

RESULT 46

AED41914
 ID AED41914 standard; protein; 107 AA.

XX AED41914;

DT 15-DEC-2005. (first entry)

DE Deimmunized PSMA J591 light chain constant region.

KW prostate tumor; cytostatic; andrology; genitourinary disease; neoplasm;
 KW antibody; prostate specific membrane antigen; PSMA;
 KW light chain constant region.

XX Mus musculus.

XX WO2005094882-A1.

XX 13-OCT-2005.

XX 03-MAR-2004; 2004WO-US006543.

XX 03-MAR-2004; 2004WO-US006543.

XX (MILL-) MILLENNIUM PHARM INC.

XX Horvath CJ, Webb IJ;

XX WPI; 2005-703269/72.

XX N-PSDB; AED41913.

PT Treating prostate cancer in a subject by administering to the subject 2-
 PT 24 doses of an antibody or its antigen binding fragment that binds to the
 PT extracellular domain of prostate specific membrane antigen (PSMA), and is
 PT coupled to DM1.

XX Disclosure; SEQ ID NO 134; 291pp; English.

XX The invention relates to a method of treating prostate cancer, in a
 CC subject which comprises administering to the subject two to twenty-four
 CC doses of an antibody or its antigen binding fragment, which binds to the
 CC extracellular domain of prostate specific membrane antigen (PSMA) and
 CC which is coupled to DM1, where each dose comprises 175-500 mg/m² of the
 CC antibody or its antigen binding fragment, to thus treat the subject. The
 CC method is useful for treating prostate cancer. The present sequence
 CC represents the amino acid sequence of a mouse prostate specific membrane

CC antigen (PSMA) antibody heavy chain.

XX Sequence 107 AA;

Query Match 100.0%; Score 553; DB 9; Length 107;
 Best Local Similarity 100.0%; Pred. No. 4.3e-48;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 107
 DB 61 SKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 107

RESULT 47

AED49132
 ID AED49132 standard; protein; 107 AA.

XX AED49132;

DT 15-DEC-2005 (first entry)

DE Light chain constant region - Igkc.

KW antibody engineering; heavy chain; light chain; variable region;
 KW constant region.

XX Homo sapiens.

XX Synthetic.

XX WO2005098039-A2.

XX 20-OCT-2005.

XX 28-MAR-2005; 2005WO-US010086.

XX 31-MAR-2004; 2004US-0558090P.

XX (CENZ) CENTOCOR INC.

XX Lu J;

XX WPI; 2005-725786/74.

PT Selecting, generating, comparing or analyzing human antibody amino acid
 PT or nucleic acid sequences comprises accessing antibody sequence databases
 PT and classifying sequences into groups, superfamilies, and/or subfamilies.

XX Disclosure; SEQ ID NO 40; 51pp; English.

XX This sequence represents the light chain constant region from a consensus
 CC antibody sequence which was used in the method of the invention for
 CC selecting, generating, comparing or analyzing human or human derived
 CC antibody or antibody fusion protein amino acid or nucleic acid sequences.
 CC The method comprises: (a) accessing antibody sequence databases and
 CC collecting constant, complementarity determining regions (CDR), and/or
 CC variable region sequences; (b) subjecting the data collected in step (a)
 CC to Algorithm 1, where the sequences are classified into groups,
 CC superfamilies, and/or subfamilies; (c) performing sequence alignment
 CC on all sequences assigned to a given subfamily in step (b); (d) displaying
 CC subfamily multiple sequence alignment result of step (c); (e) accessing
 CC antibody sequence databases and collecting variable region sequences; (f)
 CC subjecting the data collected in step (e) to Algorithm 2, where the
 CC variable region sequences are classified into superfamilies and
 CC subfamilies; (g) performing multiple sequence alignment on all sequences
 CC assigned to a given subfamily in step (f); (h) displaying subfamily
 CC multiple sequence alignment results of step (g); (i) subjecting the
 CC multiple sequence alignment data generated in step (g) or (h) to
 CC Algorithm 3, where each amino acid substitution is examined and the
 CC substitution's frequency of occurrence at a given position is calculated;

CC (j) determining the constant region subfamily prototype sequence and
CC substitutions; (k) displaying the constant region subfamily prototype
CC sequence and substitutions generated by step (j); (l) determining the
CC variable region subfamily prototype sequence and substitutions; (m)
CC displaying the variable region subfamily prototype sequence and
CC substitutions generated by step (l); and (n) exporting the displayed
CC results from step (d), (h), (k) or (m) to a web interface, where the
CC displays can be viewed and BLAST searching can be performed. The method,
CC computer programs, data and databases, computer readable media, computer
CC systems, and apparatus are useful for selecting, generating, comparing or
CC analyzing human or human derived antibody or antibody fusion protein
CC amino acid or nucleic acid sequences and are used for research,
CC diagnostic and/or therapeutic products.

XX Sequence 107 AA;

Query Match 100.0%; Score 553; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIPTPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIPTPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 48

AED28066
ID AED28066 standard; protein; 107 AA.

AC AED28066;

XX 15-DEC-2005 (first entry)

XX Human kappa light chain constant region (CL).

DE Gene therapy; antibody therapy; inflammation; antinflammatory;
KW thrombosis; anticoagulant; thrombolytic; cardiovascular disease;
KW hematological disease; peripheral arterial occlusive disease; vasotropic;
KW ischemia; monoclonal antibody; light chain constant region.

XX Homo sapiens.

OS US2005226876-A1.

XX 13-OCT-2005.

XX 08-APR-2005; 2005US-00102403.

XX 13-APR-2004; 2004EP-00008722.

XX (GRAU/) GRAUS Y.

PA (HIMB/) HIMBER J.

PA (JANS/) JANSEN-MOLENAAR M.

PA (KLIN/) KLING D.

PA (KOPE/) KOPETZKI E.

PA (PARR/) PARREN P.

PA (REBE/) REBERS F.

PA (STEL/) STEINER B.

PA (STRE/) STERN A.

PA (STRE/) STREIN P.

PA (STUB/) STUBENRAUCH K.

PA (VWIN/) VAN DE WINKEL J.

XX (VUUG/) VAN VUGT M.

XX Graus Y, Himber J, Jansen-Molenaar M, Kling D, Kopetzki E;

PI Farren P, Rebers F, Steiner B, Stern A, Strein P, Stubenrauch K;

PI Van De Winkel J, Van Vugt M;

XX WPI; 2005-723886/74.

XX New antibody containing a Fc part from human origin, binding to P-
PT selectin and non-binding to complement factor C1q, for preparing a
PT medicament for treating e.g., peripheral arterial occlusive disease.

XX Disclosure; SEQ ID NO 23; 50pp; English.

XX The invention relates to an antibody containing a Fc part from human
CC origin, binding to P-selectin (CD62P, GMP-140, PADGEM or LECAM-3) and non
CC binding to complement factor C1q. The anti-P-selectin antibody is useful
CC in preparing a medicament for treating inflammatory or thrombotic
CC disorders, preferably peripheral arterial occlusive disease (PAOD) or
CC critical limb ischemia (CLI). It is also useful in gene therapy and in
CC antibody therapy. The present sequence is the human kappa light chain
CC constant region. This sequence is used in the construction of expression
CC plasmids for an anti-P-selectin IgG1 HuMab.

XX Sequence 107 AA;

Query Match 100.0%; Score 553; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPTPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60

Db 1 RTVAAPSVFIPTPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

Db 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 49

AED66964

ID AED66964 standard; protein; 107 AA.

XX AED66964;

XX 12-JAN-2006 (first entry)

XX Human kappa chain constant region (CL) domain consensus sequence.

DE Antibody therapy; cerebrovascular ischemia; cerebroprotective;

KW vasotropic; cardiovascular disease; neurological disease;

KW light chain constant region.

XX Homo sapiens.

OS US2005255108-A1.

XX 17-NOV-2005.

XX 28-DEC-2004; 2004US-00025712.

XX 23-JAN-1996; 96US-0093038P.

PR 22-JAN-1997; 97US-00788800.

PR 17-FEB-1999; 99US-00251852.

PR 20-DEC-2000; 2000US-00811384.

PR 31-MAR-2003; 2003US-00404286.

XX (BEDN/) BEDNAR M M.

PA (GROS/) GROSS C B.

PA (GROS/) GROSS L J.

PA (THOM/) THOMAS G R.

XX Bednar MM, Gross CE, Gross LJ, Thomas GR;

XX WPI; 2005-768272/78.

XX Increasing cerebral blood flow and/or reducing infarct size in focal

PT ischemic stroke caused by obstruction of a main cerebral artery in a

PT human mammal by co-administering tissue plasminogen activator (t-PA) and

PT anti-CD18 antibody.

XX Disclosure; SEQ ID NO 5; 26pp; English.

XX The present invention relates to a method of increasing cerebral blood flow and/or reducing infarct size in focal ischemic stroke caused by obstruction of a main cerebral artery in a human mammal. The method involves the step of co-administering therapeutically effective amounts of tissue plasminogen activator (tPA) and anti-CD18 antibody (e.g. H52) to the mammal, where neither the tPA nor the anti-CD18 antibody is administered to the mammal until about 3-5 hours after the onset of focal ischemic stroke. The present sequence is a human kappa chain constant region (CL) domain consensus sequence. This sequence is used in alignment with the Fabvib variant derived from an anti-CD18 antibody.

XX Sequence 107 AA;

Query Match 100.0%; Score 553; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 50
AEF16291

ID AEF16291 standard; protein; 107 AA.

AC AEF16291;

XX 09-MAR-2006 (first entry)

XX Humanized antibody, HuD10, light chain constant region.

DE monoclonal antibody; humanized antibody; immunoglobulin; HuD10; IgG;
KW light chain constant region; antibody engineering; therapeutic; vaccine;
KW cancer; neoplasm; inflammation; asthma; autoimmune disease;
KW viral infection; cytostatic; antiinflammatory; antiasthmatic;
KW immunosuppressive; virucide.

XX Homo sapiens.

OS Synthetic.

XX WO2005123780-A2.

PN 29-DEC-2005.

PD 08-APR-2005; 2005WO-US011996.

PF 09-APR-2004; 2004US-00822300.

PR 09-APR-2004; 2004WO-US011213.

XX (PROT-) PROTEIN DESIGN LABS INC.

PA Hinton PR, Tsurushita N, Tso YJ, Vasquez M;

XX WPI; 2006-067459/07.

DR New modified monoclonal antibody of class IgG with altered FcRn binding affinity, useful for treating a condition, e.g. cancer, inflammatory conditions such as asthma, autoimmune diseases, or viral infections.

XX Disclosure; SEQ ID NO 9; 310pp; English.

XX The invention relates to modified monoclonal antibodies of class IgG with FcRn binding affinity altered relative to that of an unmodified monoclonal antibody of class IgG. The modified monoclonal antibody of class IgG comprises a heavy chain constant region where at least amino

CC acid residues 250 and 428 are different from the residues present in the unmodified monoclonal antibody and where the unmodified monoclonal antibody is selected from the group consisting of an anti-CD25, an anti-CD3, an anti-IFNGamma, or an anti-alphabeta1 integrin. Also disclosed are: (1) a method of modifying an antibody of class IgG; (2) a method of producing a modified antibody of class IgG with an altered binding affinity for FcRn and/or an altered serum half life as compared with an unmodified antibody; (3) a vector comprising a polynucleotide encoding one or more heavy or light chain sequences; (4) a host cell comprising the vector; and (5) polynucleotide sequences encoding the modified antibodies. The unmodified monoclonal antibody is an anti-CD25 of IgG1 or IgG2M3 isotype. The modified monoclonal antibodies of the invention can be used in prophylactic and therapeutic compositions, such as vaccines, for treating a condition, e.g. cancer, inflammatory conditions such as asthma, autoimmune diseases, or viral infections. The antibodies can also be used in diagnostic applications. This sequence represents a region of a humanized antibody.

XX Sequence 107 AA;

Query Match 100.0%; Score 553; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 51
AEF38694

ID AEF38694 standard; protein; 107 AA.

XX AEF38694;

XX 23-MAR-2006 (first entry)

XX Antibody sHGM12 light chain constant region SEQ ID NO 7.

DE antiallergic; antiasthmatic; gastrointestinal-gen.; neuroprotective;
KW antiinflammatory; immunomodulator; immunostimulant; immunotherapy;
KW immune stimulation; monoclonal antibody; asthma; antiasthmatic;
KW inflammation; respiratory disease; multiple sclerosis; neuroprotective;
KW immune disorder; neurological disease; irritable bowel syndrome;
KW gastrointestinal-gen.; gastrointestinal disease; sHGM12;
KW light chain constant region.

XX Homo sapiens.

OS WO2006004988-A2.

PN 12-JAN-2006.

XX 30-JUN-2005; 2005WO-US023440.

PF 30-JUN-2004; 2004US-00881661.

PR 05-NOV-2004; 2004US-00983104.

XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.

PA Pease LR, Radhakrishnan S, Van Keulen V, Ciric B, Iijima K;
PI Kita H;

XX WPI; 2006-100770/10.

XX New purified sHGM12 polypeptides, useful for enhancing immune responses, PT modifying an existing state of immune responsiveness, immunizing PT individuals, or treating or inhibiting the development of allergic PT asthma.

KW juvenile onset diabetes; delayed hypersensitivity;
KW mycobacterium tuberculosis infection; antibacterial; sarcoidosis;
KW polymyositis; muscular-gen.; granulomatosis; vasculitis; vasotropic;
KW pernicious anemia; antianemic; inflammation; sepsis; trauma; vulnery;
KW autoimmune hemolytic anemia; myasthenia gravis;
KW graft versus host disease; hemorrhagic shock; pulmonary fibrosis;
KW B-cell lymphoma; cytostatic; antibody; immunoglobulin;
KW light chain constant region.
XX
XX
OS Homo sapiens.
XX
XX US6998253-B1.
XX
XX 14-FEB-2006.
XX
XX 31-JUL-2000; 2000US-00628568.
XX
XX 14-APR-1995; 95US-00422112.
XX (GETH) GENENTECH INC.
XX PA
XX PI Presta LG, Snedecor BR;
XX
XX WPI; 2006-151963/16.
XX
XX New nucleic acid encoding modified polypeptide with improved in vivo half
XX -life, comprises Ig constant domain or Ig-like constant domain and a
XX salvage receptor binding epitope, useful for treating, e.g. psoriasis or
XX dermatitis.
XX
XX Disclosure; SEQ ID NO 8; 38pp; English.
XX
XX The present invention provides a nucleic acid encoding a modified
XX polypeptide with an improved in vivo half-life. The modified polypeptide
XX comprises an immunoglobulin (Ig) constant domain or Ig-like constant
XX domain and a salvage receptor binding epitope within the Ig constant
XX domain or Ig-like constant domain. The invention is useful for treating
XX LFA-1-mediated disorders such as inflammatory skin diseases including
XX psoriasis, responses associated with inflammatory bowel disease (such as
XX Crohn's disease and ulcerative colitis), adult respiratory distress
XX syndrome, dermatitis, meningitis, encephalitis, uveitis, allergic
XX conditions such as eczema and asthma, skin hypersensitivity reactions
XX (including poison ivy and poison oak), atherosclerosis, leukocyte
XX adhesion deficiency, autoimmune diseases such as rheumatoid arthritis,
XX systemic lupus erythematosus, diabetes mellitus, multiple sclerosis,
XX Reynaud's syndrome, autoimmune thyroiditis, Sjogren's syndrome, juvenile
XX onset diabetes and immune responses associated with delayed
XX hypersensitivity mediated by cytokines and T-lymphocytes typically found
XX in tuberculosis, sarcoidosis, polymyositis, granulomatosis and
XX vasculitis, pernicious anemia, diseases involving leukocyte diapedesis,
XX CNS inflammatory disorder, multiple organ injury syndrome secondary to
XX septicemia or trauma, autoimmune hemolytic anemia, myasthenia gravis,
XX antigen-antibody complex mediated diseases, all types of
XX transplantations, including graft versus host or host versus graft
XX disease, hemorrhagic shock, pulmonary oxygen toxicity, pulmonary
XX fibrosis, wound repair and B-cell lymphomas. The invention is also useful
XX for detecting CD11a or CD18 in vitro or in vivo. The present sequence is
XX a human immunoglobulin (Ig) light chain kappa CL domain. This sequence is
XX used in alignment with Fab vlb variant protein derived from anti-CD18
XX antibody.
XX
XX Sequence 107 AA;
XX
XX Query Match
XX Best Local Similarity 100.0%; Score 553; DB 10; Length 107;
XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPPEAKVQWVKVDNALQSGNSQESVTEQD 60
XX
XX 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPPEAKVQWVKVDNALQSGNSQESVTEQD 60
XX
XX 61 SKDSTYSLSSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSPNRGEC 107
XX
XX |||||

Db 61 SKDSTYSLSSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSPNRGEC 107
RESULT 54
AEG09130
ID AEG09130 standard; protein; 107 AA.
XX AC AEG09130;
XX
XX 20-APR-2006 (first entry)
XX
XX Tie receptor-specific antibody E3, light constant region, SEQ ID:732.
XX
XX Tie; receptor tyrosine kinase; pharmaceutical; angiogenesis inhibition;
XX cancer; cytostatic; neoplasm; diagnosis; angiogenesis disorder;
XX antiangiogenic; wound healing; vulnery; inflammation; antiinflammatory;
XX psoriasis; antipsoriatic; rheumatoid arthritis; antiarthritis;
XX antirheumatic; retinopathy; ophthalmological; diabetic retinopathy;
XX antidiabetic; retinal neovascularization; Tie 1 receptor; antibody.
XX
XX Homo sapiens.
XX
XX WO2006020706-A2.
XX
XX 23-FEB-2006.
XX
XX 09-AUG-2005; 2005WO-US028413.
XX
XX 12-AUG-2004; 2004US-00916840.
XX 12-AUG-2004; 2004WO-US026116.
XX 02-FEB-2005; 2005US-00049536.
XX (DYAX-) DYAX CORP.
XX
XX Wood CR, Dransfield DT, Pieters H, Hoet R, Hufton SE;
XX WPI; 2006-174134/18.
XX
XX New isolated protein comprises heavy chain and light chain immunoglobulin
XX variable domain sequences, which binds to Tie1 ectodomain, useful for
XX treating, preventing, or diagnosing inflammatory diseases, cancers, or
XX retinal disorders.
XX
XX Example 33; SEQ ID NO 732; 310pp; English.
XX
XX The new invention relates to modulating Tie complex formation or
XX interactions between Tie complex components. Tie1 and Tie2 are receptor
XX tyrosine kinases. Specifically described is a protein comprising a heavy
XX chain immunoglobulin variable domain sequence and a light chain
XX immunoglobulin variable domain sequence, where the protein binds to Tie1
XX ectodomain. The protein can bind to an extracellular domain such as a Ig-
XX like C2-type domain, an EGF-like domain, and a fibonectin type III
XX repeats region. Also described are a pharmaceutical comprising the
XX protein; a method of inhibiting vascular development; a method of
XX providing a post-operative adjuvant therapy; a protein comprising SEQ ID
XX NO. 723 and 724; and a nucleic acid encoding the heavy chain (HC) or
XX light chain (LC) immunoglobulin variable domain sequence of the protein
XX above. The amino acid sequences of the HC variable domain sequence
XX comprises CDR1, CDR2, and CDR3 sequences from the E3 clone, and the LC
XX variable domain sequence comprises CDR1, CDR2, and CDR3 sequences from
XX the E3 clone. The protein also comprises the HC and/or LC immunoglobulin
XX variable domains of the E3 antibody. Preferably, the protein inhibits
XX tube formation by HUVEC cells in vitro. The protein is a Fab or an IgG.
XX The protein also has two antigen-binding sites, each of which binds to
XX Tie1. Preferably, the subject has vasculature-dependent cancer or tumor.
XX The isolated protein is useful for treating or diagnosing endothelial
XX cell disorders, blood vessel development disorders, wound healing,
XX inflammatory diseases (e.g. psoriasis and rheumatoid arthritis), cancers,
XX and retinal disorders (e.g. diabetic retinopathy, corneal
XX neovascularization, or ischemic retinopathy). This sequence is a human
XX Tie1 receptor-specific germlined F allotype E3 antibody, light constant
XX region.
XX

```
SQ Sequence 107 AA;
Query Match 100.0%; Score 553; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPDEQLKSGTASVVCILNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIPPPDEQLKSGTASVVCILNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYERKHVKVACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYLSSTLTLSKADYERKHVKVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 55
ADL22765
ID ADL22765 standard; protein; 108 AA.
XX
AC ADL22765;
XX
XX 20-MAY-2004 (first entry)
XX
DE Human antibody kappa light chain variable region.
XX
KW antibody; human; light chain variable region; therapeutic; kappa.
XX
XX Homo sapiens.
XX
XX WO2004013278-A2.
XX
PD 12-FEB-2004.
XX
PF 01-AUG-2003; 2003WO-KR001555.
XX
XX 02-AUG-2002; 2002KR-00045765.
PR
XX 02-AUG-2002; 2002KR-00045767.
PR
XX 02-AUG-2002; 2002KR-00045768.
XX
XX (YUHA-) YUHAN CORP.
XX
XX Lee J, Ko I, Song M, Kim C, Lee J, Yoo T, Kim J, Park S;
XX
XX WPI; 2004-157108/15.
DR
XX N-PSDB; ADL22764.
XX
XX New expression vectors for an antibody heavy chain variable region,
PT lambda light chain variable region or kappa light chain variable region,
PT useful in developing therapeutic antibodies, e.g. humanized or chimeric
PT antibodies.
XX
PS Example 13; Page 37; 39pp; English.
XX
XX The present invention relates to an expression vector for an antibody
CC heavy chain variable region, a lambda light chain variable region or a
CC kappa light chain variable region. The expression vectors are useful in
CC the development of therapeutic antibodies, e.g. humanized or chimeric
CC antibodies. The present sequence is a human antibody kappa light chain
CC variable region of the invention.
XX
SQ Sequence 108 AA;
Query Match 100.0%; Score 553; DB 8; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.4e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPDEQLKSGTASVVCILNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 2 RTVAAPSVFIPPPDEQLKSGTASVVCILNNFYPREAKVQWKVDNALQSGNSQESVTEQD 61

QY 61 SKDSTYLSSTLTLSKADYERKHVKVACEVTHQGLSSPVTKSFNRGEC 107
DB 62 SKDSTYLSSTLTLSKADYERKHVKVACEVTHQGLSSPVTKSFNRGEC 108

RESULT 56
ADM15047
ID ADM15047 standard; protein; 108 AA.
XX
XX ADL15047;
AC
XX 07-APR-2005 (first entry)
DT
XX
XX Human Fab light chain constant region gamma1.
DE
XX
XX Antibody production; light chain constant region; antimicrobial;
KW antibacterial; fungicide; antiinflammatory; antiarthritic; antirheumatic;
KW antiparasitic; osteopathic; gastrointestinal-gen.; cytostatic;
KW antiallergic; dermatological; neuroprotective; immunosuppressive;
KW antidiabetic; antiasthmatic; CNS-gen.; respiratory-gen.; antianemic;
KW antischlicking; immunotherapy; infection; inflammation; cancer;
KW immune disorder; genetic disorder; metabolic disorder;
KW neurological disease.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 108
FT /note
FT /note= "Interchain Cys to which effector molecules may be
FT attached"
XX
XX WO2005003169-A2.
PN
XX
XX 13-JAN-2005.
PD
XX
XX 01-JUL-2004; 2004WO-GB002810.
PF
XX
XX 01-JUL-2003; 2003GB-00015457.
PR
XX 20-AUG-2003; 2003GB-00019588.
PR
XX (CLLT ) CELLTech R & D LTD.
XX
XX Humphreys DP, Heywood SP;
XX
XX WPI; 2005-081945/09.
DR
XX N-PSDB; ADM15051.
XX
XX Antibody Fab fragment useful in detection or treatment of diseases such
PT as infectious disease, rheumatoid arthritis, cancer, asthma and diabetes,
PT comprises heavy chain constant region terminating at interchain cysteine
PT of CH1.
XX
XX Claim 9; SEQ ID NO 2; 30pp; English.
PS
XX
XX A claimed antibody Fab fragment comprises a heavy chain constant region
CC that terminates at the interchain Cys of the heavy chain constant region
CC (CH1). The interchain Cys of CH1 is covalently linked to the interchain
CC Cys of the light chain constant region (CL). One or more effector
CC molecules, such as polyethylene glycol, may be attached to the Fab
CC fragment. The effector molecule is attached to a Cys residue in the CH1
CC and CL which would otherwise be linked to each other via a disulfide
CC bond. Also claimed is a mixture containing 2 or more Fab fragments, where
CC the mixture is enriched for Fab fragments in which the CH1 domain
CC terminates at the interchain Cys, the heavy chains in the fragments are
CC not covalently bonded to the light chains, and the fragments have an
CC effector molecule attached to a Cys in the CL or CH1. Vectors comprising
CC DNA sequences encoding the CL and/or CH1 regions of an antibody Fab
CC fragment are also claimed, as well as host cells, a process for producing
CC an antibody Fab fragment, and a pharmaceutical composition comprising an
CC antibody Fab fragment. The method avoids the need to engineer modified
CC hinge regions and/or surface amino acid substitutions, which are required
CC for site-specific effector molecule attachment. The Fab fragments are
CC useful in the detection or treatment of a number of diseases or disorders
CC such as infectious disease e.g., bacterial infection, fungal infection,
CC inflammatory disease/autoimmunity e.g., rheumatoid arthritis,
```

CC osteoarthritis, inflammatory bowel disease; cancer; allergic/atopic
CC disease e.g., asthma, eczema; congenital disease e.g., cystic fibrosis,
CC sickle cell anemia; dermatological disease e.g., psoriasis; neurological
CC disease e.g., multiple sclerosis; transplants e.g., organ transplant
CC rejection, graft-versus-host disease; and metabolic/idiopathic disease
CC e.g., diabetes. The present sequence is the protein sequence of human
CC gamma 1 Fab CL. This was used in an example from the invention for the
CC creation of novel 'truncated' Fab fragments. An antibody Fab fragment
CC comprising this sequence is claimed.

SQ Sequence 108 AA;

Query Match 100.0%; Score 553; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.4e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 2 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 61
Qy 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 62 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 108

RESULT 57
AEA52525
ID AEA52525 standard; protein; 108 AA.

AC AEA52525;

DT 11-AUG-2005 (first entry)

DE Human antibody light chain constant region - SEQ ID 2.

XX multiple sclerosis; neuroprotective; light chain constant region.

OS Homo sapiens.

PN WO2005051422-A1.

PD 09-JUN-2005.

PF 16-NOV-2004; 2004WO-GB004850.

PR 21-NOV-2003; 2003GB-00027181.

PR 30-JUL-2004; 2004GB-00017115.

PA (CLLT) CELLTech R & D LTD.

PI Christie MI, Mead RJ, Robinson MK, Rapecki SE;

DR WPI; 2005-405309/41.

XX Use of an inhibitor of interleukin-17 activity (e.g. an antibody) for the
PT manufacture of a medicament for the treatment and/or prophylaxis of
PT multiple sclerosis.

PS Disclosure; SEQ ID NO 2; 55pp; English.

CC The invention comprises an inhibitor of interleukin 17 (IL-17). The
CC inhibitor of the invention is useful for the treatment and/or prophylaxis
CC of multiple sclerosis, or for manufacturing a medicament for the
CC treatment and/or prophylaxis of multiple sclerosis. The present amino
CC acid sequence represents a human antibody light chain constant region.

SQ Sequence 108 AA;

Query Match 100.0%; Score 553; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.4e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Db 2 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 61
Qy 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 62 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 108

RESULT 58
ADJ95916

ID ADJ95916 standard; protein; 109 AA.

XX AC ADJ95916;

DT 06-MAY-2004 (first entry)

DE Human kappa constant region.

XX cytostatic; antibody therapy; immunoglobulin cassette construct;
KW immunoglobulin leader molecule; immunoglobulin domain;
KW immunoglobulin therapeutic molecule; monobody; cancer; human;
KW kappa constant region.

OS Homo sapiens.

PN US2004033561-A1.

PD 19-FEB-2004.

PF 17-OCT-2002; 2002US-00272899.

PR 19-OCT-2001; 2001US-0350166P.

PR 26-JUN-2002; 2002US-0392364P.

XX (MILL-) MILLENNIUM PHARM INC.

PI O'Keefe TL, Healey JJ, Newman W, Ponath PD, Keyt BA;

DR WPI; 2004-180050/17.

DR N-PSDB; ADJ95915.

XX New isolated nucleic acid molecules having an immunoglobulin cassette
PT construct, useful for producing immunoglobulin therapeutic molecules
PT termed monobodies, used as a therapeutic group in cancer disorders.

PS Example 2; SEQ ID NO 12; 84pp; English.

XX The invention describes an isolated nucleic acid molecule comprising an
CC immunoglobulin cassette construct, wherein the immunoglobulin cassette
CC comprises an immunoglobulin leader molecule operably linked to a stable
CC immunoglobulin domain region. The methods and compositions of the present
CC invention are useful for producing immunoglobulins, in particular
CC immunoglobulin therapeutic molecules termed monobodies, used as a
CC therapeutic group in cancer disorders. This is the amino acid sequence of
CC the human kappa constant region that can be used in the creation of
CC immunoglobulin DNA cassette constructs.

SQ Sequence 109 AA;

Query Match 100.0%; Score 553; DB 8; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.4e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Db 3 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 62

Qy 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107

Db 63 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 109

RESULT 59

```
ADQ89138
ID ADQ89338 standard; protein; 109 AA.
XX
AC ADQ89338;
XX
XX 21-OCT-2004 (first entry)
XX
DE Human immunoglobulin protein #47.
XX
XX Human; immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2;
KW CCR2; inflammatory disease; autoimmune disorder; graft rejection;
KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;
KW anti-HIV; virucide; antiarteriosclerotic.
XX
XX Homo sapiens.
OS
XX US2004151721-A1.
PN
XX
XX 05-AUG-2004.
PD
XX 10-DEC-2003; 2003US-00733563.
PF
XX 19-OCT-2001; 2001US-0350166P.
PR
XX 26-JUN-2002; 2002US-0392364P.
PR
XX 17-OCT-2002; 2002US-00272899.
PR
XX (OKEE/) O'KEEFE T.
PA
PA (PONA/) PONATH P.
XX
XX O'keefe T, Ponath P;
PI
XX
XX WPI; 2004-580175/56.
DR
XX
XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,
PT useful for diagnosing and/or treating inflammatory or autoimmune
PT diseases, and HIV infection.
XX
XX Disclosure; SEQ ID NO 116; 129pp; English.
PS
XX The invention relates to humanised immunoglobulin heavy and light chains
CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an
CC immunoglobulin or its antigen binding fragment comprising the chains. The
CC humanised immunoglobulin or its antigen binding fragment preferably
CC comprises two heavy chains and two light chains. The humanised
CC immunoglobulin and its heavy and light chains are useful for the
CC diagnosis, prevention and/or treatment of diseases or conditions
CC associated with aberrant expression or activity of the CCR2 polypeptide,
CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV
CC infection and atherosclerosis. This sequence represents a human
CC immunoglobulin protein of the invention.
XX
XX Sequence 109 AA;
SQ
Query Match 100.0%; Score 553; DB 8; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.4e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 3 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 62
QY 61 SKDSTYISLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107
DB 63 SKDSTYISLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 109
RESULT 60
AEB09611
ID AEB09611 standard; protein; 109 AA.
XX
AC AEB09611;
XX
XX 08-SEP-2005 (first entry)
DT
```

```
XX
DE Human C kappa constant region SEQ ID NO 116.
XX
XX antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;
KW antibody engineering; therapeutic; diagnosis; inflammation;
KW autoimmune disease; immune disorder; graft rejection; HIV infection;
KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;
KW light chain constant region.
XX
XX Homo sapiens.
OS
XX WO2005060368-A2.
PN
XX 07-JUL-2005.
PD
XX 10-DEC-2003; 2003WO-US039599.
PF
XX 10-DEC-2003; 2003WO-US039599.
PR
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX Okeefe T, Ponath P;
PI
XX WPI; 2005-488561/49.
DR
XX N-PSDB; AEB09612.
XX
XX New humanized immunoglobulin or its antigen binding portion having
PT binding specificity for CC-chemokine receptor 2 and having a heavy chain
PT and light chain, for treating inflammatory diseases, HIV, and autoimmune
PT diseases.
XX
XX Disclosure; SEQ ID NO 116; 192pp; English.
PS
XX The invention describes a humanized immunoglobulin (I) or its antigen
CC binding portion having binding specificity for CC-chemokine receptor 2
CC (CCR2) and having a heavy chain and a light chain, where the heavy chain
CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)
CC sequence, given in specification or its portion, and the light chain
CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given
CC in specification. Also described are: a humanized immunoglobulin heavy
CC chain, or its antigen binding fragment, having binding specificity for
CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the
CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized
CC immunoglobulin light chain, or its antigen binding fragment, having
CC binding specificity for CCR2 and comprising the amino acid sequence of
CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)
CC sequence, given in specification. The following are disclosed: isolated
CC nucleic acid molecules comprising nucleic acid sequence encoding (I); a
CC construct comprising nucleic acid molecule encoding (I); and host cell
CC comprising the nucleic acid molecule. (I) is useful as a therapeutic
CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus
CC reducing inflammatory response, for use in the treatment of diseases
CC associated with leukocyte infiltration of tissue, e.g. in the treatment
CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV
CC infection and monocytic-mediated disorders such as atherosclerosis. (I) is
CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.
CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel
CC fluid), and for modulating binding function and/or leukocyte trafficking
CC modulated by CCR2. This is the amino acid sequence of human C kappa
CC constant region used in the creation of a humanized anti-CCR2-antibody.
XX
XX Sequence 109 AA;
SQ
Query Match 100.0%; Score 553; DB 9; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.4e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 3 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 62
QY 61 SKDSTYISLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107
```

```
Db 63 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 109
RESULT 61
AEC22657
ID AEC22657 standard; protein; 110 AA.
XX
AC AEC22657;
XX
DT 20-OCT-2005 (first entry)
XX
DE Ig lambda constant region.
XX
KW multispecific antibody; promoter; bispecific antibody; immunoglobulin.
XX
OS Homo sapiens.
XX
FN WO2005072112-A2.
XX
PD 11-AUG-2005.
XX
PF 30-DEC-2004; 2004WO-US043806.
XX
PR 31-DEC-2003; 2003US-0533241P.
XX
PA (VACC-) VACCINEX INC.
XX
PI Zauderer M, Paris M;
XX
WPI; 2005-648912/66.
DR N-PSDB; AEC22656.
XX
Identifying polynucleotides encoding a bispecific antibody by introducing
a first library of polynucleotides encoding immunoglobulin subunit
PT polypeptides into eukaryotic host cells capable of expressing the
PT bispecific antibody.
XX
Example 1; SEQ ID NO 27; 254pp; English.
XX
The invention relates to a method of identifying polynucleotides which
CC encode a bispecific antibody which comprises introducing a library of
CC polynucleotides encoding first and second heavy chain and light chain
CC immunoglobulin subunit polypeptides into eukaryotic host cells,
CC expression and recovery of the antibodies or their antigen-binding
CC fragments. The method is useful in identifying polynucleotides which
CC encode a bispecific antibody or its bispecific antigen-binding fragment.
CC The present sequence represents an immunoglobulin constant region.
XX
SQ Sequence 110 AA;
Query Match 100.0%; Score 553; DB 9; Length 110;
Best Local Similarity 100.0%; Pred. No. 4.5e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 4 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 63
QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 107
Db 64 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 110
RESULT 62
ADD13779
ID ADD13779 standard; protein; 117 AA.
XX
AC ADD13779;
XX
DT 01-JAN-2004 (first entry)
XX
DE Plasmid pBS MhKappaM protein.
XX

KW library; transfection; humanized monoclonal antibody; antigen;
KW T cell receptor; circular.
XX
OS Synthetic.
OS Homo sapiens.
OS Mus sp.
XX
FN EP1298207-A1.
XX
PD 02-APR-2003.
XX
PF 01-OCT-2001; 2001EP-00123596.
XX
PR 01-OCT-2001; 2001EP-00123596.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Breitling F, Moldenhauer G, Poustka A, Kuehlwein T;
XX
WPI; 2003-383833/37.
XX
Preparing library of protein-producing eukaryotic cells, useful for
producing humanized high-affinity antibodies, comprises introducing
PT specific recombination signals into chromosomal gene loci and integrating
PT a variety of DNA sequences.
XX
Example 1; Fig 12A; 75pp; German.
XX
This invention describes a novel method of preparing a library of protein
-producing eukaryotic cells comprising (a) introducing specific
CC recombination signals into one or two chromosomal gene loci, (b)
CC expanding at least one of the modified cells, (c) Transfecting many
CC different DNA sequences, each flanked by recombination signals, into the
CC expanded cells and (d) Integrating the DNA sequences into the gene loci
CC on the basis of the recombination signals and the appropriate
CC recombinase. The resulting cells express different proteins, each from an
CC integrated DNA sequence and the proteins are bound to the cell surface.
CC The method is particularly used to produce libraries of humanized
CC monoclonal antibodies, for selection of those with affinity for
CC particular antigens and useful for diagnostic or therapeutic use.
CC Libraries of T cell receptors may also be prepared. The method produces
CC libraries of high diversity; provides easy, quick and automatable
CC selection from a large number of proteins, allows relatively simple
CC alteration of the expressed gene (e.g. fusion to other protein-coding
CC sequences), is suitable for large scale protein production and allows
CC simple verification and characterization of selected cell lines. The
CC method does not require incorporation of a resistance marker. This
CC sequence represents the construct pBS MhKappaM described in the
CC disclosure of the invention.
XX
SQ Sequence 117 AA;
Query Match 100.0%; Score 553; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.8e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 11 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 70
QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 107
Db 71 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 117
RESULT 63
ADN98370
ID ADN98370 standard; protein; 121 AA.
XX
AC ADN98370;
XX
DT 29-JUL-2004 (first entry)
XX
```

DE Human IgG kappa light chain protein homologue #8.
XX cytotoxic molecule; radionuclide; toxin; chemotherapeutic agent;
KW drug discovery; antibody; protein co-ordinate data.
XX Unidentified.
OS WO2004039843-A1.
PN 13-MAY-2004.
XX 12-SEP-2003; 2003WO-SE001435.
PF 31-OCT-2002; 2002SE-00003226.
PR (AMSH) AMERSHAM BIOSCIENCES AB.
XX Axen A, Baumann H, Carredano E;
PI WPI; 2004-400141/37.
XX Novel human IgG kappa light chain and IgG heavy chain binding pocket
PT polypeptides, useful for binding cytotoxic molecules, radionuclides,
PT toxins and chemotherapeutic agents, and for drug discovery.
XX Disclosure; Fig 2; 63pp; English.
PS
XX The invention relates to an isolated and purified polypeptide (I) having
CC portion of human IgG kappa light chain starting at 93-110 and ending at
CC 187-214 amino acids of human IgG kappa light chain of sequence of 214
CC amino acids (S1) fully defined in specification, or portion of human IgG
CC heavy chain starting at 106-128 and ending at 215-225 amino acids of 225
CC amino acids sequence (S2) fully defined in specification. (I) is useful
CC for identifying a potential ligand to a human kappa-Fab constant part-
CC comprising composition which involves generating a three-dimensional
CC structure of the binding pocket of (I), employing the three-dimensional
CC structure to design a candidate ligand, providing the candidate ligand,
CC contacting the candidate ligand with a human kappa-Fab constant part-
CC comprising composition comprising the binding pocket to verify any
CC binding, and optionally, repeating the above steps of employing,
CC providing and contacting. (I) is useful for evaluating the potential or
CC ability of a chemical entity to associate with a human kappa-Fab constant
CC part-comprising composition which involves providing a virtual library of
CC chemical entities, docking the chemical entities to the binding pocket of
CC (I), defining at least one query based on the results of the docking
CC operation, screening all entities docked, while in the docked
CC conformation with the query, for evaluating the potential or ability of
CC the chemical entity to bind to the compound or the binding pocket,
CC inspection and, optionally, removal of redundancy, and providing one or
CC more of the chemical entities that bound the binding pocket and
CC experimentally testing their binding to a human kappa-Fab constant part-
CC comprising composition, and, if more than one chemical entity was tested,
CC rating the affinities of the chemical entity to human kappa-Fab constant
CC part-comprising composition. The method further involves filtering and
CC removing redundancy among the entities of the library provided. The
CC results of the docking operation are evaluated by visual inspection of
CC the contact between the interacting surface of the binding pocket and the
CC molecular surface(s). (I) is useful for identifying or isolating a ligand
CC capable of selective binding of a human kappa-Fab constant part-
CC comprising composition, in site-specific modification of a human kappa-
CC Fab constant part-comprising composition. The modification is a
CC stabilization of Fab-folding by binding a ligand selectively to the
CC compound or binding pocket. (I) is also useful in an immunological assay
CC for detecting human kappa-Fab constant part-comprising composition. (I)
CC is useful for binding cytotoxic molecules, radionuclides, toxins and
CC chemotherapeutic agents, and for drug discovery. This sequence
CC corresponds to a homologue of the human IgG kappa light chain
XX
SQ Sequence 121 AA;
Query Match 100.0%; Score 553; DB 8; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.1e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
15 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 74
61 SKDSTYLSLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
75 SKDSTYLSLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 121
RESULT 64
AED85881
ID AED85881 standard; protein; 133 AA.
XX
AC AED85881;
XX
DT 12-JAN-2006 (first entry)
XX
DE Ig kappa expression vector pMORPH_h_Igkappa_1 protein.
XX
KW immunosuppressive; hematological; cytostatic; antiinflammatory;
KW antirheumatic; antiarthritic; antibody; CD38; hematological disease;
KW inflammation; light chain.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2005103083-A2.
XX
PD 03-NOV-2005.
XX
PF 07-FEB-2005; 2005WO-IB002476.
XX
PR 06-FEB-2004; 2004US-0541911P.
PR 26-FEB-2004; 2004US-0547584P.
PR 18-MAR-2004; 2004US-0553948P.
PR 06-AUG-2004; 2004US-0599014P.
XX
PA (MORP-) MORPHOSYS AG.
XX
PI Tesar M, Jager U;
XX
WPI; 2005-734713/75.
N-PSDB; AED85872.
XX
PT New isolated human or humanized antibody or its functional fragment
PT comprising an antigen-binding region that is specific for an epitope of
PT CD38, useful for treating hematological or inflammatory disorders.
XX
PS Disclosure; Fig 9; 98pp; English.
XX
CC The invention relates to an isolated human or humanized antibody or its
CC functional fragment comprising an antigen-binding region that is specific
CC for an epitope of CD38. The antibody or its functional fragment is useful
CC for treating a disorder or condition associated with the undesired
CC presence of CD38+ cells, e.g. hematological disease, such as multiple
CC myeloma, chronic lymphocytic leukemia, chronic myelogenous leukemia,
CC acute myelogenous leukemia, and acute lymphocytic leukemia; or an
CC inflammatory disease such as rheumatoid arthritis and systemic lupus
CC erythematosus. The present sequence represents the amino acid sequence of
CC the Ig kappa expression vector pMORPH_h_Igkappa_1 protein.
XX
SQ Sequence 133 AA;
Query Match 100.0%; Score 553; DB 9; Length 133;
Best Local Similarity 100.0%; Pred. No. 5.7e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
27 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 86
61 SKDSTYLSLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107

Db 87 SKDSTYSLSTLTLSKADYERKHKVACEVTHQGLSSPVTKSFNRGEC 133

RESULT 65
ADJ95970
ID ADJ95970 standard; protein; 134 AA.
AC ADJ95970;
XX
XX
XX 06-MAY-2004 (first entry)
DT
DE Immunoglobulin DNA cassette polypeptide seqid 66.
XX
XX cytostatic; antibody therapy; immunoglobulin cassette construct;
KW immunoglobulin leader molecule; immunoglobulin domain;
KW immunoglobulin therapeutic molecule; monobody; cancer.
XX
XX Synthetic.

OS
XX US2004033561-A1.
PN
XX 19-FEB-2004.
PD
XX 17-OCT-2002; 2002US-00272899.
PF
XX 19-OCT-2001; 2001US-0350166P.
PR
XX 26-JUN-2002; 2002US-0392364P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX
XX O'keefe TL, Healey JJ, Newman W, Ponath PD, Keyt BA;
PI
XX WPI; 2004-180050/17.
DR
XX N-PSDB; ADJ95969.
XX
XX New isolated nucleic acid molecules having an immunoglobulin cassette
PT construct, useful for producing immunoglobulin therapeutic molecules
PT termed monobodies, used as a therapeutic group in cancer disorders.
XX
XX Disclosure; SEQ ID NO 66; 84pp; English.
XX
XX The invention describes an isolated nucleic acid molecule comprising an
CC immunoglobulin cassette construct, wherein the immunoglobulin cassette
CC comprises an immunoglobulin leader molecule operably linked to a stable
CC immunoglobulin domain region. The methods and compositions of the present
CC invention are useful for producing immunoglobulins, in particular
CC immunoglobulin therapeutic molecules termed monobodies, used as a
CC therapeutic group in cancer disorders. This is the amino acid sequence of
XX an immunoglobulin DNA cassette construct.

SQ Sequence 134 AA;
Query Match 100.0%; Score 553; DB 8; Length 134;
Best Local Similarity 100.0%; Pred. No. 5.7e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTRQD 60
Db 28 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTRQD 87
Qy 61 SKDSTYSLSTLTLSKADYERKHKVACEVTHQGLSSPVTKSFNRGEC 107
Db 88 SKDSTYSLSTLTLSKADYERKHKVACEVTHQGLSSPVTKSFNRGEC 134

RESULT 66
AAP93559
ID AAP93559 standard; protein; 143 AA.
XX
XX
AC AAP93559;
XX
DT 25-MAR-2003 (revised)

DT 28-JAN-1991 (first entry)
XX
XX Sequence of human kappa light chain fragment.
KW HIV; antiviral; therapy; diagnosis.
XX
XX Homo sapiens.
XX
XX Key
FH Region
FT Location/Qualifiers
FT 1..37
FT /label
FT /note= "light variable and joining"
FT 37..38
FT /note= "insert site"
FT 38..38
FT /note= "light constant"
XX
XX WO8902922-A.
XX
XX 06-APR-1989.
XX
XX 03-OCT-1988; 88WO-US003414.
XX
XX 02-OCT-1987; 87US-00104329.
PR 28-SEP-1988; 88US-00250785.
XX
XX (GETH) GENENTECH INC.
XX
XX Capon DJ, Gregory TJ;
XX
XX WPI; 1989-114397/15.
DR P-PSDB; AAP93559.
XX
XX New nucleic acid sequences encoding adhesion, esp. CD 4, variants -
PT partic. with trans-membrane domain inactivated or fused to other peptide,
PT useful esp. for treating HIV infections.
XX
XX Example; Fig 5; 78pp; English.
XX
XX It is employed in the prepn. of CD4 fusions. The insert site is given in
CC the Features Table. CD4 fusion proteins can have antiviral and
CC immunomodulatory activity are esp. useful for treating HIV infections,
CC regardless of genetic variation within the virus. They and antibodies
CC raised against them can also be used diagnostically for assaying adhesions
CC and their ligands. (Updated on 25-MAR-2003 to correct PR field.) (Updated
CC on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 143 AA;
SQ
Query Match 100.0%; Score 553; DB 1; Length 143;
Best Local Similarity 100.0%; Pred. No. 6.2e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTRQD 60
Db 37 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTRQD 96
Qy 61 SKDSTYSLSTLTLSKADYERKHKVACEVTHQGLSSPVTKSFNRGEC 107
Db 97 SKDSTYSLSTLTLSKADYERKHKVACEVTHQGLSSPVTKSFNRGEC 143
RESULT 67
AEB27727
ID AEB27727 standard; protein; 155 AA.
XX
XX AEB27727;
XX
XX 08-SEP-2005 (first entry)
DT
XX Humanized 2H7 antibody light chain sequence.
DE
XX Antibody therapy; immunotherapy; autoimmune disease;
KW

KW B-lymphocyte-restricted differentiation antigen; Bp35; arthritis;
 KW immunosuppressive; antirheumatic; antiarthritic; antiinflammatory;
 KW dermatological; gastroenteric; antitumor; antidiabetic;
 KW antiarteriosclerotic; vasotropic; thyromimetic; antidiabetic;
 KW nephrotropic; nootropic; neuroprotective; cardiant; CD20-antagonist.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO2005060999-A2.
 PN
 XX
 PD 07-JUL-2005.
 XX
 XX 07-DEC-2004; 2004WO-US040949.
 PF
 XX 19-DEC-2003; 2003US-0531363P.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Brunetta PG;
 PI
 XX WPI; 2005-488599/49.
 DR
 XX Treating autoimmune diseases, such as rheumatoid arthritis, psoriasis,
 PT inflammatory bowel disease, Crohn's disease, ulcerative colitis, eczema,
 PT asthma, lupus, atherosclerosis and diabetes, using CD20 antagonists or
 PT antibodies.
 XX
 PS Disclosure; SEQ ID NO 3; Sipp; English.
 XX
 CC The invention relates to treating autoimmune disease in a patient. The
 CC method involves detecting CD20 antigen (also called human B-lymphocyte-
 CC restricted differentiation antigen, Bp35) or CD20-positive B cells in a
 CC sample from the patient. When CD20 or CD20-positive B cells is detected
 CC in the sample, a CD20 antagonist or antibody is administered to the
 CC patient to treat the autoimmune disease. Also disclosed are CD20
 CC proteins, nucleic acids and antibodies used in the methods of the
 CC invention. The CD20 antagonist in treating autoimmune disease comprises
 CC an antibody that is not conjugated with a cytotoxic agent and comprises
 CC rituximab or humanized 2H7. The antibody is also conjugated with a
 CC cytotoxic agent. The methods and compositions of the present invention
 CC are useful for diagnosing or treating autoimmune diseases, such as
 CC rheumatoid arthritis, psoriasis, inflammatory bowel disease, Crohn's
 CC disease, ulcerative colitis, eczema, asthma, lupus, atherosclerosis,
 CC aplastic anemia, Sjogren's syndrome, autoimmune thyroiditis, diabetes,
 CC Guillain-Barre syndrome, glomerulonephritis and coronary artery disease.
 CC The method consists essentially of administering the antagonist to the
 CC mammal. The CD20 protein or nucleic acid is detected in the initial step.
 CC The present sequence represents the light chain sequence of a humanized
 CC 2H7 antibody.
 XX
 SQ Sequence 155 AA;
 Query Match 100.0%; Score 553; DB 9; Length 155;
 Best Local Similarity 100.0%; Pred. No. 6.9e-48;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 DB 49 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 108
 QY 61 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
 DB 109 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 155
 RESULT 68
 AAM52145
 ID AAM52145 standard; protein; 193 AA.
 XX
 AC AAM52145;
 XX
 DT 05-FEB-2002 (first entry)
 OS

XX Humanised HMEG1 light chain.
 DE
 XX Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
 KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
 KW
 OS Synthetic.
 OS WO200174905-A1.
 PN
 XX 11-OCT-2001.
 PD
 XX 26-MAR-2001; 2001WO-GB001324.
 PF
 XX 03-APR-2000; 2000GB-00008049.
 PR
 XX 02-OCT-2000; 2000US-0237159P.
 PR
 XX (ANTI-) ANTISOMA RES LTD.
 PA
 XX Young RJ;
 PI
 XX WPI; 2001-662969/76.
 DR
 XX Novel compound used to treat cancer has target cell-specific portion
 PT comprising humanized monoclonal antibody having specificity for
 PT polymorphic epithelial mucin, and cytotoxic portion having
 PT endonucleolytic activity.
 XX
 PS Claim 20; Fig 3; 176pp; English.
 XX
 CC The invention relates to a compound which comprises a target cell-
 CC specific portion, comprising an humanised monoclonal antibody, having
 CC specificity for polymorphic epithelial mucin (PEM) or its antigen binding
 CC fragment and a cytotoxic portion having endonucleolytic activity,
 CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
 CC compound has cytostatic activity useful for treating cancer and acting as
 CC a potential inducer of apoptosis
 XX
 SQ Sequence 193 AA;
 Query Match 100.0%; Score 553; DB 4; Length 193;
 Best Local Similarity 100.0%; Pred. No. 9.1e-48;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 DB 87 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 146
 QY 61 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
 DB 147 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 193
 RESULT 69
 AAY29770
 ID AAY29770 standard; protein; 201 AA.
 XX
 AC AAY29770;
 XX
 DT 04-NOV-1999 (first entry)
 XX
 DE P-selectin ligand and kappa chain constant region fusion protein.
 XX
 KW Human; P-selectin ligand; glycoprotein; fusion protein; infection;
 KW inflammation; intercellular adhesion; ulcerative colitis; asthma;
 KW diabetes; transplant rejection; myocardial infarction; thermal injury;
 KW metastatic condition; autoimmune thyroiditis; multiple sclerosis;
 KW Reynaud's syndrome; neutrophilic dermatosis; Sweet's syndrome;
 KW Grave's disease; glomerulonephritis; gingivitis; periodontitis;
 KW Crohn's disease; necrotising enterocolitis.
 XX
 OS Homo sapiens.
 OS Synthetic.

XX WO9943834-A2.
 XX 02-SEP-1999.
 XX 25-FEB-1999; 99WO-US004302.
 XX 27-FEB-1998; 98US-00032080.
 XX (GEMY) GENETICS INST INC.
 XX Larsen GR, Sako DS, Chang X, Veldman GM, Cumming D, Kumar R;
 PI Shaw G, Camphausen R, Davis M;
 XX WPI; 1999-527628/44.
 XX N-PSDB; AA208843.
 XX New P-selectin ligand fusion proteins, used for treating e.g.
 PT inflammation, infections, asthma, diabetes, ulcerative colitis or
 PT transplant rejection.
 XX Claim 66; Page 128-129; 145pp; English.
 XX The present invention describes P-selectin ligand fusion proteins
 CC comprising amino acids 42-60, 42-310, 42-88, 42-118 or 42-189 of
 CC the P-selectin ligand protein. The fusion proteins comprising a P-
 CC selectin ligand act as ligands for P-selectin on human endothelial cells
 CC and platelets. The isolated P-selectin ligand proteins may be useful in
 CC treating conditions characterized by P-, E- or L-selectin mediated
 CC intercellular adhesion e.g. myocardial infarction, bacterial or viral
 CC infection, metastatic conditions, inflammatory disorders, thermal injury
 CC such as burns or frostbite, autoimmune thyroiditis, experimental allergic
 CC encephalomyelitis, multiple sclerosis, multiple organ injury syndrome
 CC secondary to trauma, diabetes, Reynaud's syndrome, neutrophilic
 CC dermatosis (Sweet's syndrome), inflammatory bowel disease, Grave's
 CC disease, glomerulonephritis, gingivitis, periodontitis, haemolytic
 CC uraemic syndrome, ulcerative colitis, Crohn's disease, necrotising
 CC enterocolitis, granulocyte transfusion associated syndrome, or cytokine-
 CC induced toxicity. Isolated P-selectin ligand proteins may also be useful
 CC in organ transplantation, both to prepare organs for transplantation and
 CC to quell organ transplant rejection. P-selectin ligand proteins may be
 CC used to treat haemodialysis and leukophoresis patients or used as an
 CC antimetastatic agent. The fusion proteins can also be used to treat a
 CC condition which is affected by the protein to which the P-selectin ligand
 CC protein is fused. The fusion proteins can be used for the production of
 CC antibodies for use in therapy, detection, diagnosis and drug screening.
 CC AA208839 to AA208850 encode specifically claimed fusion proteins from the
 CC present invention, which are given in AA29766 to AA29777
 XX Sequence 201 AA;
 Query Match 100.0%; Score 553; DB 2; Length 201;
 Best Local Similarity 100.0%; Pred. No. 9.6e-48; Indels 0; Gaps 0;
 Matches 107; Conservative 0; Mismatches 0;
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 Db 95 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 154
 QY 61 SKDSTYSLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
 Db 155 SKDSTYSLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 201
 RESULT 70
 ABP51955
 ID ABP51955 standard; protein; 212 AA.
 XX ABP51955;
 XX 09-OCT-2002 (first entry)
 XX Humanised anti-CD18 kappa LC sequence SEQ ID NO:5.

XX Bacterial host; protease; degp; prc; spr; anti-VEGF antibody; antibody;
 KW humanised; Apo2 ligand; anti-CD18; anti-tissue factor; 2C4; anti-CD20;
 KW anti-vascular endothelial growth factor; anti-Her-2; anti-CD40; Fab;
 KW anti-CD11a; Fab'; Fab'2; Fab'2-leucine zipper fusion; anti-VEGF Fab.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200248376-A2.
 XX 20-JUN-2002.
 XX 07-DEC-2001; 2001WO-US047581.
 XX 14-DEC-2000; 2000US-0256162P.
 XX (GETH) GENENTECH INC.
 XX Chen CY;
 XX WPI; 2002-583522/62.
 XX Novel Escherichia coli strain useful for producing polypeptide, deficient
 PT in degp and prc encoding protease, and harboring mutant spr gene, product
 of gene suppresses growth phenotypes of strains harbouring prc mutants.
 XX Example 1; Fig 10; 63pp; English.
 XX The present invention describes an Escherichia coli strain (I) deficient
 CC in chromosomal degp and prc encoding protease degp and prc, respectively,
 CC and harbouring a mutant spr gene, the product of mutant spr gene
 CC suppresses growth phenotypes exhibited by strains harbouring prc mutants.
 CC (I) is useful for producing a polypeptide, by culturing (I) comprising
 CC nucleic acid encoding the polypeptide, which is heterologous to the
 CC strain, such that the nucleic acid is expressed, and recovering the
 CC heterologous polypeptide from the strain. The heterologous polypeptide is
 CC proteolytically sensitive. Culturing of (I) is performed in a fermentor
 CC under conditions of high- or low-cell density fermentation. The
 CC polypeptide is recovered from the periplasm or culture medium of the
 CC strain. The polypeptide is an antibody (humanised or full-length
 CC antibody) or Apo2 ligand. The antibody is an anti-CD18, anti-vascular
 CC endothelial growth factor (VEGF), anti-tissue factor, 2C4, anti-Her-2,
 CC anti-CD20, anti-CD40, or anti-CD11a antibody. The antibody is also an
 CC antibody fragment having a light chain (kappa light chain). The antibody
 CC fragment is a Fab, Fab', Fab'2 or Fab'2-leucine zipper fusion, anti-CD18
 CC Fab'2-leucine zipper fusion, anti-tissue factor Fab'2-leucine zipper
 CC fusion or anti-VEGF Fab, with or without a histidine or lysine tag, anti-
 CC tissue factor Fab'2-leucine zipper fusion with a 6-histidine tag, or anti-
 CC -CD18 Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-CD18
 CC Fab'2-leucine zipper fusion with a 6-lysine tag. The present sequence
 CC represents a humanised anti-CD18 kappa LC sequence from the present
 CC invention
 XX Sequence 212 AA;
 Query Match 100.0%; Score 553; DB 5; Length 212;
 Best Local Similarity 100.0%; Pred. No. 1e-47;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 Db 106 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165
 QY 61 SKDSTYSLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
 Db 166 SKDSTYSLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 212
 RESULT 71
 AAO31100
 ID AAO31100 standard; protein; 212 AA.
 XX

```
AC AAO311100;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human A2-G8 SCF antibody light chain variable and constant region.
XX
DE Human; antibody; stem cell factor; mast cell growth factor; asthma; SCF;
KW steel factor; c-kit ligand; gene therapy.
XX
OS Homo sapiens.
XX
XX WO2003051311-A2.
XX
XX PN 26-JUN-2003.
XX
XX PD 16-DEC-2002; 2002WO-US040227.
XX
XX PF 17-DEC-2001; 2001US-0342174P.
XX
XX PR (FARB ) BAYER CORP.
XX
XX PA Takeuchi T, Tomkinson A, Neben S;
XX
XX PI WPI; 2003-523500/49.
XX
XX DR New purified human antibody that binds to stem cell factor protein,
XX useful for preparing a composition for treating asthma.
XX
XX PT Claim 9; Page 46; 94pp; English.
XX
XX PS The invention provides human antibodies that bind to stem cell factor
XX (SCF) protein. SCF is also known as mast cell growth factor, steel factor
XX or c-kit ligand. Antibodies of the invention are useful for preparing
XX compositions for treating asthma. They are also used in gene therapy. The
XX present sequence is human SCF antibody light chain variable and constant
XX region
XX
XX SQ Sequence 212 AA;
XX
XX Query Match 100.0%; Score 553; DB 6; Length 212;
XX Best Local Similarity 100.0%; Pred. No. 1e-47;
XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
XX
XX Db 106 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165
XX
XX QY 61 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
XX
XX Db 166 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 212
XX
XX
XX RESULT 72
XX AEF11766
XX ID AEF11766 standard; protein; 212 AA.
XX
XX AC AEF11766;
XX
XX DT 09-MAR-2006 (first entry)
XX
XX DE Human SCF-binding Ab A2-G8 light chain variable + constant regions.
XX
XX KW antibody therapy; antibody engineering; asthma; inflammation;
XX antiasthmatic; stem cell factor; SCF; light chain variable region;
XX light chain constant region.
XX
XX OS Homo sapiens.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Region 22..32
XX FT /label= CDR 1
XX FT /note= "Complementarity determining region 1"
XX
```

```
FT Region 48..54
FT /label= CDR_2
FT /note= "Complementarity determining region 2"
XX
FT Region 87..94
FT /label= CDR 3
FT /note= "Complementarity determining region 3"
XX
XX WO2006002064-A2.
XX
XX PN 05-JAN-2006.
XX
XX XX 14-JUN-2005; 2005WO-US021043.
XX
XX XX 14-JUN-2004; 2004US-00867506.
XX
XX PR 14-JUN-2004; 2004US-0579462P.
XX
XX PA (AERO-) AEROVANCE INC.
XX
XX XX Neben S, Takeuchi T, Tomkinson A, Delaria K, Yan K, Wong T;
XX PI Longphre M;
XX
XX DR WPI; 2006-079812/08.
XX
XX XX New purified human antibody, which binds to stem cell factor protein,
XX useful for treating asthma or a human disorder in which stem cell factor
XX protein is expressed in certain cells.
XX
XX PS Claim 30; SEQ ID NO 77; 108pp; English.
XX
XX XX The invention relates to: a purified human antibody (IgG) or fragment
XX thereof which binds to stem cell factor protein; a preparation comprising
XX the antibody, and/or a carrier; isolated polynucleotide(s) encoding the
XX antibody; an expression vector comprising the polynucleotide(s); a host
XX cell comprising the expression vector; a method of producing a human
XX antibody; a method of treating asthma or a human disorder in which stem
XX cell factor protein is expressed in certain cells; and a method for
XX identifying a disorder in which stem cell factor protein level is
XX elevated. The purified human antibody comprises the heavy chain variable
XX region human VH3 consensus framework residues, the light chain variable
XX region human V-kappa-1 or V-lambda-1 consensus framework residues, and
XX may be optionally bound to a cytotoxic molecule or detectable label. The
XX antibody, compositions and methods are useful for treating asthma or a
XX human disorder in which stem cell factor protein is expressed in certain
XX cells. This sequence is human stem cell factor-binding antibody A2-G8
XX light chain variable and constant regions. Note: claim 9 refers to SEQ ID
XX NO:77 as heavy chain variable and constant regions, but all other
XX mentions of SEQ ID NO:77 in the specification, including claim 30, refer
XX to it as light chain variable and constant regions.
XX
XX SQ Sequence 212 AA;
XX
XX Query Match 100.0%; Score 553; DB 10; Length 212;
XX Best Local Similarity 100.0%; Pred. No. 1e-47;
XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
XX
XX Db 106 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165
XX
XX QY 61 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
XX
XX Db 166 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 212
XX
XX
XX RESULT 73
XX AEF11804
XX ID AEF11804 standard; protein; 212 AA.
XX
XX XX
XX AC AEF11804;
XX
XX XX 09-MAR-2006 (first entry)
XX
XX DE SCF-binding Ab A2-G8 light chain variable + constant regions variant 5.
XX
```

XX antibody therapy; antibody engineering; asthma; inflammation;
 KW antiasthmatic; stem cell factor; SCF; light chain variable region;
 KW light chain constant region.
 XX Homo sapiens.
 OS Synthetic.
 XX WO2006002064-A2.
 XX 05-JAN-2006.
 XX 14-JUN-2005; 2005WO-US021043.
 XX 14-JUN-2004; 2004US-00867506.
 PR 14-JUN-2004; 2004US-0579462P.
 XX (AERO-) AEROVANCE INC.
 XX Neben S, Takeuchi T, Tomkinson A, Delaria K, Yan K, Wong T;
 PI Longphre M;
 XX WPI; 2006-079812/08.
 XX New purified human antibody, which binds to stem cell factor protein,
 PT useful for treating asthma or a human disorder in which stem cell factor
 PT protein is expressed in certain cells.
 XX Claim 30; Page; 108pp; English.
 XX The invention relates to: a purified human antibody (IgG) or fragment
 CC thereof which binds to stem cell factor protein; a preparation comprising
 CC the antibody, and/or a carrier; isolated polynucleotide(s) encoding the
 CC antibody; an expression vector comprising the polynucleotide(s); a host
 CC cell comprising the expression vector; a method of producing a human
 CC cell factor protein is expressed in certain cells; and a method for
 CC cell factor protein is expressed in certain cells; and a method for
 CC identifying a disorder in which stem cell factor protein level is
 CC elevated. The purified human antibody comprises the heavy chain variable
 CC region human V-kappa-1 or V-lambda-1 consensus framework residues, and
 CC may be optionally bound to a cytotoxic molecule or detectable label. The
 CC antibody, compositions and methods are useful for treating asthma or a
 CC human disorder in which stem cell factor protein is expressed in certain
 CC cells. This sequence is a variant of human stem cell factor-binding
 CC antibody A2-G8 light chain variable and constant regions. Note: this
 CC sequence is not shown in the specification but is derived from the human
 CC stem cell factor-binding antibody A2-G8 light chain variable and constant
 CC regions (AEF11766) and SCF-binding antibody clone B9 kappa-1 light chain
 CC variable region CDR3 (AEF11779).
 XX Sequence 212 AA;
 SQ Query Match 100.0%; Score 553; DB 10; Length 212;
 Best Local Similarity 100.0%; Pred. No. 1e-47;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 DB 106 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165
 QY 61 SKDSTYSLSSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
 DB 166 SKDSTYSLSSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 212
 RESULT 74
 AEF11801
 ID AEF11801 standard; protein; 212 AA.
 XX AEF11801;
 AC AEF11801;
 DT 09-MAR-2006 (first entry)

XX SCF-binding Ab A2-G8 light chain variable + constant regions variant 2.
 DE antibody therapy; antibody engineering; asthma; inflammation;
 XX antiasthmatic; stem cell factor; SCF; light chain variable region;
 KW light chain constant region.
 XX Homo sapiens.
 OS Synthetic.
 XX WO2006002064-A2.
 XX 05-JAN-2006.
 XX 14-JUN-2005; 2005WO-US021043.
 XX 14-JUN-2004; 2004US-00867506.
 PR 14-JUN-2004; 2004US-0579462P.
 XX (AERO-) AEROVANCE INC.
 XX Neben S, Takeuchi T, Tomkinson A, Delaria K, Yan K, Wong T;
 PI Longphre M;
 XX WPI; 2006-079812/08.
 XX New purified human antibody, which binds to stem cell factor protein,
 PT useful for treating asthma or a human disorder in which stem cell factor
 PT protein is expressed in certain cells.
 XX Claim 30; Page; 108pp; English.
 XX The invention relates to: a purified human antibody (IgG) or fragment
 CC thereof which binds to stem cell factor protein; a preparation comprising
 CC the antibody, and/or a carrier; isolated polynucleotide(s) encoding the
 CC antibody; an expression vector comprising the polynucleotide(s); a host
 CC cell comprising the expression vector; a method of producing a human
 CC cell factor protein is expressed in certain cells; and a method for
 CC cell factor protein is expressed in certain cells; and a method for
 CC identifying a disorder in which stem cell factor protein level is
 CC elevated. The purified human antibody comprises the heavy chain variable
 CC region human V-kappa-1 or V-lambda-1 consensus framework residues, and
 CC may be optionally bound to a cytotoxic molecule or detectable label. The
 CC antibody, compositions and methods are useful for treating asthma or a
 CC human disorder in which stem cell factor protein is expressed in certain
 CC cells. This sequence is a variant of human stem cell factor-binding
 CC antibody A2-G8 light chain variable and constant regions. Note: this
 CC sequence is not shown in the specification but is derived from the human
 CC stem cell factor-binding antibody A2-G8 light chain variable and constant
 CC regions (AEF11766) and SCF-binding antibody clone A12 kappa-1 light chain
 CC variable region CDR3 (AEF11776).
 XX Sequence 212 AA;
 SQ Query Match 100.0%; Score 553; DB 10; Length 212;
 Best Local Similarity 100.0%; Pred. No. 1e-47;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 DB 106 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165
 QY 61 SKDSTYSLSSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
 DB 166 SKDSTYSLSSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 212
 RESULT 75
 AEF11803
 ID AEF11803 standard; protein; 212 AA.
 XX AEF11803;
 AC AEF11803;

XX	09-MAR-2006	(first entry)
DT	SCF-binding Ab A2-G8	light chain variable + constant regions variant 4.
DE	antibody therapy; antibody engineering; asthma; inflammation;	
XX	antiatheumatic; stem cell factor; SCF; light chain variable region;	
KW	light chain constant region.	
KW		
XX	Homo sapiens.	
OS	Synthetic.	
OS		
XX	WO2006002064-A2.	
PN		
XX	05-JAN-2006.	
PD		
XX	14-JUN-2005; 2005WO-US021043.	
XX		
XX	14-JUN-2004; 2004US-00867506.	
PR		
PR	14-JUN-2004; 2004US-0579462P.	
XX		
XX	(AERO-) AEROVANCE INC.	
PA		
XX	Neben S, Takeuchi T, Tomkinson A, Delaria K, Yan K, Wong T;	
PI	Longphre M;	
PI		
XX	WPI; 2006-079812/08.	
DR		
XX	New purified human antibody, which binds to stem cell factor protein,	
PT	useful for treating asthma or a human disorder in which stem cell factor	
PT	protein is expressed in certain cells.	
PT		
XX		
PS	Claim 30; Page; 108pp; English.	
XX		
CC	The invention relates to: a purified human antibody (IgG) or fragment	
CC	thereof which binds to stem cell factor protein; a preparation comprising	
CC	the antibody, and/or a carrier; isolated polynucleotide(s) encoding the	
CC	antibody; an expression vector comprising the polynucleotide(s); a host	
CC	cell comprising the expression vector; a method of producing a human	
CC	antibody; a method of treating asthma or a human disorder in which stem	
CC	cell factor protein is expressed in certain cells; and a method for	
CC	identifying a disorder in which stem cell factor protein level is	
CC	elevated. The purified human antibody comprises the heavy chain variable	
CC	region human VH3 consensus framework residues, the light chain variable	
CC	region human V-kappa-1 or V-lambda-1 consensus framework residues, and	
CC	may be optionally bound to a cytotoxic molecule or detectable label. The	
CC	antibody, compositions and methods are useful for treating asthma or a	
CC	human disorder in which stem cell factor protein is expressed in certain	
CC	cells. This sequence is a variant of human stem cell factor-binding	
CC	antibody A2-G8 light chain variable and constant regions. Note: this	
CC	sequence is not shown in the specification but is derived from the human	
CC	stem cell factor-binding antibody A2-G8 light chain variable and constant	
CC	regions (AEF11766) and SCF-binding antibody clone A8 kappa-1 light chain	
CC	variable region CDR3 (AEF11778).	
XX		
XX	Sequence 212 AA;	
XX		
XX	Query Match	
XX	Best Local Similarity 100.0%; Score 553; DB 10; Length 212;	
XX	Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
Qy	1 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALGSGNSQESVTEQD 60	
Db	106 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALGSGNSQESVTEQD 165	
Qy	61 SKDSTYLSLSSTLTLSKADYEHKKVYACEVTHQGLSSPVTKSFNRGEC 107	
Db	166 SKDSTYLSLSSTLTLSKADYEHKKVYACEVTHQGLSSPVTKSFNRGEC 212	
XX		
XX	RESULT 76	
XX	AEF11805	
ID	AEF11805 standard; protein; 212 AA.	

AEF11806	AEF11806 standard; protein; 212 AA.
ID	AEF11800
AC	AEF11800
XX	AC AEF11800;
XX	AC AEF11800;
DT	09-MAR-2006 (first entry)
DE	SCF-binding Ab A2-G8 light chain variable + constant regions variant 7.
XX	antibody therapy; antibody engineering; asthma; inflammation;
KW	antiasmatic; stem cell factor; SCF; light chain variable region;
KW	light chain constant region.
XX	Homo sapiens.
OS	Synthetic.
OS	Synthetic.
FN	WO2006002064-A2.
XX	05-JAN-2006.
XX	14-JUN-2005; 2005WO-US021043.
PF	14-JUN-2004; 2004US-00867506.
PR	14-JUN-2004; 2004US-0579462P.
XX	(AERO-) AEROVANCE INC.
PA	Neben S, Takeuchi T, Tomkinson A, Delaria K, Yan K, Wong T;
PI	Longphre M;
PI	WPI; 2006-079812/08.
DR	New purified human antibody, which binds to stem cell factor protein,
XX	useful for treating asthma or a human disorder in which stem cell factor
PT	protein is expressed in certain cells.
PT	protein is expressed in certain cells.
XX	Claim 30; Page; 108pp; English.
PS	The invention relates to: a purified human antibody (IgG) or fragment
CC	thereof which binds to stem cell factor protein; a preparation comprising
CC	the antibody, and/or a carrier; isolated polynucleotide(s) encoding the
CC	antibody; an expression vector comprising the polynucleotide(s); a host
CC	cell comprising the expression vector; a method of producing a human
CC	antibody; a method of treating asthma or a human disorder in which stem
CC	cell factor protein is expressed in certain cells; and a method for
CC	identifying a disorder in which stem cell factor protein level is
CC	elevated. The purified human antibody comprises the heavy chain variable
CC	region human V-kappa-1 or V-lambda-1 consensus framework residues, and
CC	may be optionally bound to a cytotoxic molecule or detectable label. The
CC	antibody, compositions and methods are useful for treating asthma or a
CC	human disorder in which stem cell factor protein is expressed in certain
CC	cells. This sequence is a variant of human stem cell factor-binding
CC	antibody A2-G8 light chain variable and constant regions. Note: this
CC	sequence is not shown in the specification but is derived from the human
CC	stem cell factor-binding antibody A2-G8 light chain variable and constant
CC	regions (AEF11766) and SCF-binding antibody clone D5 kappa-1 light chain
CC	variable region CDR3 (AEF11781).
XX	Sequence 212 AA;
SQ	Query Match
	Best Local Similarity 100.0%; Score 553; DB 10; Length 212;
	Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB	106 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165
QY	61 SKDSTYSLSSTLTLSKADYERHKVYACEVTHOGLSSPVTKSPNRGEC 107
DB	166 SKDSTYSLSSTLTLSKADYERHKVYACEVTHOGLSSPVTKSPNRGEC 212

AEF11800	AEF11800 standard; protein; 212 AA.
ID	AEF11800
AC	AEF11800
XX	AC AEF11800;
XX	AC AEF11800;
DT	09-MAR-2006 (first entry)
DE	SCF-binding Ab A2-G8 light chain variable + constant regions variant 1.
XX	antibody therapy; antibody engineering; asthma; inflammation;
KW	antiasmatic; stem cell factor; SCF; light chain variable region;
KW	light chain constant region.
XX	Homo sapiens.
OS	Synthetic.
OS	Synthetic.
FN	WO2006002064-A2.
XX	05-JAN-2006.
XX	14-JUN-2005; 2005WO-US021043.
PF	14-JUN-2004; 2004US-00867506.
PR	14-JUN-2004; 2004US-0579462P.
XX	(AERO-) AEROVANCE INC.
PA	Neben S, Takeuchi T, Tomkinson A, Delaria K, Yan K, Wong T;
PI	Longphre M;
PI	WPI; 2006-079812/08.
DR	New purified human antibody, which binds to stem cell factor protein,
XX	useful for treating asthma or a human disorder in which stem cell factor
PT	protein is expressed in certain cells.
PT	protein is expressed in certain cells.
XX	Claim 30; Page; 108pp; English.
PS	The invention relates to: a purified human antibody (IgG) or fragment
CC	thereof which binds to stem cell factor protein; a preparation comprising
CC	the antibody, and/or a carrier; isolated polynucleotide(s) encoding the
CC	antibody; an expression vector comprising the polynucleotide(s); a host
CC	cell comprising the expression vector; a method of producing a human
CC	antibody; a method of treating asthma or a human disorder in which stem
CC	cell factor protein is expressed in certain cells; and a method for
CC	identifying a disorder in which stem cell factor protein level is
CC	elevated. The purified human antibody comprises the heavy chain variable
CC	region human V-kappa-1 or V-lambda-1 consensus framework residues, and
CC	may be optionally bound to a cytotoxic molecule or detectable label. The
CC	antibody, compositions and methods are useful for treating asthma or a
CC	human disorder in which stem cell factor protein is expressed in certain
CC	cells. This sequence is a variant of human stem cell factor-binding
CC	antibody A2-G8 light chain variable and constant regions. Note: this
CC	sequence is not shown in the specification but is derived from the human
CC	stem cell factor-binding antibody A2-G8 light chain variable and constant
CC	regions (AEF11766) and SCF-binding antibody clone B1 kappa-1 light chain
CC	variable region CDR3 (AEF11775).
XX	Sequence 212 AA;
SQ	Query Match
	Best Local Similarity 100.0%; Score 553; DB 10; Length 212;
	Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB	106 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165
QY	61 SKDSTYSLSSTLTLSKADYERHKVYACEVTHOGLSSPVTKSPNRGEC 107
DB	166 SKDSTYSLSSTLTLSKADYERHKVYACEVTHOGLSSPVTKSPNRGEC 212

```
Db      166 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 212
RESULT 79
ID      AEF11802 standard; protein; 212 AA.
XX
AC      AEF11802;
XX
DT      09-MAR-2006 (first entry)
XX
DE      SCF-binding Ab A2-G8 light chain variable + constant regions variant 3.
XX
KW      antibody therapy; antibody engineering; asthma; inflammation;
KW      antiasthmatic; stem cell factor; SCF; light chain variable region;
KW      light chain constant region.
XX
XX      Homo sapiens.
OS      Synthetic.
OS
FN      WO2006002064-A2.
XX
XX
PD      05-JAN-2006.
XX
XX
PF      14-JUN-2005; 2005WO-US021043.
XX
XX
PR      14-JUN-2004; 2004US-00867506.
PR      14-JUN-2004; 2004US-0579462P.
XX
XX      (AERO-) AEROVANCE INC.
XX
XX      Neben S, Takeuchi T, Tomkinson A, Delaria K, Yan K, Wong T;
XX      Longphre M;
PI
XX
DR      WPI; 2006-079812/08.
XX
XX      New purified human antibody, which binds to stem cell factor protein,
PT      useful for treating asthma or a human disorder in which stem cell factor
PT      protein is expressed in certain cells.
XX
XX      Claim 30; Page; 108pp; English.
PS
XX
CC      The invention relates to: a purified human antibody (IgG) or fragment
CC      thereof which binds to stem cell factor protein; a preparation comprising
CC      the antibody, and/or a carrier; isolated polynucleotide(s) encoding the
CC      antibody; an expression vector comprising the polynucleotide(s); a host
CC      cell comprising the expression vector; a method of producing a human
CC      antibody; a method of treating asthma or a human disorder in which stem
CC      cell factor protein is expressed in certain cells; and a method for
CC      identifying a disorder in which stem cell factor protein level is
CC      elevated. The purified human antibody comprises the heavy chain variable
CC      region human VH3 consensus framework residues, the light chain variable
CC      region human V-kappa-1 or V-lambda-1 consensus framework residues, and
CC      may be optionally bound to a cytotoxic molecule or detectable label. The
CC      antibody, compositions and methods are useful for treating asthma or a
CC      human disorder in which stem cell factor protein is expressed in certain
CC      cells. This sequence is a variant of human stem cell factor-binding
CC      antibody A2-G8 light chain variable and constant regions. Note: this
CC      sequence is not shown in the specification but is derived from the human
CC      stem cell factor-binding antibody A2-G8 light chain variable and constant
CC      regions (AEF11766) and SCF-binding antibody clone D6L kappa-1 light chain
CC      variable region CDR3 (AEF11777).
XX
XX      Sequence 212 AA;
SQ
Query Match      100.0%; Score 553; DB 10; Length 212;
Best Local Similarity 100.0%; Pred. No. 1e-47;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
Db      106 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 165

RESULT 81
ID      AAE10516 standard; protein; 213 AA.
XX
XX      61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
XX
XX      167 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
XX
```


AC AAE10516;
 XX 10-DEC-2001 (first entry)
 DE Humanised high potency antibody clone 24 full length light chain.
 XX
 XX Human; light chain; respiratory syncytial virus infection; virucide;
 KW parainfluenza virus; therapy; high potency antibody; drug; cocaine;
 KW cancer cell; toxic substance.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200164751-A2.
 PN 07-SEP-2001.
 PD
 XX 01-MAR-2001; 2001WO-US006815.
 PF 01-MAR-2000; 2000US-0186252P.
 XX (MEDI-) MEDIMMUNE INC.
 XX
 PI Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;
 XX WPI; 2001-582150/65.
 DR High potency recombinant antibody, useful for preventing and treating
 XX diseases induced or caused by viruses, especially respiratory syncytial
 PT virus and parainfluenza virus, has high kinetic association rate
 PT constant.
 XX
 PS Claim 23; Page 83-84; 98pp; English.
 XX
 CC The invention relates to a high potency antibody including its
 CC immunologically active portions, fragments and segments other than
 CC vitaxin. The antibody has increased potency, high rate constant for
 CC antibody-antigen complex formation and high affinity for any desired
 CC antigen. The high potency antibody is also useful for nullifying or
 CC ameliorating the effects of addictive drugs, such as cocaine. The high
 CC potency has specificity for antigenic determinants found on microbes such
 CC as viruses, bacteria or fungi, antigens found on cancer cells and toxic
 CC substances or product of toxic substances. The high potency antibody is
 CC useful for preventing or treating a disease caused by a virus such as
 CC respiratory syncytial virus (RSV) and parainfluenza virus (PIV). The
 CC present sequence is humanised high potency antibody full length light
 CC chain variable region
 XX
 SQ Sequence 213 AA;
 Query Match 100.0%; Score 553; DB 4; Length 213;
 Best Local Similarity 100.0%; Pred. No. 1e-47;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTVAAPSVFIIPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 DB 107 RTVAAPSVFIIPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
 QY 61 SKDSTYSLSSTLTLSKADYKHKYKVCVTHQGLSSPVTKSFNRGEC 107
 DB 167 SKDSTYSLSSTLTLSKADYKHKYKVCVTHQGLSSPVTKSFNRGEC 213
 RESULT 82
 AAE10526
 ID AAE10526 standard; protein; 213 AA.
 XX
 AC AAE10526;
 XX
 DT 10-DEC-2001 (first entry)
 XX Humanised high potency antibody clone 22 full length light chain.

KW Human; light chain; respiratory syncytial virus infection; virucide;
 KW parainfluenza virus; therapy; high potency antibody; drug; cocaine;
 KW cancer cell; toxic substance.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200164751-A2.
 PN 07-SEP-2001.
 PD
 XX 01-MAR-2001; 2001WO-US006815.
 PF 01-MAR-2000; 2000US-0186252P.
 XX (MEDI-) MEDIMMUNE INC.
 XX
 PI Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;
 XX WPI; 2001-582150/65.
 DR High potency recombinant antibody, useful for preventing and treating
 XX diseases induced or caused by viruses, especially respiratory syncytial
 PT virus and parainfluenza virus, has high kinetic association rate
 PT constant.
 XX
 PS Claim 23; Page 96; 98pp; English.
 XX
 CC The invention relates to a high potency antibody including its
 CC immunologically active portions, fragments and segments other than
 CC vitaxin. The antibody has increased potency, high rate constant for
 CC antibody-antigen complex formation and high affinity for any desired
 CC antigen. The high potency antibody is also useful for nullifying or
 CC ameliorating the effects of addictive drugs, such as cocaine. The high
 CC potency has specificity for antigenic determinants found on microbes such
 CC as viruses, bacteria or fungi, antigens found on cancer cells and toxic
 CC substances or product of toxic substances. The high potency antibody is
 CC useful for preventing or treating a disease caused by a virus such as
 CC respiratory syncytial virus (RSV) and parainfluenza virus (PIV). The
 CC present sequence is humanised high potency antibody full length light
 CC chain variable region
 XX
 SQ Sequence 213 AA;
 Query Match 100.0%; Score 553; DB 4; Length 213;
 Best Local Similarity 100.0%; Pred. No. 1e-47;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTVAAPSVFIIPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 DB 107 RTVAAPSVFIIPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
 QY 61 SKDSTYSLSSTLTLSKADYKHKYKVCVTHQGLSSPVTKSFNRGEC 107
 DB 167 SKDSTYSLSSTLTLSKADYKHKYKVCVTHQGLSSPVTKSFNRGEC 213
 RESULT 83
 AAE10512
 ID AAE10512 standard; protein; 213 AA.
 XX
 AC AAE10512;
 XX
 DT 10-DEC-2001 (first entry)
 XX Humanised high potency antibody clone 26 full length light chain.
 DE Human; light chain; respiratory syncytial virus infection; virucide;
 KW parainfluenza virus; therapy; high potency antibody; drug; cocaine;
 KW cancer cell; toxic substance.
 XX
 OS Homo sapiens.
 OS Synthetic.

```
XX WO200164751-A2.
XX 07-SEP-2001.
XX 01-MAR-2001; 2001WO-US006815.
XX 01-MAR-2000; 2000US-0186252P.
XX (MEDI-) MEDIMMUNE INC.
XX Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;
XX WPI; 2001-582150/65.
XX High potency recombinant antibody, useful for preventing and treating
XX diseases induced or caused by viruses, especially respiratory syncytial
XX virus and parainfluenza virus, has high kinetic association rate
XX constant.
XX Claim 23; Page 78-79; 98pp; English.
XX The invention relates to a high potency antibody including its
XX immunologically active portions, fragments and segments other than
XX vitaxin. The antibody has increased potency, high rate constant for
XX antibody-antigen complex formation and high affinity for any desired
XX antigen. The high potency antibody is also useful for nullifying or
XX ameliorating the effects of addictive drugs, such as cocaine. The high
XX potency has specificity for antigenic determinants found on microbes such
XX as viruses, bacteria or fungi, antigens found on cancer cells and toxic
XX substances or product of toxic substances. The high potency antibody is
XX useful for preventing or treating a disease caused by a virus such as
XX respiratory syncytial virus (RSV) and parainfluenza virus (PIV). The
XX present sequence is humanised high potency antibody full length light
XX chain variable region
XX Sequence 213 AA;
XX Query Match 100.0%; Score 553; DB 4; Length 213;
XX Best Local Similarity 100.0%; Pred. No. 1e-47;
XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
XX 107 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
XX
XX 61 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTGKSFNRGEC 107
XX 167 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTGKSFNRGEC 213
XX
XX RESULT 84
XX AA010514
XX ID AA010514 standard; protein; 213 AA.
XX AC AA010514;
XX 10-DEC-2001 (first entry)
XX Humanised high potency antibody clone 18 full length light chain.
XX Human; light chain; respiratory syncytial virus infection; virucide;
XX parainfluenza virus; therapy; high potency antibody; drug; cocaine;
XX cancer cell; toxic substance.
XX Homo sapiens.
XX Synthetic.
XX WO200164751-A2.
XX 07-SEP-2001.
XX 01-MAR-2001; 2001WO-US006815.
XX PF
```

```
XX 01-MAR-2000; 2000US-0186252P.
XX (MEDI-) MEDIMMUNE INC.
XX Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;
XX WPI; 2001-582150/65.
XX High potency recombinant antibody, useful for preventing and treating
XX diseases induced or caused by viruses, especially respiratory syncytial
XX virus and parainfluenza virus, has high kinetic association rate
XX constant.
XX Claim 23; Page 80-81; 98pp; English.
XX The invention relates to a high potency antibody including its
XX immunologically active portions, fragments and segments other than
XX vitaxin. The antibody has increased potency, high rate constant for
XX antibody-antigen complex formation and high affinity for any desired
XX antigen. The high potency antibody is also useful for nullifying or
XX ameliorating the effects of addictive drugs, such as cocaine. The high
XX potency has specificity for antigenic determinants found on microbes such
XX as viruses, bacteria or fungi, antigens found on cancer cells and toxic
XX substances or product of toxic substances. The high potency antibody is
XX useful for preventing or treating a disease caused by a virus such as
XX respiratory syncytial virus (RSV) and parainfluenza virus (PIV). The
XX present sequence is humanised high potency antibody full length light
XX chain variable region
XX Sequence 213 AA;
XX Query Match 100.0%; Score 553; DB 4; Length 213;
XX Best Local Similarity 100.0%; Pred. No. 1e-47;
XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
XX 107 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
XX
XX 61 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTGKSFNRGEC 107
XX 167 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTGKSFNRGEC 213
XX
XX RESULT 85
XX AA010524
XX ID AA010524 standard; protein; 213 AA.
XX AC AA010524;
XX 10-DEC-2001 (first entry)
XX Humanised high potency antibody clone 21 full length light chain.
XX Human; light chain; respiratory syncytial virus infection; virucide;
XX parainfluenza virus; therapy; high potency antibody; drug; cocaine;
XX cancer cell; toxic substance.
XX Homo sapiens.
XX Synthetic.
XX WO200164751-A2.
XX 07-SEP-2001.
XX 01-MAR-2001; 2001WO-US006815.
XX PF
XX 01-MAR-2000; 2000US-0186252P.
XX (MEDI-) MEDIMMUNE INC.
XX Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;
XX PF
```

XX WPI; 2001-582150/65.
XX High potency recombinant antibody, useful for preventing and treating
PT diseases induced or caused by viruses, especially respiratory syncytial
PT virus and parainfluenza virus, has high kinetic association rate
PT constant.
XX Claim 23; Page 93-94; 98pp; English.
XX The invention relates to a high potency antibody including its
CC immunologically active portions, fragments and segments other than
CC vitaxin. The antibody has increased potency, high rate constant for
CC antibody-antigen complex formation and high affinity for any desired
CC antigen. The high potency antibody is also useful for nullifying or
CC ameliorating the effects of addictive drugs, such as cocaine. The high
CC potency has specificity for antigenic determinants found on microbes such
CC as viruses, bacteria or fungi, antigens found on cancer cells and toxic
CC substances or product of toxic substances. The high potency antibody is
CC useful for preventing or treating a disease caused by a virus such as
CC respiratory syncytial virus (RSV) and parainfluenza virus (PIV). The
CC present sequence is humanised high potency antibody full length light
CC chain variable region
XX
SQ Sequence 213 AA;
Query Match 100.0%; Score 553; DB 4; Length 213;
Best Local Similarity 100.0%; Pred. No. 1e-47;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIFFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIFFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
QY 61 SKDSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 213
RESULT 86
AAE10518
ID AAE10518 standard; protein; 213 AA.
AC AAE10518;
XX 10-DEC-2001 (first entry)
XX Humanised high potency antibody clone 19 full length light chain.
DE Human; light chain; respiratory syncytial virus infection; virucide;
KW parainfluenza virus; therapy; high potency antibody; drug; cocaine;
KW cancer cell; toxic substance.
XX Homo sapiens.
OS Synthetic.
XX WO200164751-A2.
PN 07-SEP-2001.
XX 01-MAR-2001; 2001WO-US006815.
PF 01-MAR-2001; 2001WO-US006815.
XX 01-MAR-2000; 2000US-0186252P.
XX (MEDI-) MEDIMUNE INC.
PA Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;
PI WPI; 2001-582150/65.
XX High potency recombinant antibody, useful for preventing and treating
PT diseases induced or caused by viruses, especially respiratory syncytial
PT virus and parainfluenza virus, has high kinetic association rate

PT constant.
XX Claim 23; Page 86; 98pp; English.
XX The invention relates to a high potency antibody including its
CC immunologically active portions, fragments and segments other than
CC vitaxin. The antibody has increased potency, high rate constant for
CC antibody-antigen complex formation and high affinity for any desired
CC antigen. The high potency antibody is also useful for nullifying or
CC ameliorating the effects of addictive drugs, such as cocaine. The high
CC potency has specificity for antigenic determinants found on microbes such
CC as viruses, bacteria or fungi, antigens found on cancer cells and toxic
CC substances or product of toxic substances. The high potency antibody is
CC useful for preventing or treating a disease caused by a virus such as
CC respiratory syncytial virus (RSV) and parainfluenza virus (PIV). The
CC present sequence is humanised high potency antibody full length light
CC chain variable region
XX
SQ Sequence 213 AA;
Query Match 100.0%; Score 553; DB 4; Length 213;
Best Local Similarity 100.0%; Pred. No. 1e-47;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIFFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIFFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
QY 61 SKDSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 213
RESULT 87
AAE10522
ID AAE10522 standard; protein; 213 AA.
AC AAE10522;
XX 10-DEC-2001 (first entry)
XX Humanised high potency antibody clone 23 full length light chain.
DE Human; light chain; respiratory syncytial virus infection; virucide;
KW parainfluenza virus; therapy; high potency antibody; drug; cocaine;
KW cancer cell; toxic substance.
XX Homo sapiens.
OS Synthetic.
XX WO200164751-A2.
PN 07-SEP-2001.
XX 01-MAR-2001; 2001WO-US006815.
PF 01-MAR-2000; 2000US-0186252P.
XX (MEDI-) MEDIMUNE INC.
PA Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;
PI WPI; 2001-582150/65.
XX High potency recombinant antibody, useful for preventing and treating
PT diseases induced or caused by viruses, especially respiratory syncytial
PT virus and parainfluenza virus, has high kinetic association rate
PT constant.
XX Claim 23; Page 91; 98pp; English.
XX The invention relates to a high potency antibody including its
CC immunologically active portions, fragments and segments other than

CC vitaxin. The antibody has increased potency, high rate constant for
CC antibody-antigen complex formation and high affinity for any desired
CC antigen. The high potency antibody is also useful for nullifying or
CC ameliorating the effects of addictive drugs, such as cocaine. The high
CC potency has specificity for antigenic determinants found on microbes such
CC as viruses, bacteria or fungi, antigens found on cancer cells and toxic
CC substances or product of toxic substances. The high potency antibody is
CC useful for preventing or treating a disease caused by a virus such as
CC respiratory syncytial virus (RSV) and parainfluenza virus (PIV). The
CC present sequence is humanised high potency antibody full length light
CC chain variable region
XX
SQ Sequence 213 AA;

Query Match 100.0%; Score 553; DB 4; Length 213;
Best Local Similarity 100.0%; Pred. No. 1e-47;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
107 RTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

DB 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
107 RTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTGKFNRGEC 107
167 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTGKFNRGEC 213

DB 167 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTGKFNRGEC 213

RESULT 88
AAE10510
ID AAE10510 standard; protein; 213 AA.
XX
AC AAE10510;
XX
DT 10-DEC-2001 (first entry)
DE Humanised high potency antibody clone 25 full length light chain.
XX
KW Human; light chain; respiratory syncytial virus infection; virucide;
KW parainfluenza virus; therapy; high potency antibody; drug; cocaine;
KW cancer cell; toxic substance.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200164751-A2.
XX
PD 07-SEP-2001.
XX
PF 01-MAR-2001; 2001WO-US006815.
XX
PR 01-MAR-2000; 2000US-0186252P.
XX
PA (MEDI-) MEDIMUNE INC.
XX
PI Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;
XX
DR WPI; 2001-582150/65.
XX
PT High potency recombinant antibody, useful for preventing and treating
PT diseases induced or caused by viruses, especially respiratory syncytial
PT virus and parainfluenza virus, has high kinetic association rate
PT constant.
XX
PS Claim 23; Page 75-76; 98pp; English.
XX
CC The invention relates to a high potency antibody including its
CC immunologically active portions, fragments and segments other than
CC vitaxin. The antibody has increased potency, high rate constant for
CC antibody-antigen complex formation and high affinity for any desired
CC antigen. The high potency antibody is also useful for nullifying or
CC ameliorating the effects of addictive drugs, such as cocaine. The high
CC potency has specificity for antigenic determinants found on microbes such
CC as viruses, bacteria or fungi, antigens found on cancer cells and toxic

CC substances or product of toxic substances. The high potency antibody is
CC useful for preventing or treating a disease caused by a virus such as
CC respiratory syncytial virus (RSV) and parainfluenza virus (PIV). The
CC present sequence is humanised high potency antibody full length light
CC chain variable region
XX
SQ Sequence 213 AA;

Query Match 100.0%; Score 553; DB 4; Length 213;
Best Local Similarity 100.0%; Pred. No. 1e-47;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
107 RTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

DB 107 RTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTGKFNRGEC 107
167 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTGKFNRGEC 213

DB 167 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTGKFNRGEC 213

RESULT 89
AAE10520
ID AAE10520 standard; protein; 213 AA.
XX
AC AAE10520;
XX
DT 10-DEC-2001 (first entry)
DE Humanised high potency antibody clone 20 full length light chain.
XX
KW Human; light chain; respiratory syncytial virus infection; virucide;
KW parainfluenza virus; therapy; high potency antibody; drug; cocaine;
KW cancer cell; toxic substance.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200164751-A2.
XX
PD 07-SEP-2001.
XX
PF 01-MAR-2001; 2001WO-US006815.
XX
PR 01-MAR-2000; 2000US-0186252P.
XX
PA (MEDI-) MEDIMUNE INC.
XX
PI Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;
XX
DR WPI; 2001-582150/65.
XX
PT High potency recombinant antibody, useful for preventing and treating
PT diseases induced or caused by viruses, especially respiratory syncytial
PT virus and parainfluenza virus, has high kinetic association rate
PT constant.
XX
PS Claim 23; Page 88-89; 98pp; English.
XX
CC The invention relates to a high potency antibody including its
CC immunologically active portions, fragments and segments other than
CC vitaxin. The antibody has increased potency, high rate constant for
CC antibody-antigen complex formation and high affinity for any desired
CC antigen. The high potency antibody is also useful for nullifying or
CC ameliorating the effects of addictive drugs, such as cocaine. The high
CC potency has specificity for antigenic determinants found on microbes such
CC as viruses, bacteria or fungi, antigens found on cancer cells and toxic
CC substances or product of toxic substances. The high potency antibody is
CC useful for preventing or treating a disease caused by a virus such as
CC respiratory syncytial virus (RSV) and parainfluenza virus (PIV). The
CC present sequence is humanised high potency antibody full length light
CC chain variable region
XX

```

SQ Sequence 213 AA;
  Query Match          100.0%; Score 553; DB 4; Length 213;
  Best Local Similarity 100.0%; Pred. No. 1e-47;
  Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||
Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
   |||||
Db 167 SKDSTYSLSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 90
AAB83157
ID AAB83157 standard; protein; 213 AA.
AC AAB83157;
XX
XX
DT 02-JUL-2001 (first entry)
XX
DE Ganglioside GM2 antibody-related protein #2.
XX
KW Ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer.
XX
OS Unidentified.
XX
PN WO200123431-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006775.
XX
PR 30-SEP-1999; 95JP-00278292.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Nakamura K, Niwa R;
XX
DR WPI; 2001-266142/27.
XX
CC Monoclonal antibodies against ganglioside GM2 combined with drugs,
PT radioisotopes or proteins for treatment and diagnosis of cancer.
XX
PS Claim 43; Page 65-67; 80pp; Japanese.
XX
CC The present invention relates to derivatives of an antibody against
CC ganglioside GM2. The antibody may be a monoclonal antibody or its
CC fragments. The antibody is combined with a radioactive isotope, protein
CC or small drug in the treatment and diagnosis of cancer
XX
SQ Sequence 213 AA;
  Query Match          100.0%; Score 553; DB 4; Length 213;
  Best Local Similarity 100.0%; Pred. No. 1e-47;
  Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||
Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
   |||||
Db 167 SKDSTYSLSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 91
ABP66573
ID ABP66573 standard; protein; 213 AA.
XX
AC ABP66573;

XX
DT 04-DEC-2002 (first entry)
XX
DE Human RSV antibody variable light chain.
XX
KW Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
KW complementarity determining region; respiratory syncytial virus;
KW virucide; pulmonary; antiinflammatory; cardiant; anti-Hiv; vaccine;
KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;
KW bronchopulmonary dysplasia; congenital heart disease;
KW congenital immunodeficiency; acquired immunodeficiency.
XX
OS Homo sapiens.
XX
PN WO200243660-A2.
XX
PD 06-JUN-2002.
XX
PF 28-NOV-2001; 2001WO-US044807.
XX
PR 28-NOV-2000; 2000US-00724396.
XX
PA (MEDI-) MEDIUMUNE INC.
XX
PI Young JF, Koenig S, Johnson LS;
XX
DR WPI; 2002-706803/76.
XX
CC Antibody for treating respiratory syncytial virus (RSV) infection,
PT comprises a variable heavy/light domain or complementarity determining
PT regions 1 - 3 of variable light/heavy chains, that immunospecifically
PT binds to RSV antigen.
XX
PS Disclosure; Page 254; 298pp; English.
XX
CC The invention relates to a novel antibody comprising a variable heavy
CC (VH) domain, variable light (VL) domain, VH complementarity determining
CC region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the
CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)
CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
CC and immunostimulant activity. The polynucleotides of the invention may
CC have a use in a vaccine, and in gene therapy. The antibody is useful for
CC treating or ameliorating a RSV infection in a human. The antibody is also
CC useful for preventing, treating or ameliorating one or more symptoms
CC associated with RSV infection in a mammal, e.g. cystic fibrosis.
CC bronchopulmonary dysplasia, congenital heart disease, congenital
CC immunodeficiency or acquired immunodeficiency, or after a bone marrow
CC transplant. The sequence represents a variable domain of a human RSV
CC antibody of the invention
XX
SQ Sequence 213 AA;
  Query Match          100.0%; Score 553; DB 5; Length 213;
  Best Local Similarity 100.0%; Pred. No. 1e-47;
  Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||
Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
   |||||
Db 167 SKDSTYSLSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 92
ABP66591
ID ABP66591 standard; protein; 213 AA.
XX
AC ABP66591;
XX

```

```
DT 04-DEC-2002 (first entry)
XX Human RSV antibody variable light chain.
DE
XX
XX Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
KW complementarity determining region; respiratory syncytial virus;
KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;
KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;
KW bronchopulmonary dysplasia; congenital heart disease;
KW congenital immunodeficiency; acquired immunodeficiency.
XX
OS Homo sapiens.
XX
XX WO200243660-A2.
XX
XX 06-JUN-2002.
XX
XX 28-NOV-2001; 2001WO-US044807.
XX
XX 28-NOV-2000; 2000US-00724396.
XX
XX 28-NOV-2000; 2000US-00724531.
XX
XX (MEDI-) MEDIUMMUNE INC.
XX
XX Young JF, Koenig S, Johnson LS;
XX
XX WPI; 2002-706803/76.
XX
XX Antibody for treating respiratory syncytial virus (RSV) infection,
XX comprises a variable heavy/light domain or complementarity determining
XX regions 1 - 3 of variable light/heavy chains, that immunospecifically
XX binds to RSV antigen.
XX
XX Disclosure; Page 274-275; 298pp; English.
XX
XX The invention relates to a novel antibody comprising a variable heavy
XX (VH) domain, variable light (VL) domain, VH complementarity determining
XX region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the
XX antibody immunospecifically binds to a respiratory syncytial virus (RSV)
XX antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
XX invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
XX and immunostimulant activity. The polynucleotides of the invention may
XX have a use in a vaccine, and in gene therapy. The antibody is useful for
XX treating or ameliorating a RSV infection in a human. The antibody is also
XX useful for preventing, treating or ameliorating one or more symptoms
XX associated with RSV infection in a mammal, e.g. cystic fibrosis,
XX bronchopulmonary dysplasia, congenital heart disease, congenital
XX immunodeficiency or acquired immunodeficiency, or after a bone marrow
XX transplant. The sequence represents a variable domain of a human RSV
XX antibody of the invention
XX
XX SQ Sequence 213 AA;
XX
XX Query Match 100.0%; Score 553; DB 5; Length 213;
XX Best Local Similarity 100.0%; Pred. No. 1e-47;
XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
XX Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
XX
XX QY 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
XX Db 167 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
XX
XX RESULT 93
XX ABP66607
XX ID ABP66607 standard; protein; 213 AA.
XX
XX AC ABP66607;
XX
XX DT 04-DEC-2002 (first entry)
XX
```

```
XX Human RSV antibody variable light chain.
DE
XX
XX Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
KW complementarity determining region; respiratory syncytial virus;
KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;
KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;
KW bronchopulmonary dysplasia; congenital heart disease;
KW congenital immunodeficiency; acquired immunodeficiency.
XX
OS Homo sapiens.
XX
XX WO200243660-A2.
XX
XX 06-JUN-2002.
XX
XX 28-NOV-2001; 2001WO-US044807.
XX
XX 28-NOV-2000; 2000US-00724396.
XX
XX 28-NOV-2000; 2000US-00724531.
XX
XX (MEDI-) MEDIUMMUNE INC.
XX
XX Young JF, Koenig S, Johnson LS;
XX
XX WPI; 2002-706803/76.
XX
XX Antibody for treating respiratory syncytial virus (RSV) infection,
XX comprises a variable heavy/light domain or complementarity determining
XX regions 1 - 3 of variable light/heavy chains, that immunospecifically
XX binds to RSV antigen.
XX
XX Disclosure; Page 292-293; 298pp; English.
XX
XX The invention relates to a novel antibody comprising a variable heavy
XX (VH) domain, variable light (VL) domain, VH complementarity determining
XX region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the
XX antibody immunospecifically binds to a respiratory syncytial virus (RSV)
XX antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
XX invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
XX and immunostimulant activity. The polynucleotides of the invention may
XX have a use in a vaccine, and in gene therapy. The antibody is useful for
XX treating or ameliorating a RSV infection in a human. The antibody is also
XX useful for preventing, treating or ameliorating one or more symptoms
XX associated with RSV infection in a mammal, e.g. cystic fibrosis,
XX bronchopulmonary dysplasia, congenital heart disease, congenital
XX immunodeficiency or acquired immunodeficiency, or after a bone marrow
XX transplant. The sequence represents a variable domain of a human RSV
XX antibody of the invention
XX
XX SQ Sequence 213 AA;
XX
XX Query Match 100.0%; Score 553; DB 5; Length 213;
XX Best Local Similarity 100.0%; Pred. No. 1e-47;
XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
XX Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
XX
XX QY 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
XX Db 167 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
XX
XX RESULT 94
XX ABP66605
XX ID ABP66605 standard; protein; 213 AA.
XX
XX AC ABP66605;
XX
XX DT 04-DEC-2002 (first entry)
XX
```

DE Human RSV antibody variable light chain.

XX Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
 KW complementarity determining region; respiratory syncytial virus;
 KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;
 KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;
 KW bronchopulmonary dysplasia; congenital heart disease;
 KW congenital immunodeficiency; acquired immunodeficiency.

XX Homo sapiens.

OS WO200243660-A2.

PN 06-JUN-2002.

XX 28-NOV-2001; 2001WO-US044807.

XX 28-NOV-2000; 2000US-00724396.

PR 28-NOV-2000; 2000US-00724531.

XX (MEDI-) MEDIUMMUNE INC.

PA Young JF, Koenig S, Johnson LS;
 PI WPI; 2002-706803/76.

XX Antibody for treating respiratory syncytial virus (RSV) infection,
 PT comprises a variable heavy/light domain or complementarity determining
 PT regions 1 - 3 of variable light/heavy chains, that immunospecifically
 PT binds to RSV antigen.

XX Disclosure; Page 290; 298pp; English.

XX The invention relates to a novel antibody comprising a variable heavy
 CC (VH) domain, variable light (VL) domain, VH complementarity determining
 CC region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the
 CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)
 CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
 CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
 CC and immunostimulant activity. The polynucleotides of the invention may
 CC have a use in a vaccine, and in gene therapy. The antibody is useful for
 CC treating or ameliorating a RSV infection in a human. The antibody is also
 CC useful for preventing, treating or ameliorating one or more symptoms
 CC associated with RSV infection in a mammal, e.g. cystic fibrosis,
 CC bronchopulmonary dysplasia, congenital heart disease, congenital
 CC immunodeficiency or acquired immunodeficiency, or after a bone marrow
 CC transplant. The sequence represents a variable domain of a human RSV
 CC antibody of the invention

XX Sequence 213 AA;

Query Match 100.0%; Score 553; DB 5; Length 213;
 Best Local Similarity 100.0%; Pred. No. 1e-47;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 DB 107 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYLSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
 DB 167 SKDSTYLSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 95
 ABP66569
 ID ABP66569 standard; protein; 213 AA.
 XX
 AC ABP66569;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human RSV antibody variable light chain.

XX Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
 KW complementarity determining region; respiratory syncytial virus;
 KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;
 KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;
 KW bronchopulmonary dysplasia; congenital heart disease;
 KW congenital immunodeficiency; acquired immunodeficiency.

XX Homo sapiens.

OS WO200243660-A2.

PN 06-JUN-2002.

XX 28-NOV-2001; 2001WO-US044807.

XX 28-NOV-2000; 2000US-00724396.

PR 28-NOV-2000; 2000US-00724531.

XX (MEDI-) MEDIUMMUNE INC.

PA Young JF, Koenig S, Johnson LS;
 PI WPI; 2002-706803/76.

XX Antibody for treating respiratory syncytial virus (RSV) infection,
 PT comprises a variable heavy/light domain or complementarity determining
 PT regions 1 - 3 of variable light/heavy chains, that immunospecifically
 PT binds to RSV antigen.

XX Disclosure; Page 290; 298pp; English.

XX The invention relates to a novel antibody comprising a variable heavy
 CC (VH) domain, variable light (VL) domain, VH complementarity determining
 CC region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the
 CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)
 CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
 CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
 CC and immunostimulant activity. The polynucleotides of the invention may
 CC have a use in a vaccine, and in gene therapy. The antibody is useful for
 CC treating or ameliorating a RSV infection in a human. The antibody is also
 CC useful for preventing, treating or ameliorating one or more symptoms
 CC associated with RSV infection in a mammal, e.g. cystic fibrosis,
 CC bronchopulmonary dysplasia, congenital heart disease, congenital
 CC immunodeficiency or acquired immunodeficiency, or after a bone marrow
 CC transplant. The sequence represents a variable domain of a human RSV
 CC antibody of the invention

XX Sequence 213 AA;

Query Match 100.0%; Score 553; DB 5; Length 213;
 Best Local Similarity 100.0%; Pred. No. 1e-47;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 DB 107 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYLSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
 DB 167 SKDSTYLSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 95
 ABP66569
 ID ABP66569 standard; protein; 213 AA.
 XX
 AC ABP66569;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human RSV antibody variable light chain.

```
KW Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
KW complementarity determining region; respiratory syncytial virus;
KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;
KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;
KW bronchopulmonary dysplasia; congenital heart disease;
KW congenital immunodeficiency; acquired immunodeficiency.
XX
OS Homo sapiens.
XX
XX WO200243660-A2.
XX
XX 06-JUN-2002.
XX
XX 28-NOV-2001; 2001WO-US044807.
XX
XX 28-NOV-2000; 2000US-00724396.
XX
XX 28-NOV-2000; 2000US-00724531.
XX
XX (MEDI-) MEDIUMMUNE INC.
XX
XX Young JF, Koenig S, Johnson LS;
XX WPI; 2002-706803/76.
XX
XX Antibody for treating respiratory syncytial virus (RSV) infection,
XX comprises a variable heavy/light domain or complementarity determining
XX regions 1 - 3 of variable light/heavy chains, that immunospecifically
XX binds to RSV antigen.
XX
XX Disclosure; Page 267-268; 298pp; English.
XX
XX The invention relates to a novel antibody comprising a variable heavy
XX (VH) domain, variable light (VL) domain, VH complementarity determining
XX region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the
XX antibody immunospecifically binds to a respiratory syncytial virus (RSV)
XX antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
XX invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
XX and immunostimulant activity. The polynucleotides of the invention may
XX have a use in a vaccine, and in gene therapy. The antibody is useful for
XX treating or ameliorating a RSV infection in a human. The antibody is also
XX useful for preventing, treating or ameliorating one or more symptoms
XX associated with RSV infection in a mammal, e.g. cystic fibrosis,
XX bronchopulmonary dysplasia, congenital heart disease, congenital
XX immunodeficiency or acquired immunodeficiency, or after a bone marrow
XX transplant. The sequence represents a variable domain of a human RSV
XX antibody of the invention
XX
XX Sequence 213 AA;
XX
XX Query Match 100.0%; Score 553; DB 5; Length 213;
XX Best Local Similarity 100.0%; Pred. No. 1e-47;
XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
XX |
XX 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
XX |
XX
XX QY 61 SKDSTYSLSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
XX |
XX 167 SKDSTYSLSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213
XX |
XX
XX RESULT 97
XX ABP66597
XX ID ABP66597 standard; protein; 213 AA.
XX
XX AC ABP66597;
XX
XX 04-DEC-2002 (first entry)
XX
XX Human RSV antibody variable light chain.
XX
XX Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
```

```
KW complementarity determining region; respiratory syncytial virus;
KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;
KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;
KW bronchopulmonary dysplasia; congenital heart disease;
KW congenital immunodeficiency; acquired immunodeficiency.
XX
OS Homo sapiens.
XX
XX WO200243660-A2.
XX
XX 06-JUN-2002.
XX
XX 28-NOV-2001; 2001WO-US044807.
XX
XX 28-NOV-2000; 2000US-00724396.
XX
XX 28-NOV-2000; 2000US-00724531.
XX
XX (MEDI-) MEDIUMMUNE INC.
XX
XX Young JF, Koenig S, Johnson LS;
XX WPI; 2002-706803/76.
XX
XX Antibody for treating respiratory syncytial virus (RSV) infection,
XX comprises a variable heavy/light domain or complementarity determining
XX regions 1 - 3 of variable light/heavy chains, that immunospecifically
XX binds to RSV antigen.
XX
XX Disclosure; Page 281; 298pp; English.
XX
XX The invention relates to a novel antibody comprising a variable heavy
XX (VH) domain, variable light (VL) domain, VH complementarity determining
XX region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the
XX antibody immunospecifically binds to a respiratory syncytial virus (RSV)
XX antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
XX invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
XX and immunostimulant activity. The polynucleotides of the invention may
XX have a use in a vaccine, and in gene therapy. The antibody is useful for
XX treating or ameliorating a RSV infection in a human. The antibody is also
XX useful for preventing, treating or ameliorating one or more symptoms
XX associated with RSV infection in a mammal, e.g. cystic fibrosis,
XX bronchopulmonary dysplasia, congenital heart disease, congenital
XX immunodeficiency or acquired immunodeficiency, or after a bone marrow
XX transplant. The sequence represents a variable domain of a human RSV
XX antibody of the invention
XX
XX Sequence 213 AA;
XX
XX Query Match 100.0%; Score 553; DB 5; Length 213;
XX Best Local Similarity 100.0%; Pred. No. 1e-47;
XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
XX |
XX 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
XX |
XX
XX QY 61 SKDSTYSLSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
XX |
XX 167 SKDSTYSLSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213
XX |
XX
XX RESULT 98
XX ABP66581
XX ID ABP66581 standard; protein; 213 AA.
XX
XX AC ABP66581;
XX
XX 04-DEC-2002 (first entry)
XX
XX Human RSV antibody variable light chain.
XX
XX Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
KW complementarity determining region; respiratory syncytial virus;
```


KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;
 KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;
 KW bronchopulmonary dysplasia; congenital heart disease;
 KW congenital immunodeficiency; acquired immunodeficiency.
 XX
 OS Homo sapiens.
 XX
 XX WO200243660-A2.
 XX
 XX PD 06-JUN-2002.
 XX
 XX PF 28-NOV-2001; 2001WO-US044807.
 XX
 XX PR 28-NOV-2000; 2000US-00724396.
 XX
 XX PR 28-NOV-2000; 2000US-00724531.
 XX
 XX PA (MEDI-) MEDIUMMUNE INC.
 XX
 XX PI Young JF, Koenig S, Johnson LS;
 XX
 XX DR WPI; 2002-706803/76.
 XX
 XX PT Antibody for treating respiratory syncytial virus (RSV) infection,
 PT comprises a variable heavy/light domain or complementarity determining
 PT regions 1 - 3 of variable light/heavy chains, that immunospecifically
 PT binds to RSV antigen.
 XX
 XX PS Disclosure; Page 263; 298pp; English.
 XX
 XX CC The invention relates to a novel antibody comprising a variable heavy
 CC (VH) domain, variable light (VL) domain, VH complementarity determining
 CC region (CDR)-1, VH CDR2, VL CDR3, VL CDR1 or VL CDR3, where the
 CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)
 CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
 CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
 CC and immunostimulant activity. The polynucleotides of the invention may
 CC have a use in a vaccine, and in gene therapy. The antibody is useful for
 CC treating or ameliorating a RSV infection in a human. The antibody is also
 CC useful for preventing, treating or ameliorating one or more symptoms
 CC associated with RSV infection in a mammal, e.g. cystic fibrosis,
 CC bronchopulmonary dysplasia, congenital heart disease, congenital
 CC immunodeficiency or acquired immunodeficiency, or after a bone marrow
 CC transplant. The sequence represents a variable domain of a human RSV
 CC antibody of the invention
 XX
 XX SQ Sequence 213 AA;

Query Match 100.0%; Score 553; DB 5; Length 213;
 Best Local Similarity 100.0%; Pred. No. 1e-47;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 DB 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
 OY 61 SKDSTYLSLSTLTLSKADYEHKVKVACEVTHQGLSSPVTKSFNRGEC 107
 DB 167 SKDSTYLSLSTLTLSKADYEHKVKVACEVTHQGLSSPVTKSFNRGEC 213

RESULT 99
 ABP66589
 ID ABP66589 standard; protein; 213 AA.
 XX
 AC ABP66589;
 XX
 XX DT 04-DEC-2002 (first entry)
 XX
 XX DE Human RSV antibody variable light chain.
 XX
 XX KW Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
 KW complementarity determining region; respiratory syncytial virus;
 KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;

KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;
 KW bronchopulmonary dysplasia; congenital heart disease;
 KW congenital immunodeficiency; acquired immunodeficiency.
 XX
 OS Homo sapiens.
 XX
 XX PN WO200243660-A2.
 XX
 XX PD 06-JUN-2002.
 XX
 XX PF 28-NOV-2001; 2001WO-US044807.
 XX
 XX PR 28-NOV-2000; 2000US-00724396.
 XX
 XX PR 28-NOV-2000; 2000US-00724531.
 XX
 XX PA (MEDI-) MEDIUMMUNE INC.
 XX
 XX PI Young JF, Koenig S, Johnson LS;
 XX
 XX DR WPI; 2002-706803/76.
 XX
 XX PT Antibody for treating respiratory syncytial virus (RSV) infection,
 PT comprises a variable heavy/light domain or complementarity determining
 PT regions 1 - 3 of variable light/heavy chains, that immunospecifically
 PT binds to RSV antigen.
 XX
 XX PS Disclosure; Page 272; 298pp; English.
 XX
 XX CC The invention relates to a novel antibody comprising a variable heavy
 CC (VH) domain, variable light (VL) domain, VH complementarity determining
 CC region (CDR)-1, VH CDR2, VL CDR3, VL CDR1 or VL CDR3, where the
 CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)
 CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
 CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
 CC and immunostimulant activity. The polynucleotides of the invention may
 CC have a use in a vaccine, and in gene therapy. The antibody is useful for
 CC treating or ameliorating a RSV infection in a human. The antibody is also
 CC useful for preventing, treating or ameliorating one or more symptoms
 CC associated with RSV infection in a mammal, e.g. cystic fibrosis,
 CC bronchopulmonary dysplasia, congenital heart disease, congenital
 CC immunodeficiency or acquired immunodeficiency, or after a bone marrow
 CC transplant. The sequence represents a variable domain of a human RSV
 CC antibody of the invention
 XX
 XX SQ Sequence 213 AA;

Query Match 100.0%; Score 553; DB 5; Length 213;
 Best Local Similarity 100.0%; Pred. No. 1e-47;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 DB 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
 OY 61 SKDSTYLSLSTLTLSKADYEHKVKVACEVTHQGLSSPVTKSFNRGEC 107
 DB 167 SKDSTYLSLSTLTLSKADYEHKVKVACEVTHQGLSSPVTKSFNRGEC 213

RESULT 100
 ABP66563
 ID ABP66563 standard; protein; 213 AA.
 XX
 AC ABP66563;
 XX
 XX DT 04-DEC-2002 (first entry)
 XX
 XX DE Human RSV antibody variable light chain.
 XX
 XX KW Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
 KW complementarity determining region; respiratory syncytial virus;
 KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;
 KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;

KW bronchopulmonary dysplasia; congenital heart disease;
KW congenital immunodeficiency; acquired immunodeficiency.

OS Homo sapiens.

PN WO200243660-A2.

XX 06-JUN-2002.

PD 28-NOV-2001; 2001WO-US044807.

XX 28-NOV-2000; 2000US-00724396.

PR 28-NOV-2000; 2000US-00724531.

XX (MEDI-) MEDIUMMUNE INC.

PA Young JF, Koenig S, Johnson LS;

XX WPI; 2002-706803/76.

DR Antibody for treating respiratory syncytial virus (RSV) infection,
XX comprises a variable heavy/light domain or complementarity determining
PT regions 1 - 3 of variable light/heavy chains, that immunospecifically
PT binds to RSV antigen.

XX Disclosure; Page 243; 298pp; English.

CC The invention relates to a novel antibody comprising a variable heavy
CC (VH) domain, variable light (VL) domain, VH complementarity determining
CC region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the
CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)
CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
CC and immunostimulant activity. The polynucleotides of the invention may
CC have a use in a vaccine, and in gene therapy. The antibody is useful for
CC treating or ameliorating a RSV infection in a human. The antibody is also
CC useful for preventing, treating or ameliorating one or more symptoms
CC associated with RSV infection in a mammal, e.g. cystic fibrosis,
CC bronchopulmonary dysplasia, congenital heart disease, congenital
CC immunodeficiency or acquired immunodeficiency, or after a bone marrow
CC transplant. The sequence represents a variable domain of a human RSV
CC antibody of the invention

XX SQ Sequence 213 AA;

Query Match 100.0%; Score 553; DB 5; Length 213;
Best Local Similarity 100.0%; Pred. No. 1e-47;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
Qy 61 SKDSTYSLSLTILTSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSLTILTSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213

Search completed: June 12, 2006, 17:09:46
Job time : 96.2929 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 11:56:42 ; Search time 11.4069 Seconds
(without alignments)
902.540 Million cell updates/sec

Title: US-10-733-563-112

Perfect score: 553

Sequence: 1 RTVAAPSVFIFPPSDEQLKLS.....EVTHQGLSSPVTKSFNRGEC 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.*

1: pirl.*

2: pirl.*

3: pirl.*

4: pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553	100.0	215	2 JE0243	Ig kappa chain NIG
2	553	100.0	215	2 JE0244	Ig kappa chain NIG
3	553	100.0	215	2 JE0242	Ig kappa chain NIG
4	550	99.5	135	2 S52059	JC-kappa protein -
5	548	99.1	106	1 K3HU	Ig kappa chain C r
6	537	97.1	216	2 JE0241	Ig kappa chain Am3
7	520	94.0	215	2 A23746	Ig kappa chain V-I
8	513	92.8	99	2 A37927	Ig kappa chain C r
9	507	91.7	99	2 S26653	Ig kappa chain C r
10	372	67.3	240	2 S06084	Ig kappa chain pre
11	367	66.4	106	1 K1RTB	Ig kappa chain C r
12	366	66.2	178	2 PT0219	Ig kappa chain V-C
13	359	64.9	106	1 K1RTA	Ig kappa chain C r
14	358	64.7	217	2 S42772	Ig kappa chain - m
15	358	64.7	218	2 S68241	Ig kappa chain V r
16	358	64.7	219	2 S38865	Ig kappa chain - m
17	352	63.7	218	2 JC5810	monoclonal antibod
18	352	63.7	219	2 S52028	Ig kappa chain - m
19	352	63.7	219	2 PC4203	Ig kappa chain (mo
20	352	63.7	219	2 S16112	Ig kappa chain V r
21	352	63.7	220	2 A31790	Ig kappa chain V r
22	352	63.7	225	2 S37484	Ig kappa chain - m
23	352	63.7	234	2 S14337	Ig kappa chain pre
24	352	63.7	234	2 S01320	Ig kappa chain pre
25	352	63.7	235	2 S25058	Ig kappa chain - m
26	350	63.3	106	1 K1MS	Ig kappa chain C r
27	350	63.3	126	2 I54782	gene Pvt-1a/Ig-Ck
28	348	62.9	225	2 JL0029	Ig kappa chain pre
29	345	62.4	230	2 S33161	Ig kappa chain - s

30	321	58.0	214	2 S68212	Ig kappa chain (Ma
31	312	56.4	210	2 A56169	Ig kappa chain V r
32	308.5	55.8	106	2 G20907	Ig kappa-B4 chain
33	306.5	55.4	106	1 K4RBBS	Ig kappa-2 chain C
34	277.5	50.2	229	2 A20969	Ig kappa chain pre
35	257.5	46.6	103	1 K4RB	Ig kappa-B4 chain
36	256	46.3	104	2 F53275	Ig kappa-1 chain C
37	246.5	44.6	104	1 K9RB	Ig kappa-B9 chain
38	245	44.3	238	2 A49633	Ig lambda-like cha
39	241	43.6	104	1 K5RBV	Ig kappa chain C r
40	237	42.9	118	2 A4518	Ig lambda chain J-C re
41	231	41.8	103	2 B26167	Ig lambda chain C
42	231	41.8	213	2 A21177	Ig light chain pre
43	225	40.7	108	1 K3FG	Ig light chain C r
44	223.5	40.4	103	1 K5RB	Ig kappa-B5 chain
45	222	40.1	197	2 S29593	Ig kappa chain (WM

ALIGNMENTS

RESULT 1

JE0243

Ig kappa chain NIG93 precursor - human

C:Species: Homo sapiens (man)

C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0243

R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T

submitted to JIPID, November 1998

A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy

A:Reference number: JE0243

A:Accession: JE0243

A:Molecule type: protein

A:Residues: 1-215 <ALI>

A:Cross-references: UNIPARC:UPI0000176984

A:Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-90/Domain: immunoglobulin homology <INM>

Query Match 100.0%; Score 553; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 1.6e-46;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKLSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQD 60

DB 109 RTVAAPSVFIFPPSDEQLKLSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQD 168

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

DB 169 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 2

JE0244

Ig kappa chain NIG2 precursor - human

C:Species: Homo sapiens (man)

C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0244

R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T

submitted to JIPID, November 1998

A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy

A:Reference number: JE0243

A:Accession: JE0244

A:Molecule type: protein

A:Residues: 1-215 <ALI>

A:Cross-references: UNIPARC:UPI0000176982

A:Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-90/Domain: immunoglobulin homology <INM>

Query Match 100.0%; Score 553; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 1.6e-46;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKLSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQD 60

Db	109	RTVAAPSVFI	PPSPDEQLKSGTASVVC	LNFFYPREAKVQWKVDNALQSGNSQESVTEQD	168
QY	61	SKDSTVSL	STLTLSKADYKHKVYACEV	THQGLSSPVTKSFNRGEC	107
Db	169	SKDSTVSL	STLTLSKADYKHKVYACEV	THQGLSSPVTKSFNRGEC	215
RESULT 3					
JE0242					
Ig kappa chain NIG26 precursor - human					
C:Species: Homo sapiens (man)					
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000					
C:Accession: JE0242					
R:Alim, M.A.; Yanaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T					
submitted to JIPID, November 1998					
A:Description: Structure relationship of kappatype light chains with AL amyloidosis: Mul					
A:Reference number: JE0241					
A:Accession: JE0242					
A:Molecule type: protein					
A:Residues: 1-215 <ALI>					
A:Cross-references: UNIPARC:UPI0000176983					
C:Superfamily: immunoglobulin V region; immunoglobulin homology					
F;16-91/Domain: immunoglobulin homology <IMM>					
Query Match 100.0%; Score 553; DB 2; Length 215;					
Best Local Similarity 100.0%; Pred. NO. 1.6e-46;					
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	RTVAAPSVFI	PPSPDEQLKSGTASVVC	LNFFYPREAKVQWKVDNALQSGNSQESVTEQD	60
Db	109	RTVAAPSVFI	PPSPDEQLKSGTASVVC	LNFFYPREAKVQWKVDNALQSGNSQESVTEQD	168
QY	61	SKDSTVSL	STLTLSKADYKHKVYACEV	THQGLSSPVTKSFNRGEC	107
Db	169	SKDSTVSL	STLTLSKADYKHKVYACEV	THQGLSSPVTKSFNRGEC	215
RESULT 4					
S52059					
JC-kappa protein - human					
C:Species: Homo sapiens (man)					
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 08-Sep-2000					
C:Accession: S52059					
R:Frances, V.; Pandrau-Garcia, D.; Guret, C.; Ho, S.; Wang, Z.; Duvert, V.; Saeland, S.;					
EMBO J. 13, 5937-5943, 1994					
A:Title: A surrogate 15 kDa JC-kappa protein is expressed in combination with mu heavy c					
A:Reference number: S52059; MUID:95112804; PMID:7813432					
A:Accession: S52059					
A:Status: preliminary					
A:Molecule type: mRNA					
A:Residues: 1-135 <FRA>					
A:Cross-references: UNIPARC:UPI00001184D0					
C:Superfamily: pre-B cell omega light chain; immunoglobulin homology					
Query Match 99.5%; Score 550; DB 2; Length 135;					
Best Local Similarity 99.1%; Pred. NO. 1.8e-46;					
Matches 106; Conservative 1; Mismatches 0; Indels 0; Gaps 0;					
QY	1	RTVAAPSVFI	PPSPDEQLKSGTASVVC	LNFFYPREAKVQWKVDNALQSGNSQESVTEQD	60
Db	29	RTVAAPSVFI	PPSPDEQLKSGTASVVC	LNFFYPREAKVQWKVDNALQSGNSQESVTEQD	88
QY	61	SKDSTVSL	STLTLSKADYKHKVYACEV	THQGLSSPVTKSFNRGEC	107
Db	89	SKDSTVSL	STLTLSKADYKHKVYACEV	THQGLSSPVTKSFNRGEC	135
RESULT 5					
K3HU					
Ig kappa chain C region - human					
C:Species: Homo sapiens (man)					
C:Date: 31-Dec-1980 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004					

C:Accession: B90562; A91651; A90806; A94417; A91639; A92047; A94242; B37927; A02116; S021
R:Gotlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelman, G.M.
Biochemistry 9, 3155-3161, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VI. Amino acid sequence
A:Reference number: A90562; MUID:71064023; PMID:5489770
A:Contents: myeloma protein Eu
A:Accession: B90562
A:Molecule type: protein
A:Residues: 1-106 <GOT>
A:Cross-references: UNIPROT:P01834; UNIPARC:UPI000002F106
A:Note: this sequence has the Inv (3) allotypic marker, 45-Ala and 83-Val
R:Galli, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Contents: annotation; Eu, disulfide bonds
R:Suter, L.; Barnikol, H.U.; Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972
A:Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sub
A:Reference number: A91651; MUID:72188439; PMID:5027703
A:Contents: Bence Jones protein Ti
A:Accession: A91651
A:Molecule type: protein
A:Residues: 1-106 <SUT>
A:Cross-references: UNIPARC:UPI000002F106
R:Hieter, P.A.; Max, E.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.
Cell 22, 197-207, 1980
A:Title: Cloned human and mouse kappa immunoglobulin constant and J region genes conserve
A:Reference number: A90806; MUID:81042304; PMID:6775818
A:Accession: A90806
A:Molecule type: DNA
A:Residues: 1-106 <HIE>
A:Cross-references: UNIPARC:UPI000002F106; GB:J00241; NID:933140; PIDN:CAA23823.1; PID:91
A:Note: the sequence was determined from the germline gene
R:Hilschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne, N
in Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74, 1
A:Reference number: A94417
A:Contents: Bence Jones protein Roy
A:Accession: A94417
A:Molecule type: protein
A:Residues: 1-44, 'A', 46-56, 'Q', 58-82, 'L', 84-106 <HIL>
A:Cross-references: UNIPARC:UPI000017376D
A:Note: this sequence has the Inv (1,2) allotypic marker, 45-Ala and 83-Leu
R:Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967
A:Title: Die vollständige Aminosäuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ) .
A:Reference number: A91639; MUID:68242259; PMID:5586923
A:Contents: Bence Jones protein Cum
A:Accession: A91639
A:Molecule type: protein
A:Residues: 1-56, 'Q', 58-106 <HI2>
A:Cross-references: UNIPARC:UPI000017376E
R:Titani, K.; Shinoda, T.; Putnam, F.W.
J. Biol. Chem. 244, 3550-3560, 1969
A:Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete
A:Reference number: A92047; MUID:69234734; PMID:4893682
A:Contents: Bence Jones protein Ag
A:Accession: A92047
A:Molecule type: protein
A:Residues: 1-13, 'N', 15-106 <TIT>
A:Cross-references: UNIPARC:UPI000017376F
R:Kohler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.
Science 169, 56-59, 1970
A:Title: Macroglobulin structure: variable sequence of light and heavy chains.
A:Reference number: A94242; MUID:70201507; PMID:5447531
A:Contents: Waldenström's macroglobulin Ou
A:Accession: A94242
A:Molecule type: protein
A:Residues: 1-13, 'N', 15-106 <KOH>
A:Cross-references: UNIPARC:UPI000017376F
R:Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.
Am. J. Hum. Genet. 48, 613-620, 1991
A:Title: Km typing with PCR: application to population screening.

A;Reference number: A37927; MUID:91150772; PMID:1900145
A;Accession: B37927
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 8-106 <KUR>
A;Cross-references: UNIPARC:UPI0000173770
A;Note: allotype Inv(3)
R;Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances the
A;Reference number: S02572; MUID:98005152; PMID:3115831
A;Contents: annotation
C;Genetics:

A;Gene: GDB:IGKC
A;Cross-references: GDB:120088; OMIM:147200
A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into larger complexes
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-88/Domain: immunoglobulin homology <IMM>
F;26-86/Disulfide bonds: #status experimental
F;106/Disulfide bonds: interchain (to heavy chain) #status experimental

Query Match 99.1%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.1e-46;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TVAAPSVFIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 61
DB 1 TVAAPSVFIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 62 KDSYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 KDSYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106

RESULT 6
JE0241
IG kappa chain Am37 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
A;Accession: JE0241
R;Alim, M.A.; Yanaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
submitted to JIPID, November 1998
A;Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul
A;Reference number: JE0241
A;Accession: JE0241
A;Molecule type: protein
A;Residues: 1-216 <ALI>
A;Cross-references: UNIPARC:UPI0000176981
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-92/Domain: immunoglobulin homology <IMM>

Query Match 97.1%; Score 537; DB 2; Length 216;
Best Local Similarity 97.2%; Pred. No. 5.7e-45;
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 110 RTVAAPSVFIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 169
QY 61 SKDSTYSLSTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 170 SKDSTYSLSTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 216

RESULT 7
A23746
IG kappa chain V-III (KAU cold agglutinin) - human
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: A23746

R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin
A;Reference number: A23746; MUID:91151575; PMID:1993660
A;Accession: A23746

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-215 <LEO>
A;Cross-references: UNIPARC:UPI0000176985
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 94.0%; Score 520; DB 2; Length 215;
Best Local Similarity 98.1%; Pred. No. 2.6e-43;
Matches 104; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 109 RTVAAPSVFIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 168
QY 61 SKDSTYSLSTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106
DB 169 SKDSTYSLSTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 8
A37927
IG kappa chain C region (allotype Inv(1,2)) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 21-Jan-2000
C;Accession: A37927
R;Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.
Am. J. Hum. Genet. 48, 613-620, 1991

A;Title: Km typing with PCR: application to population screening.
A;Reference number: A37927; MUID:91150772; PMID:1900145
A;Accession: A37927
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-99 <KUR>

A;Cross-references: UNIPARC:UPI0000176ED6
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;12-81/Domain: immunoglobulin homology <IMM>

Query Match 92.8%; Score 513; DB 2; Length 99;
Best Local Similarity 99.0%; Pred. No. 5e-43;
Matches 98; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 FIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 68
DB 1 FIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 69 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 99

RESULT 9
S26653
IG kappa chain C region - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C;Accession: S26653
R;Ehrlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.
Hum. Antibodies Hybridomas 1, 23-26, 1990
A;Title: Potential of primate monoclonal antibodies to substitute for human antibodies:
A;Reference number: S26652; MUID:91355693; PMID:2129418
A;Accession: S26653
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-99 <EHR>
A;Cross-references: UNIPARC:UPI0000176ED5; EMBL:X65287

C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;19-88/Domain: immunoglobulin homology <IMM>

Query Match 91.7%; Score 507; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.9e-42;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQSVTEQDS 61
Db 1 TVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQSVTEQDS 60
QY 62 KDSTYLSLSTLTLSKADYKHKVYACVTHQGLSSPVTK 100
Db 61 KDSTYLSLSTLTLSKADYKHKVYACVTHQGLSSPVTK 99

RESULT 10
S06084
Ig kappa chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S06084
R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.

Nucleic Acids Res. 17, 7992, 1989
A;Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA
A;Reference number: S06084; MUID:90016888; PMID:2508067
A;Accession: S06084
A;Molecule type: mRNA
A;Residues: 1-240 <CRO>
A;Cross-references: UNIPARC:UPI0000113764; EMBL:X16129; NID:956457; PIDN:CAA34256.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-240/Product: Ig kappa chain #status predicted <MAT>
F;153-222/Domain: immunoglobulin homology <IMM>

Query Match 67.3%; Score 372; DB 2; Length 240;
Best Local Similarity 65.4%; Pred. No. 7.4e-29;
Matches 70; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQSVTEQD 60
Db 134 RADAAPTIVSIFPPSTEQLATGGASVVCLLMNNFYPRDISVKWKIDGTERDGLVDSVTDQD 193
QY 61 SKDSTYLSLSTLTLSKADYKHKVYACVTHQGLSSPVTKSFNRGEC 107
Db 194 SKDSTYMSLSTLSKADYKESHNLTYCEVVHKTSSSPVVKSFNRNEC 240

RESULT 11
K1RTB
Ig kappa chain C region (allele b) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A93901; A92807; A02117
R;Sheppard, H.W.; Gutman, G.A.
Proc. Natl. Acad. Sci. U.S.A. 78, 7064-7068, 1981
A;Title: Allelic forms of rat kappa chain genes: evidence for strong selection at the le
A;Reference number: A93901; MUID:82082587; PMID:6273908
A;Accession: A93901
A;Molecule type: DNA
A;Residues: 1-106 <SHE>

A;Cross-references: UNIPROT:P01835; UNIPARC:UPI000012DB83; GB:V01241; GB:J00745; GB:J025
A;Experimental source: strain LOU
R;Starace, V.; Querinjean, P.
J. Immunol. 115, 59-62, 1975
A;Title: The primary structure of a rat kappa Bence Jones protein: phylogenetic relation
A;Reference number: A92807; MUID:75212238; PMID:807630
A;Contents: Bence Jones protein S211
A;Accession: A92807
A;Molecule type: protein
A;Residues: 1,'N',3-29,'K',31-47,49-78,'Q',80-86,'Q',88-98,'W',99,'N',101-106 <STA>

A;Cross-references: UNIPARC:UPI0000173771
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lai
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer
F;19-88/Domain: immunoglobulin homology <IMM>
F;26-96/Disulfide bonds: #status predicted
F;106/Disulfide bonds: interchain (to heavy chain) #status predicted

Query Match 66.4%; Score 367; DB 1; Length 106;
Best Local Similarity 65.4%; Pred. No. 8.7e-29;
Matches 68; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 4 AAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQSVTEQDSKD 63
Db 3 AAPTVSIFPPSTEQLATGGASVVCLLMNNFYPRDISVKWKIDGTERDGLVDSVTDQDSKD 62
QY 64 STYLSLSTLTLSKADYKHKVYACVTHQGLSSPVTKSFNRGEC 107
Db 63 STYMSLSTLTLSKADYKESHNLTYCEVVHKTSSSPVVKSFNRNEC 106

RESULT 12
PT0219
Ig kappa chain V-C region (PLC18) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jan-2000
C;Accession: PT0219
R;Lammers, B.M.; Beaman, K.D.; Kim, Y.B.
Mol. Immunol. 28, 877-880, 1991
A;Title: Sequence analysis of porcine immunoglobulin light chain cDNAs.
A;Reference number: PT0219; MUID:91342694; PMID:1715030
A;Accession: PT0219
A;Molecule type: mRNA
A;Residues: 1-178 <LAM>
A;Cross-references: UNIPARC:UPI00001151A1; GB:M59321; NID:g164508; PIDN:AAA03520.1; PID:
A;Experimental source: spleen, strain Minnesota Miniature
A;Note: the authors translated the codon CTC for residue 141 as Ser
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;12-18/Domain: V region (fragment) <VRG>
F;19-51/Region: complementarity-determining 1
F;52-60/Region: complementarity-determining 2
F;61-70/Region: framework 2
F;71-178/Domain: C region <CRG>
F;96-156/Disulfide bonds: #status predicted
F;176/Disulfide bonds: interchain #status predicted

Query Match 66.2%; Score 366; DB 2; Length 178;
Best Local Similarity 64.5%; Pred. No. 2e-28;
Matches 69; Conservative 13; Mismatches 25; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQSVTEQD 60
Db 70 RADAKPSVFIPPSPDEQLATPTVSVCLINNFFPREISVKWKVDGVQSSGHGPDVTEQD 129
QY 61 SKDSTYLSLSTLTLSKADYKHKVYACVTHQGLSSPVTKSFNRGEC 107
Db 130 SKDSTYLSLSTLSLTQVLSHNLNYSCEVTHKTLASPLVTSFNRNEC 176

RESULT 13
K1RTA
Ig kappa chain C region (allele a) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Aug-1982 #sequence_revision 10-Sep-1982 #text_change 09-Jul-2004
C;Accession: A02118
R;Sheppard, H.W.; Gutman, G.A.
Proc. Natl. Acad. Sci. U.S.A. 78, 7064-7068, 1981
A;Title: Allelic forms of rat kappa chain genes: evidence for strong selection at the le
A;Reference number: A93901; MUID:82082587; PMID:6273908
A;Accession: A02118

```
Query Match      64.7%; Score 358; DB 2; Length 218;
Best Local Similarity 61.7%; Pred No. 1.5e-27;
Matches 66; Conservative 15; Mismatches 26; Indels

Qy   1   RTVAAPSVFPTPSDEQLSKGTASVCLNNFYPREAKVQWKVDNALQSGH
      | | | | | | | | | | | | | | | | | | : | : | :
Db   112 RADAAFTVTPSPSSEQLTGGASVCLNNFYPKDINVKRKIDGSRQNQ
      | | | | | | | | | | | | | | | | | | : | : | :

Qy   61 SKDSTYSLSTLTLKADYBKHYACEVTHQGLSSPVTKSFNRGEC 107
      | | | | | | | | | | | | | | | | | | : | : | :
Db   172 SKDSTYSMSSTLTLDKEYERHNSYTCEAHTKYSTSPIVKSFNRGEC 218
      | | | | | | | | | | | | | | | | | | : | : | :
```

Search completed: June 10, 2006, 12:06:43
Job time : 12.4069 secs

RESULT 14
S42772
IG kappa chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S42772
R;Schellekens, G.A.
submitted to the EMBL Data Library, November 1993
A;Reference number: S42771
A;Accession: S42772
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-217 <SCH>
A;Cross-references: UNIPARC:UPI00001161CD; EMBL:X75536; NID:G414143; PIDN:CAA53226.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-93/Domain: immunoglobulin homology <IMM>

	Query Match	64.7%;	Score 358;	DB 2;	Length 217;	
	Best Local Similarity	61.7%;	Pred. No. 1.5e-27;			
	Matches	66;	Conservative 15;	Mismatches 26;	Indels 0;	Gaps 0;
Oy	1	RTVAAPSVTFFPPSDEOLKSGTASVCLLNFPYPREAKVQWKVDNALQSGNSOESVTEQD	60			
Dd	111	RADAAPTVSIFPSSSEQLTSGGASVCFLLNFPYKDINVKWDIGDSRQGVNLNSMTDQD	170			
Oy	61	SKDSTYSLSLTLLSLKADYEKKHYACEVTHQGLSSPVTGSFNRGEC	107			
Dd	171	SKDSTYSMSLTLLTKDEYERHNSYTCEATHKTSTSPIVKSFNRGEC	217			

RESULT 15
S68241
IG kappa chain V region (Mab13-1) - mouse (fragment)
N/Alternate names: immunoglobulin light chain
C/Species: Mus musculus (house mouse)
C/Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C/Accession: S68241; S68214
R/R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
submitted to the EMBL Data Library, March 1994
A/Description: Specific peroxidase activity by formation of an antibody L-chain-porphyrin
A/Reference number: S68241
A/Accession: S68241
A/Molecule type: mRNA
A/Residues: 1-218 <UNK>
A/Cross-references: UNIPARC:UPI000011B263; EMBL:D29670; NID:G473962; PIDN:BAA06141.1; PI
R/R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995

THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 11:49:06 ; Search time 88.042 Seconds
(without alignments)
1124.198 Million cell updates/sec

Title: US-10-733-563-112
Perfect score: 553
Sequence: 1 RTVAAPSVFIPPSDQLKS.....EVTHQGLSPVTKSFNRGEC 107

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.2*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	553	100.0	120	2	Q6P5R5_HUMAN	Q6P5R5 homo sapien
2	553	100.0	234	2	Q5EFE6_HUMAN	Q5EFE6 homo sapien
3	553	100.0	234	2	Q7Z473_HUMAN	Q7Z473 homo sapien
4	553	100.0	235	2	Q6GMV9_HUMAN	Q6GMV9 homo sapien
5	553	100.0	235	2	Q6GMW0_HUMAN	Q6GMW0 homo sapien
6	553	100.0	235	2	Q6PJP2_HUMAN	Q6PJP2 homo sapien
7	553	100.0	236	2	Q502W4_HUMAN	Q502W4 homo sapien
8	553	100.0	236	2	Q6GMW1_HUMAN	Q6GMW1 homo sapien
9	553	100.0	236	2	Q6GMX0_HUMAN	Q6GMX0 homo sapien
10	553	100.0	236	2	Q6GMX8_HUMAN	Q6GMX8 homo sapien
11	553	100.0	236	2	Q6GMX9_HUMAN	Q6GMX9 homo sapien
12	553	100.0	236	2	Q6P5S8_HUMAN	Q6P5S8 homo sapien
13	553	100.0	236	2	Q6PIH4_HUMAN	Q6PIH4 homo sapien
14	553	100.0	236	2	Q6PIH7_HUMAN	Q6PIH7 homo sapien
15	553	100.0	236	2	Q6PIH8_HUMAN	Q6PIH8 homo sapien
16	553	100.0	236	2	Q6PIT5_HUMAN	Q6PIT5 homo sapien
17	553	100.0	236	2	Q7Z3V4_HUMAN	Q7Z3V4 homo sapien
18	553	100.0	239	2	Q6P491_HUMAN	Q6P491 homo sapien
19	553	100.0	239	2	Q8TCD0_HUMAN	Q8TCD0 homo sapien
20	553	100.0	240	2	Q6PIH6_HUMAN	Q6PIH6 homo sapien
21	549	99.3	239	2	Q8NEK0_HUMAN	Q8NEK0 homo sapien
22	548	99.1	106	1	KAC_HUMAN	Q01834 homo sapien
23	548	99.1	234	2	Q569T9_HUMAN	Q569T9 homo sapien
24	369	66.7	234	2	Q4KM66_RAT	Q4KM66 rattus norv
25	369	66.7	234	2	Q5M838_RAT	Q5M838 rattus norv
26	367	66.4	106	1	KACB_RAT	P01835 rattus norv
27	359	64.9	106	1	KACA_RAT	Q612C0 rattus norv
28	358	64.7	219	2	Q65ZC0_MOUSE	Q65ZC0 mus musculus
29	352	63.7	234	2	Q5XKG4_MOUSE	Q5XKG4 mus musculus
30	352	63.7	235	2	Q58EV6_MOUSE	Q58EV6 mus musculus
31	352	63.7	235	2	Q5XFY8_MOUSE	Q5XFY8 mus musculus

RESULT 1									
Q6P5R5_HUMAN									
ID	Q6P5R5_HUMAN	PRELIMINARY;	PRT;	120	AA.				
AC	Q6P5R5;								
DT	05-JUL-2004,	integrated into UniProtKB/TREMBL.							
DT	05-JUL-2004,	sequence version 1.							
DT	21-FEB-2006,	entry version 19.							
DE	IGKC protein.								
GN	Name=IGKC;								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;								
OC	Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	NUCLEOTIDE SEQUENCE.								
RC	TISSUE=Glandular pool- thyroid;								
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;								
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,								
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,								
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,								
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,								
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,								
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,								
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,								
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallaby S.J.,								
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,								
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,								
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,								
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,								
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,								
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,								
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,								
RA	Butterfield Y.S.N., Krzywinaki M.I., Skaleka U., Smailus D.E.,								
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;								
RT	"Generation and initial analysis of more than 15,000 full-length human								
RT	and mouse cDNA sequences."								
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).								
RN	[2]								
RP	NUCLEOTIDE SEQUENCE.								
RC	TISSUE=Glandular pool- thyroid;								
RG	NIH MGC Project;								
RL	Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.								
CC	-!- FUNCTION: Beta-2-microglobulin is the beta-chain of major								
CC	histocompatibility complex class I molecules (By similarity).								
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms								
CC	Distributed under the Creative Commons Attribution-NoDerivs License								
CC	-----								
CC	EMBL; BC062732; AAH62732.1; -; mRNA.								
CC	HSSP; P01837; 1KCU.								
DR	SMR; Q6P5R5; 3-120.								
DR	Ensembl; ENSG00000163245; Homo sapiens.								
DR	GO; GO:0030106; F:MHC class I receptor activity; IEA.								

Q52195	mus musculus
Q71698	mus musculus
Q3KQK1	mus musculus
Q569Y8	mus musculus
Q58EU4	mus musculus
Q66J67	mus musculus
Q58EU8	mus musculus
Q52164	mus musculus
Q63ZX4	mus musculus
P01837	mus musculus
P01839	oryctolagus
O569I7	homo sapien
Q6LEJ1	oryctolagus
Q6LEJ2	oryctolagus

ALIGNMENTS

32	352	63.7	236	2	Q52195_MOUSE
33	352	63.7	236	2	Q71698_MOUSE
34	352	63.7	237	2	Q3KQK1_MOUSE
35	352	63.7	237	2	Q569Y8_MOUSE
36	352	63.7	238	2	Q58EU4_MOUSE
37	352	63.7	238	2	Q66J67_MOUSE
38	352	63.7	239	2	Q58EU8_MOUSE
39	352	63.7	240	2	Q52164_MOUSE
40	352	63.7	241	2	Q63ZX4_MOUSE
41	350	63.3	106	1	KAC_MOUSE
42	306.5	55.4	106	1	KACB_RABIT
43	292	52.8	189	2	O569I7_HUMAN
44	259.5	46.9	116	2	Q6LEJ1_RABIT
45	259.5	46.9	116	2	Q6LEJ2_RABIT

DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
 DR GO; GO:0019895; P:antigen processing, endogenous antigen via . . . ; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig.cl.
 DR InterPro; IPR003006; Ig.MHC.
 DR Pfam; PF07654; Cl-set; 1.
 DR SMART; SM00407; IGcl; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Immune response; Immunoglobulin domain; MHC I.
 SQ SEQUENCE 120 AA; 13153 MW; B42FA2928C5C8F1F CRC64;

Query Match 100.0%; Score 553; DB 2; Length 120;
 Best Local Similarity 100.0%; Pred. No. 4.5e-47;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 |||||
 Db 14 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 73
 |||||

Qy 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 |||||
 Db 74 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 120
 |||||

RESULT 2
 QSEFE6_HUMAN
 ID QSEFE6_HUMAN PRELIMINARY; PRT; 234 AA.
 AC QSEFE6;
 DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 15-MAR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE Anti-Rhd monoclonal T125 kappa light chain precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC Gaucher C., Klein P., Beliard R.;
 RA "Sequence determination of the recombinant human anti-Rhd monoclonal antibody T125";
 RT Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 RL
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 CC EMBL; AY894991; AAW82027.1; -; mRNA.
 DR SMR; OSEFE6; 22-234.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig.cl.
 DR InterPro; IPR003006; Ig.MHC.
 DR InterPro; IPR003596; Ig_v.
 DR InterPro; IPR013106; V-set.
 DR Pfam; PF07654; Cl-set; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL 1 20 Potential.
 FT CHAIN 21 234 anti-Rhd monoclonal T125 kappa light chain.
 FT
 SQ SEQUENCE 234 AA; 25698 MW; 866DCD1E4FD7D5EA CRC64;

Query Match 100.0%; Score 553; DB 2; Length 234;
 Best Local Similarity 100.0%; Pred. No. 9.9e-47;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 |||||
 Db 128 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 187
 |||||

Qy 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 |||||
 Db 188 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 234
 |||||

RESULT 3
 Q72473_HUMAN
 ID Q72473_HUMAN PRELIMINARY; PRT; 234 AA.
 AC Q72473;
 DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2003, sequence version 1.
 DT 07-FEB-2006, entry version 21.
 DE IGKC protein.
 DE IGKC protein.
 GN Name=IGKC;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RG NIH MGC Project;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 CC EMBL; BC056256; AAH56256.1; -; mRNA.
 DR HSSP; P01834; lHEZ.
 DR SMR; Q72473; 22-234.
 DR Ensembl; ENSG00000163245; Homo sapiens.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig.cl.
 DR InterPro; IPR003006; Ig.MHC.
 DR InterPro; IPR003596; Ig_v.
 DR InterPro; IPR013106; V-set.
 DR Pfam; PF07654; Cl-set; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 100.0%; Score 553; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. NO. 9.9e-47;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFPPSPDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 128 RTVAAPSVFPPSPDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 187
QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 188 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 4
ID Q6GMV9_HUMAN PRELIMINARY; PRT; 235 AA.
AC Q6GMV9;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; BC073793; AAH73793.1; -; mRNA.
DR SNR; Q6GMV9; 21-235.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;

Query Match 100.0%; Score 553; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. NO. 1e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFPPSPDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 129 RTVAAPSVFPPSPDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 188
QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 189 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 235

RESULT 5
Q6GMW0_HUMAN
ID Q6GMW0_HUMAN PRELIMINARY; PRT; 235 AA.
AC Q6GMW0;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE IGKV1-5 protein.
GN Name=IGKV1-5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Director MSC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; BC073792; AAH73792.1; -; mRNA.
DR SNR; Q6GMW0; 21-233.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; C1-set; 1.

```
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;

Query Match 100.0%; Score 553; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 129 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 188

QY 61 SKDSTVSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 189 SKDSTVSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 235

RESULT 6
Q6PJF2 HUMAN PRELIMINARY; PRT; 235 AA.
AC Q6PJF2;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 16.
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs license
CC -----
DR EMBL; BC016380; AAH16380.1; -; mRNA.
DR HSP; P01837; 1KCU.
DR SNR; Q6PJF2.21-235.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
```

```
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25521 MW; F33A145A396BA285 CRC64;

Query Match 100.0%; Score 553; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 129 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 188

QY 61 SKDSTVSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 189 SKDSTVSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 235

RESULT 7
Q502W4 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q502W4;
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-JUN-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs license
CC -----
DR EMBL; BC095489; AAH95489.1; -; mRNA.
DR Ensembl; ENSG00000163245; Homo sapiens.
```

```
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25936 MW; E2DF79AC18756AA9 CRC64;

Query Match 100.0%; Score 553; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 130 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 189

QY 61 SKDSTYLSLTSLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 190 SKDSTYLSLTSLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 8
Q6GMW1 HUMAN
ID Q6GMW1_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NCBIOTIDE SEQUENCE.
[1]
TI TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
TI TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
```

```
DR EMBL; BC073791; AAH73791.1; -; mRNA.
DR SWR; Q6GMW1; 24-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IGC1; 1.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;

Query Match 100.0%; Score 553; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 130 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 189

QY 61 SKDSTYLSLTSLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 190 SKDSTYLSLTSLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 9
Q6GMX0 HUMAN
ID Q6GMX0_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMX0;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NCBIOTIDE SEQUENCE.
[1]
TI TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
TI TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
```


RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]

RP NUCLEOTIDE SEQUENCE
 RC TISSUE=Primary B-Cells;
 RG NIH MGC Project;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC

CC EMBL; BC073763; AAH73763.1; -; mRNA.
 CC SMR; Q6GMX9; 23-236.

DR Ensembl; ENSG0000163245; Homo sapiens.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig-cl.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR013106; V-set.

DR Pfam; PF07654; Cl-set; 1.

DR SMART; SM00409; IG; 1.

DR SMART; SM00407; IGcl; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG LIKE; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.

SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CRPF7 CRC64;

Query Match 100.0%; Score 553; DB 2; Length 236;

Best Local Similarity 100.0%; Pred. No. 1e-46;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

DB 130 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 189

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

DB 190 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 12

Q6P5S8 HUMAN

ID Q6P5S8 HUMAN PRELIMINARY; PRT; 236 AA.

AC Q6P5S8;

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.

DT 07-FEB-2006, entry version 15.

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Glandular pool- thyroid;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]

RN NUCLEOTIDE SEQUENCE.

RC TISSUE=Glandular pool- thyroid;

RA Strausberg R.;

RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.

CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms

CC Distributed under the Creative Commons Attribution-NoDerivs License

CC EMBL; BC062704; AAH62704.1; -; mRNA.

DR HSSP; P01837; 1KCU

DR SMR; Q6P5S8; 21-236.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig-cl.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR InterPro; IPR013106; V-set.

DR Pfam; PF07654; Cl-set; 1.

DR SMART; SM00409; IG; 1.

DR SMART; SM00407; IGcl; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG LIKE; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

KW Hypothetical protein.

SQ SEQUENCE 236 AA; 25773 MW; 953E37BEB4FF5F27 CRC64;

Query Match 100.0%; Score 553; DB 2; Length 236;

Best Local Similarity 100.0%; Pred. No. 1e-46;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

DB 130 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 189

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

DB 190 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 13

Q6PIH4 HUMAN

ID Q6PIH4 HUMAN PRELIMINARY; PRT; 236 AA.

AC Q6PIH4;

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.

DT 07-FEB-2006, entry version 16.

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Lung;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG Strauberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BC034146; AAH34146.1; -; mRNA.
DR HSSP; P01607; IAR2.
DR SMR; Q6PIH4; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; BE01A28CD06EE26 CRC64;

Query Match 100.0%; Score 553; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 130 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 189

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 190 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 14
ID Q6PIH7_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6PIH7;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BC034141; AAH34141.1; -; mRNA.
DR HSSP; P01607; IAR2.
DR SMR; Q6PIH7; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 236 AA; 8BC561106861213F CRC64;

Query Match 100.0%; Score 553; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 130 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 189

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 190 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 15
ID Q6PIL8_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6PIL8;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BC032451; AAH32451.1; -; mRNA.
DR HSSP; P01837; IKCU.
DR SNR; Q6PIL8; 21-236.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;

Query Match 100.0%; Score 553; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNALQGNLSQESVTEQD 60
DB |||||
130 RTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNALQGNLSQESVTEQD 189
|||

QY 61 SKDSTYLSSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB |||||
190 SKDSTYLSSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236
|||

Search completed: June 10, 2006, 12:05:26
Job time : 90.042 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 12:05:52 ; Search time 18.476 Seconds
(without alignments)
506.917 Million cell updates/sec

Title: US-10-733-563-112
Perfect score: 553
Sequence: 1 RTVAAPSVFIFFPSPDEQLK.....EVTHOGLSPVTKSNRGEC 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents:AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pdp:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pdp:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pdp:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pdp:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PTUS_COMB.pdp:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pdp:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles.pdp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	107	1	US-08-422-101-8
2	553	100.0	107	1	US-08-422-091-8
3	553	100.0	107	1	US-08-422-092-8
4	553	100.0	107	1	US-08-788-800-5
5	553	100.0	107	2	US-08-422-093-8
6	553	100.0	107	2	US-08-422-112-8
7	553	100.0	107	2	US-09-301-593-20
8	553	100.0	107	2	US-09-628-568A-8
9	553	100.0	212	2	US-10-011-125A-5
10	553	100.0	213	2	US-08-630-820-6
11	553	100.0	213	2	US-08-397-411-12
12	553	100.0	213	2	US-09-273-453-6
13	553	100.0	213	2	US-09-996-288-209
14	553	100.0	213	2	US-09-996-288-211
15	553	100.0	213	2	US-09-996-288-213
16	553	100.0	213	2	US-09-996-288-215
17	553	100.0	213	2	US-09-996-288-217
18	553	100.0	213	2	US-09-996-288-219
19	553	100.0	213	2	US-09-996-288-221
20	553	100.0	213	2	US-09-996-288-223
21	553	100.0	213	2	US-09-996-288-225
22	553	100.0	213	2	US-09-996-288-227
23	553	100.0	213	2	US-09-996-288-229
24	553	100.0	213	2	US-09-996-288-231
25	553	100.0	213	2	US-09-996-288-233
26	553	100.0	213	2	US-09-996-288-235

ALIGNMENTS

RESULT 1

US-08-422-101-8
; Sequence 8, Application US/08422101
; Patent No. 5739277
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,101
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-422-101-8

Query Match 100.0%; Score 553; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.3e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSPDEQLKSGTASVVLNNFPYBREAKVQWKVDNALQSGNSQESVTEQD 60

```
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 2
US-08-422-091-8
; Sequence 8, Application US/08422091
; Patent No. 5747035
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,091
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-9881
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-422-091-8

Query Match 100.0%; Score 553; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.3e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 3
US-08-422-092-8
; Sequence 8, Application US/08422092
; Patent No. 5869046
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
```

```
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,092
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-422-092-8

Query Match 100.0%; Score 553; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.3e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 4
US-08-788-800-5
; Sequence 5, Application US/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: winPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
```

```
; FILING DATE: 22-Jan-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0987r1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-788-800-5

Query Match 100.0%; Score 553; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.3e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 5
US-08-422-093-8
; Sequence 8, Application US/08422093
; Patent No. 6096871
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,093
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-422-093-8
```

```
Query Match 100.0%; Score 553; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.3e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 6
US-08-422-112-8
; Sequence 8, Application US/08422112
; Patent No. 6121022
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,112
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-422-112-8

Query Match 100.0%; Score 553; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.3e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 7
US-09-301-593-20
```

```
; Sequence 20, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Legier, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-20

Query Match      100.0%; Score 553; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.3e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 8
US-09-628-568A-8
; Sequence 8, Application US/09628568A
; Patent No. 6998253
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Snedecor, Bradley R.
; TITLE OF INVENTION: ALTERED POLYPEPTIDES WITH INCREASED HALF-LIFE
; FILE REFERENCE: 11669.161USC1
; CURRENT APPLICATION NUMBER: US/09/628,568A
; CURRENT FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 08/422,112
; PRIOR FILING DATE: 1995-04-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-628-568A-8

Query Match      100.0%; Score 553; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.3e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 9
```

```
US-10-011-125A-5
; Sequence 5, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 5
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6828121
US-10-011-125A-5

Query Match      100.0%; Score 553; DB 2; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.6e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 106 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 166 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 212

RESULT 10
US-08-630-820-6
; Sequence 6, Application US/08630820
; Patent No. 6008023
; GENERAL INFORMATION:
; APPLICANT: Oppen, Martin
; APPLICANT: Bosslet, Klaus
; APPLICANT: Czech, Joerg
; TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES.
; TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
; TITLE OF INVENTION: IN E. COLI
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,820
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 19513676.4
; FILING DATE: 11-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/306
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
```

1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60 QY

RESULT 13
US-09-996-288-209 ; Sequence 209, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James

```
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 209
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-209

Query Match      100.0%; Score 553; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.6e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNFPYPRKAKVQWKVDNALQSGNSQESVTEQD 60
Db      107 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNFPYPRKAKVQWKVDNALQSGNSQESVTEQD 166

QY      61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db      167 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 14
US-09-996-288-211
; Sequence 211, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 211
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-211

Query Match      100.0%; Score 553; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.6e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNFPYPRKAKVQWKVDNALQSGNSQESVTEQD 60
Db      107 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNFPYPRKAKVQWKVDNALQSGNSQESVTEQD 166

QY      61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db      167 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 15
US-09-996-288-213
; Sequence 213, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
```

```
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 213
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-213

Query Match      100.0%; Score 553; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.6e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNFPYPRKAKVQWKVDNALQSGNSQESVTEQD 60
Db      107 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNFPYPRKAKVQWKVDNALQSGNSQESVTEQD 166

QY      61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db      167 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

Search completed: June 10, 2006, 12:08:43
Job time : 18.476 secs
```


GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 12, 2006, 17:10:25 ; Search time 99.6545 Seconds

(without alignments)
497.358 Million cell updates/sec

Title: US-10-733-563-112

Perfect score: 553

Sequence: 1 RTVAAPSVFIPPSDEQLKS.....EVTHQGLSSPVTKFNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553	100.0	107	3	US-09-301-593-20
2	553	100.0	107	3	US-09-811-384-5
3	553	100.0	107	3	US-09-990-586-97
4	553	100.0	107	3	US-09-990-586-99
5	553	100.0	107	4	US-10-121-464-18
6	553	100.0	107	4	US-10-269-805-67
7	553	100.0	107	4	US-10-159-006-20
8	553	100.0	107	4	US-10-310-113-166
9	553	100.0	107	4	US-10-310-113-168
10	553	100.0	107	4	US-10-230-880-97
11	553	100.0	107	4	US-10-230-880-99
12	553	100.0	107	4	US-10-366-709-54
13	553	100.0	107	4	US-10-404-286-5
14	553	100.0	107	4	US-10-656-769-4
15	553	100.0	107	4	US-10-679-620-60
16	553	100.0	107	4	US-10-730-563-112
17	553	100.0	107	5	US-10-815-449-10
18	553	100.0	107	5	US-10-684-957-4
19	553	100.0	107	5	US-10-886-838-8
20	553	100.0	107	5	US-10-822-300-9
21	553	100.0	107	5	US-10-687-118-9
22	553	100.0	107	5	US-10-872-932A-41
23	553	100.0	107	5	US-10-891-658-8
24	553	100.0	107	5	US-10-937-596-29
25	553	100.0	107	5	US-10-893-576-44
26	553	100.0	107	5	US-10-810-881A-40
27	553	100.0	107	5	US-10-981-936-40

28	553	100.0	107	5	US-10-993-866-40	Sequence 40, Appl
29	553	100.0	107	5	US-10-988-207-21	Sequence 21, Appl
30	553	100.0	107	5	US-10-982-440-67	Sequence 67, Appl
31	553	100.0	107	5	US-10-935-005B-71	Sequence 71, Appl
32	553	100.0	107	6	US-11-001-980-4	Sequence 4, Appl
33	553	100.0	107	6	US-11-001-980-8	Sequence 8, Appl
34	553	100.0	107	6	US-11-132-143-60	Sequence 60, Appl
35	553	100.0	107	6	US-11-102-403-23	Sequence 23, Appl
36	553	100.0	107	6	US-11-025-712-5	Sequence 5, Appl
37	553	100.0	107	6	US-11-075-351-61	Sequence 61, Appl
38	553	100.0	107	6	US-11-061-821-40	Sequence 40, Appl
39	553	100.0	107	6	US-11-102-621-9	Sequence 9, Appl
40	553	100.0	107	6	US-11-122-622-97	Sequence 97, Appl
41	553	100.0	107	6	US-11-122-622-99	Sequence 99, Appl
42	553	100.0	107	6	US-11-218-813-134	Sequence 134, Appl
43	553	100.0	107	6	US-11-149-309-18	Sequence 18, Appl
44	553	100.0	109	4	US-10-272-899A-12	Sequence 12, Appl
45	553	100.0	109	4	US-10-733-563-116	Sequence 116, Appl
46	553	100.0	110	6	US-11-024-251-27	Sequence 27, Appl
47	553	100.0	134	4	US-10-272-899A-66	Sequence 66, Appl
48	553	100.0	212	4	US-10-011-125-5	Sequence 5, Appl
49	553	100.0	212	4	US-10-320-231A-77	Sequence 77, Appl
50	553	100.0	212	5	US-10-867-506-77	Sequence 77, Appl
51	553	100.0	213	3	US-09-796-848A-38	Sequence 38, Appl
52	553	100.0	213	3	US-09-796-848A-40	Sequence 40, Appl
53	553	100.0	213	3	US-09-796-848A-42	Sequence 42, Appl
54	553	100.0	213	3	US-09-796-848A-44	Sequence 44, Appl
55	553	100.0	213	3	US-09-796-848A-46	Sequence 46, Appl
56	553	100.0	213	3	US-09-796-848A-48	Sequence 48, Appl
57	553	100.0	213	3	US-09-796-848A-50	Sequence 50, Appl
58	553	100.0	213	3	US-09-796-848A-52	Sequence 52, Appl
59	553	100.0	213	3	US-09-796-848A-54	Sequence 54, Appl
60	553	100.0	213	3	US-09-996-288-209	Sequence 209, Appl
61	553	100.0	213	3	US-09-996-288-211	Sequence 211, Appl
62	553	100.0	213	3	US-09-996-288-213	Sequence 213, Appl
63	553	100.0	213	3	US-09-996-288-215	Sequence 215, Appl
64	553	100.0	213	3	US-09-996-288-217	Sequence 217, Appl
65	553	100.0	213	3	US-09-996-288-219	Sequence 219, Appl
66	553	100.0	213	3	US-09-996-288-221	Sequence 221, Appl
67	553	100.0	213	3	US-09-996-288-223	Sequence 223, Appl
68	553	100.0	213	3	US-09-996-288-225	Sequence 225, Appl
69	553	100.0	213	3	US-09-996-288-227	Sequence 227, Appl
70	553	100.0	213	3	US-09-996-288-229	Sequence 229, Appl
71	553	100.0	213	3	US-09-996-288-231	Sequence 231, Appl
72	553	100.0	213	3	US-09-996-288-233	Sequence 233, Appl
73	553	100.0	213	3	US-09-996-288-235	Sequence 235, Appl
74	553	100.0	213	3	US-09-996-288-237	Sequence 237, Appl
75	553	100.0	213	3	US-09-996-288-239	Sequence 239, Appl
76	553	100.0	213	3	US-09-996-288-241	Sequence 241, Appl
77	553	100.0	213	3	US-09-996-288-243	Sequence 243, Appl
78	553	100.0	213	3	US-09-996-288-245	Sequence 245, Appl
79	553	100.0	213	3	US-09-996-288-247	Sequence 247, Appl
80	553	100.0	213	3	US-09-996-288-251	Sequence 251, Appl
81	553	100.0	213	3	US-09-996-288-253	Sequence 253, Appl
82	553	100.0	213	3	US-09-996-288-255	Sequence 255, Appl
83	553	100.0	213	3	US-09-996-288-257	Sequence 257, Appl
84	553	100.0	213	3	US-09-996-265-209	Sequence 209, Appl
85	553	100.0	213	3	US-09-996-265-211	Sequence 211, Appl
86	553	100.0	213	3	US-09-996-265-213	Sequence 213, Appl
87	553	100.0	213	3	US-09-996-265-215	Sequence 215, Appl
88	553	100.0	213	3	US-09-996-265-217	Sequence 217, Appl
89	553	100.0	213	3	US-09-996-265-219	Sequence 219, Appl
90	553	100.0	213	3	US-09-996-265-221	Sequence 221, Appl
91	553	100.0	213	3	US-09-996-265-223	Sequence 223, Appl
92	553	100.0	213	3	US-09-996-265-225	Sequence 225, Appl
93	553	100.0	213	3	US-09-996-265-227	Sequence 227, Appl
94	553	100.0	213	3	US-09-996-265-229	Sequence 229, Appl
95	553	100.0	213	3	US-09-996-265-231	Sequence 231, Appl
96	553	100.0	213	3	US-09-996-265-233	Sequence 233, Appl
97	553	100.0	213	3	US-09-996-265-235	Sequence 235, Appl
98	553	100.0	213	3	US-09-996-265-237	Sequence 237, Appl
99	553	100.0	213	3	US-09-996-265-239	Sequence 239, Appl
100	553	100.0	213	3	US-09-996-265-241	Sequence 241, Appl

101	553	100.0	213	3	US-09-996-265-243	Sequence 243, App	174	553	100.0	213	5	US-10-962-285-223	Sequence 223, App
102	553	100.0	213	3	US-09-996-265-245	Sequence 245, App	175	553	100.0	213	5	US-10-962-285-225	Sequence 225, App
103	553	100.0	213	3	US-09-996-265-247	Sequence 247, App	176	553	100.0	213	5	US-10-962-285-227	Sequence 227, App
104	553	100.0	213	3	US-09-996-265-251	Sequence 251, App	177	553	100.0	213	5	US-10-962-285-229	Sequence 229, App
105	553	100.0	213	3	US-09-996-265-253	Sequence 253, App	178	553	100.0	213	5	US-10-962-285-231	Sequence 231, App
106	553	100.0	213	3	US-09-996-265-255	Sequence 255, App	179	553	100.0	213	5	US-10-962-285-233	Sequence 233, App
107	553	100.0	213	3	US-09-996-265-257	Sequence 257, App	180	553	100.0	213	5	US-10-962-285-235	Sequence 235, App
108	553	100.0	213	4	US-10-135-636-7	Sequence 7, Appli	181	553	100.0	213	5	US-10-962-285-237	Sequence 237, App
109	553	100.0	213	4	US-10-150-475A-4	Sequence 4, Appli	182	553	100.0	213	5	US-10-962-285-239	Sequence 239, App
110	553	100.0	213	4	US-10-150-475A-8	Sequence 8, Appli	183	553	100.0	213	5	US-10-962-285-241	Sequence 241, App
111	553	100.0	213	4	US-10-281-479A-46	Sequence 46, Appli	184	553	100.0	213	5	US-10-962-285-243	Sequence 243, App
112	553	100.0	213	4	US-10-281-479A-73	Sequence 73, Appli	185	553	100.0	213	5	US-10-962-285-245	Sequence 245, App
113	553	100.0	213	4	US-10-281-479A-74	Sequence 74, Appli	186	553	100.0	213	5	US-10-962-285-247	Sequence 247, App
114	553	100.0	213	4	US-10-281-479A-75	Sequence 75, Appli	187	553	100.0	213	5	US-10-962-285-251	Sequence 251, App
115	553	100.0	213	4	US-10-138-727A-42	Sequence 42, Appli	188	553	100.0	213	5	US-10-962-285-253	Sequence 253, App
116	553	100.0	213	4	US-10-275-180A-46	Sequence 46, Appli	189	553	100.0	213	5	US-10-962-285-255	Sequence 255, App
117	553	100.0	213	4	US-10-275-180A-73	Sequence 73, Appli	190	553	100.0	213	5	US-10-962-285-257	Sequence 257, App
118	553	100.0	213	4	US-10-275-180A-74	Sequence 74, Appli	191	553	100.0	213	5	US-10-880-028-49	Sequence 49, Appli
119	553	100.0	213	4	US-10-275-180A-75	Sequence 75, Appli	192	553	100.0	213	5	US-10-880-320-49	Sequence 49, Appli
120	553	100.0	213	4	US-10-286-132A-46	Sequence 46, Appli	193	553	100.0	213	5	US-10-916-758-18	Sequence 18, Appli
121	553	100.0	213	4	US-10-286-132A-73	Sequence 73, Appli	194	553	100.0	213	5	US-10-403-180-209	Sequence 209, App
122	553	100.0	213	4	US-10-286-132A-74	Sequence 74, Appli	195	553	100.0	213	5	US-10-403-180-211	Sequence 211, App
123	553	100.0	213	4	US-10-286-132A-75	Sequence 75, Appli	196	553	100.0	213	5	US-10-403-180-213	Sequence 213, App
124	553	100.0	213	4	US-10-435-299-12	Sequence 12, Appli	197	553	100.0	213	5	US-10-403-180-215	Sequence 215, App
125	553	100.0	213	4	US-10-474-832-3	Sequence 3, Appli	198	553	100.0	213	5	US-10-403-180-217	Sequence 217, App
126	553	100.0	213	4	US-10-704-522-4	Sequence 4, Appli	199	553	100.0	213	5	US-10-403-180-219	Sequence 219, App
127	553	100.0	213	4	US-10-704-522-8	Sequence 8, Appli	200	553	100.0	213	5	US-10-403-180-221	Sequence 221, App
128	553	100.0	213	4	US-10-645-215-4	Sequence 4, Appli	201	553	100.0	213	5	US-10-403-180-223	Sequence 223, App
129	553	100.0	213	4	US-10-645-215-8	Sequence 8, Appli	202	553	100.0	213	5	US-10-403-180-225	Sequence 225, App
130	553	100.0	213	4	US-10-818-765-3	Sequence 3, Appli	203	553	100.0	213	5	US-10-403-180-227	Sequence 227, App
131	553	100.0	213	5	US-10-900-230-209	Sequence 209, App	204	553	100.0	213	5	US-10-403-180-229	Sequence 229, App
132	553	100.0	213	5	US-10-900-230-211	Sequence 211, App	205	553	100.0	213	5	US-10-403-180-231	Sequence 231, App
133	553	100.0	213	5	US-10-900-230-213	Sequence 213, App	206	553	100.0	213	5	US-10-403-180-233	Sequence 233, App
134	553	100.0	213	5	US-10-900-230-215	Sequence 215, App	207	553	100.0	213	5	US-10-403-180-235	Sequence 235, App
135	553	100.0	213	5	US-10-900-230-217	Sequence 217, App	208	553	100.0	213	5	US-10-403-180-237	Sequence 237, App
136	553	100.0	213	5	US-10-900-230-219	Sequence 219, App	209	553	100.0	213	5	US-10-403-180-239	Sequence 239, App
137	553	100.0	213	5	US-10-900-230-221	Sequence 221, App	210	553	100.0	213	5	US-10-403-180-241	Sequence 241, App
138	553	100.0	213	5	US-10-900-230-223	Sequence 223, App	211	553	100.0	213	5	US-10-403-180-243	Sequence 243, App
139	553	100.0	213	5	US-10-900-230-225	Sequence 225, App	212	553	100.0	213	5	US-10-403-180-245	Sequence 245, App
140	553	100.0	213	5	US-10-900-230-227	Sequence 227, App	213	553	100.0	213	5	US-10-403-180-247	Sequence 247, App
141	553	100.0	213	5	US-10-900-230-229	Sequence 229, App	214	553	100.0	213	5	US-10-403-180-251	Sequence 251, App
142	553	100.0	213	5	US-10-900-230-231	Sequence 231, App	215	553	100.0	213	5	US-10-403-180-253	Sequence 253, App
143	553	100.0	213	5	US-10-900-230-233	Sequence 233, App	216	553	100.0	213	5	US-10-403-180-255	Sequence 255, App
144	553	100.0	213	5	US-10-900-230-235	Sequence 235, App	217	553	100.0	213	5	US-10-403-180-257	Sequence 257, App
145	553	100.0	213	5	US-10-900-230-237	Sequence 237, App	218	553	100.0	213	6	US-11-021-874-15	Sequence 15, Appli
146	553	100.0	213	5	US-10-900-230-239	Sequence 239, App	219	553	100.0	213	6	US-11-021-874-18	Sequence 18, Appli
147	553	100.0	213	5	US-10-900-230-241	Sequence 241, App	220	553	100.0	213	6	US-11-021-874-19	Sequence 19, Appli
148	553	100.0	213	5	US-10-900-230-243	Sequence 243, App	221	553	100.0	213	6	US-11-021-874-21	Sequence 21, Appli
149	553	100.0	213	5	US-10-900-230-245	Sequence 245, App	222	553	100.0	213	6	US-11-005-677-3	Sequence 3, Appli
150	553	100.0	213	5	US-10-900-230-247	Sequence 247, App	223	553	100.0	213	6	US-11-006-136-3	Sequence 3, Appli
151	553	100.0	213	5	US-10-900-230-251	Sequence 251, App	224	553	100.0	213	6	US-11-136-538-8	Sequence 8, Appli
152	553	100.0	213	5	US-10-900-230-253	Sequence 253, App	225	553	100.0	213	6	US-11-136-538-9	Sequence 9, Appli
153	553	100.0	213	5	US-10-900-230-255	Sequence 255, App	226	553	100.0	213	6	US-11-172-320-4	Sequence 4, Appli
154	553	100.0	213	5	US-10-900-230-257	Sequence 257, App	227	553	100.0	213	6	US-11-172-320-8	Sequence 8, Appli
155	553	100.0	213	5	US-10-822-300-118	Sequence 118, App	228	553	100.0	213	6	US-11-174-186-42	Sequence 42, Appli
156	553	100.0	213	5	US-10-822-300-135	Sequence 135, App	229	553	100.0	213	6	US-11-120-338-13	Sequence 13, Appli
157	553	100.0	213	5	US-10-849-615-67	Sequence 67, Appli	230	553	100.0	213	6	US-11-120-338-16	Sequence 16, Appli
158	553	100.0	213	5	US-10-822-231-3	Sequence 3, Appli	231	553	100.0	213	6	US-11-173-969-4	Sequence 4, Appli
159	553	100.0	213	5	US-10-947-432-1	Sequence 1, Appli	232	553	100.0	213	6	US-11-173-969-8	Sequence 8, Appli
160	553	100.0	213	5	US-10-861-049-15	Sequence 15, Appli	233	553	100.0	213	6	US-11-102-621-118	Sequence 118, App
161	553	100.0	213	5	US-10-861-049-18	Sequence 18, Appli	234	553	100.0	213	6	US-11-102-621-135	Sequence 135, App
162	553	100.0	213	5	US-10-861-049-19	Sequence 19, Appli	235	553	100.0	213	6	US-11-107-028-31	Sequence 31, Appli
163	553	100.0	213	5	US-10-861-049-21	Sequence 21, Appli	236	553	100.0	213	6	US-11-107-028-44	Sequence 44, Appli
164	553	100.0	213	5	US-10-632-815-6	Sequence 6, Appli	237	553	100.0	213	6	US-11-158-505-34	Sequence 34, Appli
165	553	100.0	213	5	US-10-985-584-5	Sequence 5, Appli	238	553	100.0	213	6	US-11-106-820-24	Sequence 24, Appli
166	553	100.0	213	5	US-10-728-723-198	Sequence 198, App	239	553	100.0	213	6	US-11-106-820-29	Sequence 29, Appli
167	553	100.0	213	5	US-10-962-285-209	Sequence 209, App	240	553	100.0	213	6	US-11-106-820-44	Sequence 44, Appli
168	553	100.0	213	5	US-10-962-285-211	Sequence 211, App	241	553	100.0	213	6	US-11-143-077-13	Sequence 13, Appli
169	553	100.0	213	5	US-10-962-285-213	Sequence 213, App	242	553	100.0	213	6	US-11-143-077-16	Sequence 16, Appli
170	553	100.0	213	5	US-10-962-285-215	Sequence 215, App	243	553	100.0	213	6	US-11-124-620-6	Sequence 6, Appli
171	553	100.0	213	5	US-10-962-285-217	Sequence 217, App	244	553	100.0	213	6	US-11-143-386-13	Sequence 13, Appli
172	553	100.0	213	5	US-10-962-285-219	Sequence 219, App	245	553	100.0	213	6	US-11-143-386-16	Sequence 16, Appli
173	553	100.0	213	5	US-10-962-285-221	Sequence 221, App	246	553	100.0	213	6	US-11-187-364-13	Sequence 13, Appli

247	553	100.0	213	6	US-11-187-364-28	Sequence 28, Appl	320	553	100.0	214	6	US-11-010-797-4	Sequence 4, Appl
248	553	100.0	213	6	US-11-208-422-24	Sequence 24, Appl	321	553	100.0	214	6	US-11-085-368-19	Sequence 19, Appl
249	553	100.0	213	6	US-11-208-422-26	Sequence 26, Appl	322	553	100.0	214	6	US-11-085-368-91	Sequence 91, Appl
250	553	100.0	213	6	US-11-208-422-39	Sequence 39, Appl	323	553	100.0	214	6	US-11-025-712-11	Sequence 11, Appl
251	553	100.0	214	3	US-09-940-166A-2	Sequence 2, Appl	324	553	100.0	214	6	US-11-094-625-9	Sequence 9, Appl
252	553	100.0	214	3	US-09-811-384-11	Sequence 11, Appl	325	553	100.0	214	6	US-11-102-621-129	Sequence 129, Appl
253	553	100.0	214	3	US-09-949-558-128	Sequence 128, App	326	553	100.0	214	6	US-11-128-900-71	Sequence 71, Appl
254	553	100.0	214	3	US-09-996-288-249	Sequence 249, App	327	553	100.0	214	6	US-11-154-337-14	Sequence 14, Appl
255	553	100.0	214	3	US-09-875-221A-128	Sequence 128, App	328	553	100.0	214	6	US-11-154-337-16	Sequence 16, Appl
256	553	100.0	214	3	US-09-996-265-249	Sequence 249, App	329	553	100.0	214	6	US-11-154-337-16	Sequence 16, Appl
257	553	100.0	214	4	US-10-253-366-1	Sequence 1, Appl	330	553	100.0	214	6	US-11-182-908-13	Sequence 13, Appl
258	553	100.0	214	4	US-10-153-382-19	Sequence 19, Appl	331	553	100.0	214	6	US-11-182-908-15	Sequence 15, Appl
259	553	100.0	214	4	US-10-229-567-11	Sequence 11, Appl	332	553	100.0	214	6	US-11-005-728-163	Sequence 163, App
260	553	100.0	214	4	US-10-316-694-1	Sequence 1, Appl	333	553	100.0	214	6	US-11-049-536-700	Sequence 700, App
261	553	100.0	214	4	US-10-356-974-1	Sequence 1, Appl	334	553	100.0	214	6	US-11-183-205-55	Sequence 55, Appl
262	553	100.0	214	4	US-10-310-454-4	Sequence 4, Appl	335	553	100.0	214	6	US-11-199-739-700	Sequence 700, App
263	553	100.0	214	4	US-10-364-953-1	Sequence 1, Appl	336	553	100.0	214	6	US-11-199-739-724	Sequence 724, App
264	553	100.0	214	4	US-10-364-953-3	Sequence 3, Appl	337	553	100.0	214	6	US-11-208-422-19	Sequence 19, Appl
265	553	100.0	214	4	US-10-364-953-4	Sequence 4, Appl	338	553	100.0	214	6	US-11-208-422-19	Sequence 19, Appl
266	553	100.0	214	4	US-10-364-953-11	Sequence 11, Appl	339	553	100.0	215	3	US-09-972-656-100	Sequence 100, App
267	553	100.0	214	4	US-10-364-953-13	Sequence 13, Appl	340	553	100.0	215	3	US-09-791-153A-47	Sequence 47, Appl
268	553	100.0	214	4	US-10-423-299-1	Sequence 1, Appl	341	553	100.0	215	4	US-10-408-901-32	Sequence 32, Appl
269	553	100.0	214	4	US-10-423-299-3	Sequence 3, Appl	342	553	100.0	215	4	US-10-408-901-40	Sequence 40, Appl
270	553	100.0	214	4	US-10-408-901-36	Sequence 36, Appl	343	553	100.0	215	4	US-10-408-901-48	Sequence 48, Appl
271	553	100.0	214	4	US-10-408-901-44	Sequence 44, Appl	344	553	100.0	215	4	US-10-408-901-52	Sequence 52, Appl
272	553	100.0	214	4	US-10-411-037-55	Sequence 55, Appl	345	553	100.0	215	5	US-10-818-068-26	Sequence 26, Appl
273	553	100.0	214	4	US-10-435-299-5	Sequence 5, Appl	346	553	100.0	215	5	US-10-684-957-18	Sequence 18, Appl
274	553	100.0	214	4	US-10-404-286-11	Sequence 11, Appl	347	553	100.0	215	5	US-10-684-957-20	Sequence 20, Appl
275	553	100.0	214	4	US-10-411-026-55	Sequence 55, Appl	348	553	100.0	215	5	US-10-684-957-22	Sequence 22, Appl
276	553	100.0	214	4	US-10-410-962-55	Sequence 55, Appl	349	553	100.0	215	5	US-10-823-300-141	Sequence 141, App
277	553	100.0	214	4	US-10-411-049-55	Sequence 55, Appl	350	553	100.0	215	5	US-10-724-274-26	Sequence 26, Appl
278	553	100.0	214	4	US-10-659-825-1	Sequence 1, Appl	351	553	100.0	215	5	US-10-724-274-32	Sequence 32, Appl
279	553	100.0	214	4	US-10-467-546-3	Sequence 3, Appl	352	553	100.0	215	5	US-10-830-956-32	Sequence 32, Appl
280	553	100.0	214	4	US-10-379-392-170	Sequence 170, App	353	553	100.0	215	5	US-10-830-956-32	Sequence 32, Appl
281	553	100.0	214	4	US-10-379-392-175	Sequence 175, App	354	553	100.0	215	5	US-10-916-758-12	Sequence 12, Appl
282	553	100.0	214	4	US-10-410-930-55	Sequence 55, Appl	355	553	100.0	215	5	US-10-916-758-16	Sequence 16, Appl
283	553	100.0	214	4	US-10-410-997-55	Sequence 55, Appl	356	553	100.0	215	6	US-11-102-621-141	Sequence 141, App
284	553	100.0	214	4	US-10-411-012-55	Sequence 55, Appl	357	553	100.0	215	6	US-11-166-906-2	Sequence 2, Appl
285	553	100.0	214	4	US-10-287-994-55	Sequence 55, Appl	358	553	100.0	216	5	US-10-684-957-33	Sequence 33, Appl
286	553	100.0	214	4	US-10-762-967-2	Sequence 2, Appl	359	553	100.0	217	5	US-10-937-596-5	Sequence 5, Appl
287	553	100.0	214	4	US-10-410-913-55	Sequence 55, Appl	360	553	100.0	217	6	US-11-056-776-2	Sequence 2, Appl
288	553	100.0	214	4	US-10-813-483-3	Sequence 3, Appl	361	553	100.0	217	6	US-11-182-908-23	Sequence 23, Appl
289	553	100.0	214	5	US-10-635-908-15	Sequence 15, Appl	362	553	100.0	218	3	US-09-802-077-9	Sequence 9, Appl
290	553	100.0	214	5	US-10-635-908-17	Sequence 17, Appl	363	553	100.0	218	3	US-09-802-096-9	Sequence 9, Appl
291	553	100.0	214	5	US-10-612-497-71	Sequence 71, Appl	364	553	100.0	218	3	US-09-920-171-13	Sequence 13, Appl
292	553	100.0	214	5	US-10-776-649-71	Sequence 71, Appl	365	553	100.0	218	3	US-09-920-171-15	Sequence 15, Appl
293	553	100.0	214	5	US-10-835-641-24	Sequence 24, Appl	366	553	100.0	218	3	US-09-920-171-17	Sequence 17, Appl
294	553	100.0	214	5	US-10-900-230-249	Sequence 249, App	367	553	100.0	218	3	US-09-920-171-19	Sequence 19, Appl
295	553	100.0	214	5	US-10-822-300-129	Sequence 129, App	368	553	100.0	218	3	US-09-920-171-24	Sequence 24, Appl
296	553	100.0	214	5	US-10-410-980-55	Sequence 55, Appl	369	553	100.0	218	3	US-09-917-410-2	Sequence 2, Appl
297	553	100.0	214	5	US-10-877-532-1	Sequence 1, Appl	370	553	100.0	218	3	US-09-925-179-9	Sequence 9, Appl
298	553	100.0	214	5	US-10-728-420B-113	Sequence 113, App	371	553	100.0	218	3	US-09-925-179-67	Sequence 67, Appl
299	553	100.0	214	5	US-10-914-015-113	Sequence 113, App	372	553	100.0	218	3	US-09-792-938-1	Sequence 1, Appl
300	553	100.0	214	5	US-10-644-277-64	Sequence 64, Appl	373	553	100.0	218	4	US-10-171-452A-39	Sequence 39, Appl
301	553	100.0	214	5	US-10-949-683-1	Sequence 1, Appl	374	553	100.0	218	4	US-10-171-452A-57	Sequence 57, Appl
302	553	100.0	214	5	US-10-666-332-3	Sequence 3, Appl	375	553	100.0	218	4	US-10-113-996-13	Sequence 13, Appl
303	553	100.0	214	5	US-10-503-504-8	Sequence 8, Appl	376	553	100.0	218	4	US-10-113-996-15	Sequence 15, Appl
304	553	100.0	214	5	US-10-891-658-44	Sequence 44, Appl	377	553	100.0	218	4	US-10-113-996-17	Sequence 17, Appl
305	553	100.0	214	5	US-10-484-280-14	Sequence 14, Appl	378	553	100.0	218	4	US-10-113-996-19	Sequence 19, Appl
306	553	100.0	214	5	US-10-410-897-55	Sequence 55, Appl	379	553	100.0	218	4	US-10-113-996-24	Sequence 24, Appl
307	553	100.0	214	5	US-10-492-261-55	Sequence 55, Appl	380	553	100.0	218	4	US-10-293-869-1	Sequence 1, Appl
308	553	100.0	214	5	US-10-962-285-249	Sequence 249, App	381	553	100.0	218	4	US-10-353-708-37	Sequence 37, Appl
309	553	100.0	214	5	US-10-880-028-41	Sequence 41, Appl	382	553	100.0	218	4	US-10-353-708-57	Sequence 57, Appl
310	553	100.0	214	5	US-10-880-320-41	Sequence 41, Appl	383	553	100.0	218	4	US-10-378-567-3	Sequence 3, Appl
311	553	100.0	214	5	US-10-500-184-26	Sequence 26, Appl	384	553	100.0	218	4	US-10-449-566-98	Sequence 98, Appl
312	553	100.0	214	5	US-10-916-758-20	Sequence 20, Appl	385	553	100.0	218	4	US-10-449-566-102	Sequence 102, App
313	553	100.0	214	5	US-10-778-915-2	Sequence 2, Appl	386	553	100.0	218	4	US-10-449-566-119	Sequence 119, App
314	553	100.0	214	5	US-10-403-180-249	Sequence 249, App	387	553	100.0	218	4	US-10-318-397-21	Sequence 21, Appl
315	553	100.0	214	6	US-11-004-054-19	Sequence 19, Appl	388	553	100.0	218	4	US-10-317-747-21	Sequence 21, Appl
316	553	100.0	214	6	US-11-004-054-22	Sequence 22, Appl	389	553	100.0	218	4	US-10-731-984-4	Sequence 4, Appl
317	553	100.0	214	6	US-11-013-966-3	Sequence 3, Appl	390	553	100.0	218	4	US-10-731-984-28	Sequence 28, Appl
318	553	100.0	214	6	US-11-077-171-2	Sequence 2, Appl	391	553	100.0	218	4	US-10-833-642-1	Sequence 1, Appl
319	553	100.0	214	6	US-11-084-729-1	Sequence 1, Appl	392	553	100.0	218	4	US-10-813-483-1	Sequence 1, Appl

393	553	100.0	218	4	US-10-813-483-2	Sequence 2, Appli	466	553	100.0	232	4	US-10-006-771A-6	Sequence 6, Appli
394	553	100.0	218	5	US-10-757-863-1	Sequence 1, Appli	467	553	100.0	232	4	US-10-377-109-4	Sequence 4, Appli
395	553	100.0	218	5	US-10-791-619-13	Sequence 13, Appli	468	553	100.0	232	4	US-10-877-363-3	Sequence 3, Appli
396	553	100.0	218	5	US-10-791-619-15	Sequence 15, Appli	469	553	100.0	232	5	US-10-922-651-3	Sequence 3, Appli
397	553	100.0	218	5	US-10-791-619-17	Sequence 17, Appli	470	553	100.0	232	5	US-10-861-049-3	Sequence 23, Appli
398	553	100.0	218	5	US-10-791-619-19	Sequence 19, Appli	471	553	100.0	232	5	US-10-985-584-23	Sequence 23, Appli
399	553	100.0	218	5	US-10-791-619-24	Sequence 24, Appli	472	553	100.0	232	6	US-11-021-874-3	Sequence 3, Appli
400	553	100.0	218	5	US-10-714-000-1	Sequence 1, Appli	473	553	100.0	232	6	US-11-106-820-23	Sequence 23, Appli
401	553	100.0	218	5	US-10-698-073-6	Sequence 6, Appli	474	553	100.0	232	6	US-11-190-364-21	Sequence 21, Appli
402	553	100.0	218	5	US-10-698-073-8	Sequence 8, Appli	475	553	100.0	232	6	US-11-147-780-21	Sequence 21, Appli
403	553	100.0	218	5	US-10-698-073-10	Sequence 10, Appli	476	553	100.0	233	4	US-10-153-382-11	Sequence 11, Appli
404	553	100.0	218	5	US-10-698-073-12	Sequence 12, Appli	477	553	100.0	233	4	US-10-071-485-69	Sequence 69, Appli
405	553	100.0	218	5	US-10-698-073-17	Sequence 17, Appli	478	553	100.0	233	4	US-10-404-724-68	Sequence 68, Appli
406	553	100.0	218	5	US-10-968-237-9	Sequence 9, Appli	479	553	100.0	233	4	US-10-377-121-16	Sequence 16, Appli
407	553	100.0	218	5	US-10-968-237-67	Sequence 67, Appli	480	553	100.0	233	4	US-10-377-121-20	Sequence 20, Appli
408	553	100.0	218	5	US-10-985-584-14	Sequence 14, Appli	481	553	100.0	233	4	US-10-656-769-40	Sequence 40, Appli
409	553	100.0	218	5	US-10-937-596-33	Sequence 33, Appli	482	553	100.0	233	4	US-10-663-244-150	Sequence 150, App
410	553	100.0	218	5	US-10-982-470-1	Sequence 1, Appli	483	553	100.0	233	4	US-10-663-244-151	Sequence 151, App
411	553	100.0	218	5	US-10-923-327-6	Sequence 6, Appli	484	553	100.0	233	4	US-10-660-128-9	Sequence 9, Appli
412	553	100.0	218	5	US-10-923-327-8	Sequence 8, Appli	485	553	100.0	233	5	US-10-612-497-15	Sequence 15, Appli
413	553	100.0	218	5	US-10-923-327-10	Sequence 10, Appli	486	553	100.0	233	5	US-10-612-497-67	Sequence 67, Appli
414	553	100.0	218	5	US-10-923-327-12	Sequence 12, Appli	487	553	100.0	233	5	US-10-776-649-15	Sequence 15, Appli
415	553	100.0	218	5	US-10-923-327-17	Sequence 17, Appli	488	553	100.0	233	5	US-10-776-649-67	Sequence 67, Appli
416	553	100.0	218	6	US-11-013-966-1	Sequence 1, Appli	489	553	100.0	233	5	US-10-835-641-25	Sequence 25, Appli
417	553	100.0	218	6	US-11-013-966-2	Sequence 2, Appli	490	553	100.0	233	5	US-10-769-144-6	Sequence 6, Appli
418	553	100.0	218	6	US-11-158-839-1	Sequence 1, Appli	491	553	100.0	233	5	US-10-985-581-69	Sequence 69, Appli
419	553	100.0	218	6	US-11-158-839-11	Sequence 11, Appli	492	553	100.0	233	5	US-10-903-191-6	Sequence 6, Appli
420	553	100.0	218	6	US-11-158-505-4	Sequence 4, Appli	493	553	100.0	233	6	US-11-085-368-11	Sequence 11, Appli
421	553	100.0	218	6	US-11-158-505-28	Sequence 28, Appli	494	553	100.0	233	6	US-11-085-368-47	Sequence 47, Appli
422	553	100.0	218	6	US-11-004-590-229	Sequence 229, App	495	553	100.0	233	6	US-11-031-485-16	Sequence 16, Appli
423	553	100.0	218	6	US-11-136-250-11	Sequence 11, Appli	496	553	100.0	233	6	US-11-031-485-54	Sequence 54, Appli
424	553	100.0	218	6	US-11-194-989-37	Sequence 37, Appli	497	553	100.0	233	6	US-11-128-900-15	Sequence 15, Appli
425	553	100.0	218	6	US-11-195-207-37	Sequence 37, Appli	498	553	100.0	233	6	US-11-128-900-67	Sequence 67, Appli
426	553	100.0	218	6	US-11-195-207-37	Sequence 37, Appli	499	553	100.0	233	6	US-11-182-908-17	Sequence 17, Appli
427	553	100.0	218	6	US-11-208-422-16	Sequence 16, Appli	500	553	100.0	233	6	US-11-182-908-17	Sequence 17, Appli
428	553	100.0	218	6	US-11-208-422-17	Sequence 17, Appli	501	553	100.0	234	3	US-11-218-813-130	Sequence 130, App
429	553	100.0	219	3	US-11-208-428-72	Sequence 72, Appli	502	553	100.0	234	3	US-09-740-002-24	Sequence 24, Appli
430	553	100.0	219	3	US-09-726-258-72	Sequence 72, Appli	503	553	100.0	234	3	US-09-800-729-150	Sequence 150, App
431	553	100.0	219	3	US-09-972-656-92	Sequence 92, Appli	504	553	100.0	234	3	US-09-848-832-4	Sequence 4, Appli
432	553	100.0	219	3	US-09-972-656-94	Sequence 94, Appli	505	553	100.0	234	3	US-09-833-245-2210	Sequence 2210, Ap
433	553	100.0	219	3	US-09-972-656-104	Sequence 104, App	506	553	100.0	234	4	US-10-153-382-15	Sequence 15, Appli
434	553	100.0	219	3	US-09-972-656-106	Sequence 106, App	507	553	100.0	234	4	US-10-026-925-55	Sequence 55, Appli
435	553	100.0	219	4	US-10-226-435A-11	Sequence 11, Appli	508	553	100.0	234	4	US-10-225-108A-4	Sequence 4, Appli
436	553	100.0	219	5	US-10-487-332-11	Sequence 11, Appli	509	553	100.0	234	4	US-10-292-088-24	Sequence 24, Appli
437	553	100.0	219	5	US-10-487-326-11	Sequence 11, Appli	510	553	100.0	234	4	US-10-292-088-48	Sequence 48, Appli
438	553	100.0	219	5	US-10-486-908-11	Sequence 11, Appli	511	553	100.0	234	4	US-10-292-088-72	Sequence 72, Appli
439	553	100.0	219	5	US-10-478-265-11	Sequence 11, Appli	512	553	100.0	234	4	US-10-292-088-88	Sequence 88, Appli
440	553	100.0	219	5	US-10-512-527-11	Sequence 11, Appli	513	553	100.0	234	4	US-10-461-148-2	Sequence 2, Appli
441	553	100.0	219	5	US-10-497-475-11	Sequence 11, Appli	514	553	100.0	234	4	US-10-325-698-24	Sequence 24, Appli
442	553	100.0	219	5	US-10-880-028-45	Sequence 45, Appli	515	553	100.0	234	4	US-10-684-109-85	Sequence 85, Appli
443	553	100.0	219	5	US-10-880-320-45	Sequence 45, Appli	516	553	100.0	234	4	US-10-684-109-91	Sequence 91, Appli
444	553	100.0	219	6	US-11-080-587-8	Sequence 8, Appli	517	553	100.0	234	4	US-10-684-109-97	Sequence 97, Appli
445	553	100.0	219	6	US-11-224-623-11	Sequence 11, Appli	518	553	100.0	234	4	US-10-684-109-103	Sequence 103, App
446	553	100.0	219	6	US-11-194-989-12	Sequence 12, Appli	519	553	100.0	234	4	US-10-684-109-109	Sequence 109, App
447	553	100.0	219	6	US-11-195-207-12	Sequence 12, Appli	520	553	100.0	234	5	US-10-612-497-115	Sequence 115, App
448	553	100.0	219	6	US-11-155-843-177	Sequence 177, App	521	553	100.0	234	5	US-10-612-497-69	Sequence 69, Appli
449	553	100.0	219	6	US-11-259-232-72	Sequence 72, Appli	522	553	100.0	234	5	US-10-776-649-17	Sequence 17, Appli
450	553	100.0	220	3	US-09-301-593-17	Sequence 17, Appli	523	553	100.0	234	5	US-10-776-649-69	Sequence 69, Appli
451	553	100.0	220	3	US-09-917-410-5	Sequence 5, Appli	524	553	100.0	234	5	US-10-938-353-4	Sequence 4, Appli
452	553	100.0	220	3	US-09-995-693-1	Sequence 1, Appli	525	553	100.0	234	5	US-10-938-353-8	Sequence 8, Appli
453	553	100.0	220	4	US-10-232-408-1	Sequence 1, Appli	526	553	100.0	234	5	US-10-938-353-12	Sequence 12, Appli
454	553	100.0	220	4	US-10-159-006-17	Sequence 17, Appli	527	553	100.0	234	6	US-11-085-368-15	Sequence 15, Appli
455	553	100.0	220	4	US-10-737-208A-5	Sequence 5, Appli	528	553	100.0	234	6	US-11-085-368-55	Sequence 55, Appli
456	553	100.0	220	5	US-10-644-277-4	Sequence 4, Appli	529	553	100.0	234	6	US-11-128-900-17	Sequence 17, Appli
457	553	100.0	220	5	US-10-644-277-20	Sequence 20, Appli	530	553	100.0	234	6	US-11-128-900-69	Sequence 69, Appli
458	553	100.0	220	5	US-10-644-277-40	Sequence 40, Appli	531	553	100.0	234	6	US-11-041-095-25	Sequence 25, Appli
459	553	100.0	220	5	US-10-644-277-68	Sequence 68, Appli	532	553	100.0	234	6	US-11-264-096-2210	Sequence 2210, Ap
460	553	100.0	220	5	US-10-644-277-92	Sequence 92, Appli	533	553	100.0	235	3	US-09-800-729-152	Sequence 152, App
461	553	100.0	220	5	US-10-880-028-19	Sequence 19, Appli	534	553	100.0	235	3	US-09-910-059-17	Sequence 17, Appli
462	553	100.0	220	5	US-10-880-028-27	Sequence 27, Appli	535	553	100.0	235	3	US-09-910-059-52	Sequence 52, Appli
463	553	100.0	220	5	US-10-880-320-19	Sequence 19, Appli	536	553	100.0	235	3	US-09-910-059-97	Sequence 97, Appli
464	553	100.0	220	5	US-10-880-320-27	Sequence 27, Appli	537	553	100.0	235	3	US-09-910-059-99	Sequence 99, Appli
465	553	100.0	220	6	US-11-040-071-2	Sequence 2, Appli	538	553	100.0	235	3	US-09-833-245-2209	Sequence 2209, Ap

539	553	100.0	235	4	US-10-153-382-7	Sequence 7, Appli	612	553	100.0	236	6	US-11-144-248-52	Sequence 52, Appl
540	553	100.0	235	4	US-10-180-648-4	Sequence 4, Appli	613	553	100.0	236	6	US-11-144-222-47	Sequence 47, Appl
541	553	100.0	235	4	US-10-656-769-38	Sequence 38, Appl	614	553	100.0	236	6	US-11-144-222-48	Sequence 48, Appl
542	553	100.0	235	4	US-10-608-710-2	Sequence 2, Appli	615	553	100.0	236	6	US-11-144-222-51	Sequence 51, Appl
543	553	100.0	235	5	US-10-612-497-14	Sequence 14, Appl	616	553	100.0	236	6	US-11-144-222-52	Sequence 52, Appl
544	553	100.0	235	5	US-10-612-497-65	Sequence 65, Appl	617	553	100.0	236	6	US-11-086-289-4	Sequence 4, Appli
545	553	100.0	235	5	US-10-776-649-14	Sequence 14, Appl	618	553	100.0	236	6	US-11-086-289-8	Sequence 8, Appli
546	553	100.0	235	5	US-10-776-649-65	Sequence 65, Appl	619	553	100.0	236	6	US-11-086-289-20	Sequence 20, Appl
547	553	100.0	235	5	US-10-723-003-42	Sequence 42, Appl	620	553	100.0	236	6	US-11-106-820-19	Sequence 19, Appl
548	553	100.0	235	5	US-10-938-353-32	Sequence 32, Appl	621	553	100.0	236	6	US-11-182-343-47	Sequence 47, Appl
549	553	100.0	235	5	US-10-938-353-44	Sequence 44, Appl	622	553	100.0	236	6	US-11-182-343-48	Sequence 48, Appl
550	553	100.0	235	5	US-10-938-353-60	Sequence 60, Appl	623	553	100.0	236	6	US-11-182-343-51	Sequence 51, Appl
551	553	100.0	235	5	US-10-492-228-11	Sequence 11, Appl	624	553	100.0	236	6	US-11-182-343-52	Sequence 52, Appl
552	553	100.0	235	5	US-10-492-228-70	Sequence 70, Appl	625	553	100.0	236	6	US-11-190-364-17	Sequence 17, Appl
553	553	100.0	235	6	US-11-019-180-2	Sequence 2, Appli	626	553	100.0	236	6	US-11-147-780-17	Sequence 17, Appl
554	553	100.0	235	6	US-11-085-368-7	Sequence 7, Appli	627	553	100.0	236	6	US-11-264-096-237	Sequence 237, App
555	553	100.0	235	6	US-11-085-368-43	Sequence 43, Appl	628	553	100.0	237	3	US-09-056-160B-100	Sequence 100, App
556	553	100.0	235	6	US-11-004-639-42	Sequence 42, Appl	629	553	100.0	237	3	US-09-940-166A-6	Sequence 6, Appli
557	553	100.0	235	6	US-11-128-900-14	Sequence 14, Appl	630	553	100.0	237	4	US-10-194-975-109	Sequence 109, App
558	553	100.0	235	6	US-11-128-900-65	Sequence 65, Appl	631	553	100.0	237	4	US-10-020-786-8	Sequence 8, Appli
559	553	100.0	235	6	US-11-086-289-16	Sequence 16, Appl	632	553	100.0	237	4	US-10-020-786-10	Sequence 10, Appl
560	553	100.0	235	6	US-11-166-994-2	Sequence 2, Appli	633	553	100.0	237	4	US-10-227-694-1	Sequence 1, Appli
561	553	100.0	235	6	US-11-264-096-2209	Sequence 2209, Ap	634	553	100.0	237	4	US-10-227-694-4	Sequence 4, Appli
562	553	100.0	236	3	US-09-859-053-30	Sequence 30, Appl	635	553	100.0	237	4	US-10-234-671-100	Sequence 100, App
563	553	100.0	236	3	US-09-859-053-34	Sequence 34, Appl	636	553	100.0	237	4	US-10-409-938-25	Sequence 25, Appl
564	553	100.0	236	3	US-09-859-053-38	Sequence 38, Appl	637	553	100.0	237	4	US-10-663-244-146	Sequence 146, App
565	553	100.0	236	3	US-09-833-245-237	Sequence 237, App	638	553	100.0	237	4	US-10-663-244-152	Sequence 152, App
566	553	100.0	236	4	US-10-006-593-69	Sequence 69, Appl	639	553	100.0	237	4	US-10-663-244-153	Sequence 153, App
567	553	100.0	236	4	US-10-401-344-4	Sequence 4, Appli	640	553	100.0	237	4	US-10-763-967-6	Sequence 6, Appli
568	553	100.0	236	4	US-10-307-724-69	Sequence 69, Appl	641	553	100.0	237	5	US-10-754-212-2	Sequence 2, Appli
569	553	100.0	236	4	US-10-108-260A-4281	Sequence 4281, Ap	642	553	100.0	237	5	US-10-754-212-5	Sequence 5, Appli
570	553	100.0	236	4	US-10-038-591-47	Sequence 47, Appl	643	553	100.0	237	5	US-10-697-995-2	Sequence 2, Appli
571	553	100.0	236	4	US-10-038-591-48	Sequence 48, Appl	644	553	100.0	237	5	US-10-697-995-5	Sequence 5, Appli
572	553	100.0	236	4	US-10-038-591-51	Sequence 51, Appl	645	553	100.0	237	5	US-10-697-995-8	Sequence 8, Appli
573	553	100.0	236	4	US-10-038-591-52	Sequence 52, Appl	646	553	100.0	237	5	US-10-697-995-11	Sequence 11, Appl
574	553	100.0	236	4	US-10-800-250-30	Sequence 30, Appl	647	553	100.0	237	5	US-10-697-995-17	Sequence 17, Appl
575	553	100.0	236	4	US-10-800-250-34	Sequence 34, Appl	648	553	100.0	237	5	US-10-697-995-20	Sequence 20, Appl
576	553	100.0	236	4	US-10-800-250-38	Sequence 38, Appl	649	553	100.0	237	5	US-10-974-517-100	Sequence 100, App
577	553	100.0	236	4	US-10-625-105-30	Sequence 30, Appl	650	553	100.0	237	6	US-11-077-717-10	Sequence 10, Appl
578	553	100.0	236	4	US-10-625-105-34	Sequence 34, Appl	651	553	100.0	237	6	US-11-071-291-8	Sequence 8, Appli
579	553	100.0	236	4	US-10-625-105-38	Sequence 38, Appl	652	553	100.0	237	6	US-11-071-291-10	Sequence 10, Appl
580	553	100.0	236	4	US-10-775-444A-47	Sequence 47, Appl	653	553	100.0	237	6	US-11-054-669-109	Sequence 109, App
581	553	100.0	236	4	US-10-775-444A-48	Sequence 48, Appl	654	553	100.0	238	4	US-10-216-484-50	Sequence 50, Appl
582	553	100.0	236	4	US-10-775-444A-51	Sequence 51, Appl	655	553	100.0	238	4	US-10-216-484-52	Sequence 52, Appl
583	553	100.0	236	4	US-10-775-444A-52	Sequence 52, Appl	656	553	100.0	238	4	US-10-216-484-54	Sequence 54, Appl
584	553	100.0	236	5	US-10-858-186-20	Sequence 20, Appl	657	553	100.0	238	4	US-10-216-484-107	Sequence 107, App
585	553	100.0	236	5	US-10-737-290-69	Sequence 69, Appl	658	553	100.0	238	4	US-10-216-484-109	Sequence 109, App
586	553	100.0	236	5	US-10-723-003-56	Sequence 56, Appl	659	553	100.0	238	4	US-10-216-484-127	Sequence 127, App
587	553	100.0	236	5	US-10-910-901-4	Sequence 4, Appli	660	553	100.0	238	4	US-10-216-484-129	Sequence 129, App
588	553	100.0	236	5	US-10-910-901-8	Sequence 8, Appli	661	553	100.0	238	4	US-10-216-484-131	Sequence 131, App
589	553	100.0	236	5	US-10-910-901-12	Sequence 12, Appl	662	553	100.0	238	4	US-10-171-452A-38	Sequence 38, Appl
590	553	100.0	236	5	US-10-910-901-16	Sequence 16, Appl	663	553	100.0	238	4	US-10-171-452A-56	Sequence 56, Appl
591	553	100.0	236	5	US-10-938-353-16	Sequence 16, Appl	664	553	100.0	238	4	US-10-384-933-50	Sequence 50, Appl
592	553	100.0	236	5	US-10-938-353-20	Sequence 20, Appl	665	553	100.0	238	4	US-10-384-933-52	Sequence 52, Appl
593	553	100.0	236	5	US-10-938-353-28	Sequence 28, Appl	666	553	100.0	238	4	US-10-384-933-54	Sequence 54, Appl
594	553	100.0	236	5	US-10-938-353-36	Sequence 36, Appl	667	553	100.0	238	4	US-10-384-933-107	Sequence 107, App
595	553	100.0	236	5	US-10-938-353-48	Sequence 48, Appl	668	553	100.0	238	4	US-10-384-933-109	Sequence 109, App
596	553	100.0	236	5	US-10-938-353-52	Sequence 52, Appl	669	553	100.0	238	4	US-10-384-933-127	Sequence 127, App
597	553	100.0	236	5	US-10-938-353-55	Sequence 56, Appl	670	553	100.0	238	4	US-10-384-933-129	Sequence 129, App
598	553	100.0	236	5	US-10-917-073A-5	Sequence 5, Appli	671	553	100.0	238	4	US-10-384-933-131	Sequence 131, App
599	553	100.0	236	5	US-10-917-073A-6	Sequence 6, Appli	672	553	100.0	238	4	US-10-353-708-38	Sequence 38, Appl
600	553	100.0	236	5	US-10-961-567A-6	Sequence 6, Appli	673	553	100.0	238	4	US-10-353-708-56	Sequence 56, Appl
601	553	100.0	236	5	US-10-728-723-18	Sequence 18, Appl	674	553	100.0	238	4	US-10-663-244-144	Sequence 144, App
602	553	100.0	236	6	US-11-131-648-20	Sequence 20, Appl	675	553	100.0	238	4	US-10-663-244-145	Sequence 145, App
603	553	100.0	236	6	US-11-131-648-49	Sequence 49, Appl	676	553	100.0	238	4	US-10-663-244-147	Sequence 147, App
604	553	100.0	236	6	US-11-031-485-12	Sequence 12, Appl	677	553	100.0	238	4	US-10-663-244-148	Sequence 148, App
605	553	100.0	236	6	US-11-031-485-20	Sequence 20, Appl	678	553	100.0	238	4	US-10-663-244-149	Sequence 149, App
606	553	100.0	236	6	US-11-031-485-58	Sequence 58, Appl	679	553	100.0	238	4	US-10-467-253-14	Sequence 14, Appl
607	553	100.0	236	6	US-11-056-776-3	Sequence 3, Appli	680	553	100.0	238	4	US-10-731-984-3	Sequence 3, Appli
608	553	100.0	236	6	US-11-004-639-56	Sequence 56, Appl	681	553	100.0	238	5	US-10-731-984-27	Sequence 27, Appl
609	553	100.0	236	6	US-11-144-248-47	Sequence 47, Appl	682	553	100.0	238	5	US-10-937-046-10	Sequence 10, Appl
610	553	100.0	236	6	US-11-144-248-48	Sequence 48, Appl	683	553	100.0	238	5	US-10-497-475-19	Sequence 19, Appl
611	553	100.0	236	6	US-11-144-248-51	Sequence 51, Appl	684	553	100.0	238	5	US-10-943-640-2	Sequence 2, Appli

685	553	100.0	238	6	US-11-034-655-2	Sequence 2, Appl	758	553	100.0	239	6	US-11-031-485-36	Sequence 36, Appl
686	553	100.0	238	6	US-11-034-655-11	Sequence 11, Appl	759	553	100.0	239	6	US-11-031-485-44	Sequence 44, Appl
687	553	100.0	238	6	US-11-034-655-13	Sequence 13, Appl	760	553	100.0	239	6	US-11-031-485-66	Sequence 66, Appl
688	553	100.0	238	6	US-11-034-655-15	Sequence 15, Appl	761	553	100.0	239	6	US-11-031-485-68	Sequence 68, Appl
689	553	100.0	238	6	US-11-031-485-1	Sequence 1, Appl	762	553	100.0	239	6	US-11-004-639-14	Sequence 14, Appl
690	553	100.0	238	6	US-11-031-485-4	Sequence 4, Appl	763	553	100.0	239	6	US-11-139-499-6	Sequence 6, Appl
691	553	100.0	238	6	US-11-031-485-8	Sequence 8, Appl	764	553	100.0	239	6	US-11-086-289-12	Sequence 12, Appl
692	553	100.0	238	6	US-11-031-485-28	Sequence 28, Appl	765	553	100.0	239	6	US-11-041-095-19	Sequence 19, Appl
693	553	100.0	238	6	US-11-031-485-40	Sequence 40, Appl	766	553	100.0	239	6	US-11-177-648-10	Sequence 10, Appl
694	553	100.0	238	6	US-11-031-485-48	Sequence 48, Appl	767	553	100.0	239	6	US-11-271-090-4	Sequence 4, Appl
695	553	100.0	238	6	US-11-031-485-51	Sequence 1, Appl	768	553	100.0	240	3	US-09-301-593-28	Sequence 28, Appl
696	553	100.0	238	6	US-11-158-505-3	Sequence 3, Appl	769	553	100.0	240	3	US-09-301-593-36	Sequence 36, Appl
697	553	100.0	238	6	US-11-158-505-25	Sequence 25, Appl	770	553	100.0	240	3	US-09-799-514-8	Sequence 8, Appl
698	553	100.0	238	6	US-11-158-505-27	Sequence 27, Appl	771	553	100.0	240	3	US-10-159-006-28	Sequence 28, Appl
699	553	100.0	238	6	US-11-177-648-34	Sequence 34, Appl	772	553	100.0	240	4	US-10-159-006-36	Sequence 36, Appl
700	553	100.0	238	6	US-11-177-648-35	Sequence 35, Appl	773	553	100.0	240	4	US-10-153-006-36	Sequence 8, Appl
701	553	100.0	238	6	US-11-177-648-36	Sequence 36, Appl	774	553	100.0	240	4	US-10-630-406-8	Sequence 24, Appl
702	553	100.0	238	6	US-11-177-648-37	Sequence 37, Appl	775	553	100.0	240	5	US-10-938-353-24	Sequence 24, Appl
703	553	100.0	238	6	US-11-177-648-38	Sequence 38, Appl	776	553	100.0	240	5	US-10-805-177-139	Sequence 139, App
704	553	100.0	238	6	US-11-177-648-39	Sequence 39, Appl	777	553	100.0	240	6	US-11-073-453-8	Sequence 8, Appl
705	553	100.0	238	6	US-11-177-648-40	Sequence 40, Appl	778	553	100.0	241	5	US-10-723-003-22	Sequence 22, Appl
706	553	100.0	238	6	US-11-177-648-80	Sequence 80, Appl	779	553	100.0	241	6	US-11-031-485-24	Sequence 24, Appl
707	553	100.0	239	3	US-09-758-173-6	Sequence 6, Appl	780	553	100.0	241	6	US-11-031-485-62	Sequence 62, Appl
708	553	100.0	239	3	US-09-825-012-9	Sequence 9, Appl	781	553	100.0	241	6	US-11-004-639-22	Sequence 22, Appl
709	553	100.0	239	3	US-09-249-011A-22	Sequence 22, Appl	782	553	100.0	241	6	US-11-106-820-15	Sequence 15, Appl
710	553	100.0	239	3	US-09-948-429B-6	Sequence 6, Appl	783	553	100.0	241	6	US-11-190-364-14	Sequence 14, Appl
711	553	100.0	239	3	US-09-992-600A-8	Sequence 8, Appl	784	553	100.0	242	3	US-11-147-780-14	Sequence 14, Appl
712	553	100.0	239	3	US-09-924-340-8	Sequence 8, Appl	785	553	100.0	242	3	US-09-819-266-26	Sequence 26, Appl
713	553	100.0	239	3	US-09-992-095B-8	Sequence 8, Appl	786	553	100.0	242	3	US-09-726-258-51	Sequence 51, Appl
714	553	100.0	239	3	US-09-992-095B-8	Sequence 8, Appl	787	553	100.0	242	3	US-09-726-258-62	Sequence 56, Appl
715	553	100.0	239	4	US-10-124-905-6	Sequence 6, Appl	788	553	100.0	242	6	US-11-259-232-51	Sequence 51, Appl
716	553	100.0	239	4	US-10-000-489-8	Sequence 8, Appl	789	553	100.0	242	6	US-11-259-232-56	Sequence 56, Appl
717	553	100.0	239	4	US-10-000-986-8	Sequence 8, Appl	790	553	100.0	242	6	US-11-259-232-62	Sequence 62, Appl
718	553	100.0	239	4	US-10-154-678-8	Sequence 8, Appl	791	553	100.0	245	3	US-09-797-941A-6	Sequence 6, Appl
719	553	100.0	239	4	US-10-124-807-6	Sequence 6, Appl	792	553	100.0	245	5	US-10-965-585-6	Sequence 6, Appl
720	553	100.0	239	4	US-10-291-532-6	Sequence 6, Appl	793	553	100.0	247	5	US-10-466-164-69	Sequence 69, Appl
721	553	100.0	239	4	US-10-404-724-6	Sequence 6, Appl	794	553	100.0	247	5	US-10-887-230-50	Sequence 50, Appl
722	553	100.0	239	4	US-10-404-724-10	Sequence 10, Appl	795	553	100.0	258	3	US-09-979-948C-4	Sequence 4, Appl
723	553	100.0	239	4	US-10-404-724-12	Sequence 12, Appl	796	553	100.0	259	3	US-09-979-948C-6	Sequence 6, Appl
724	553	100.0	239	4	US-10-404-724-39	Sequence 39, Appl	797	553	100.0	260	4	US-10-264-049-2296	Sequence 2296, Ap
725	553	100.0	239	4	US-10-404-724-41	Sequence 41, Appl	798	553	100.0	271	5	US-10-887-230-46	Sequence 46, Appl
726	553	100.0	239	4	US-10-404-724-43	Sequence 43, Appl	799	553	100.0	290	6	US-11-041-095-13	Sequence 13, Appl
727	553	100.0	239	4	US-10-404-724-45	Sequence 45, Appl	800	553	100.0	291	6	US-11-041-095-60	Sequence 60, Appl
728	553	100.0	239	4	US-10-404-724-47	Sequence 47, Appl	801	553	100.0	323	3	US-09-746-359A-60	Sequence 60, Appl
729	553	100.0	239	4	US-10-404-724-49	Sequence 49, Appl	802	553	100.0	323	3	US-09-951-268-41	Sequence 41, Appl
730	553	100.0	239	4	US-10-292-088-8	Sequence 8, Appl	803	553	100.0	323	3	US-09-745-752A-60	Sequence 60, Appl
731	553	100.0	239	4	US-10-292-088-16	Sequence 16, Appl	804	553	100.0	323	3	US-10-424-658-60	Sequence 60, Appl
732	553	100.0	239	4	US-10-292-088-32	Sequence 32, Appl	805	553	100.0	323	5	US-10-471-151-29	Sequence 29, Appl
733	553	100.0	239	4	US-10-292-088-40	Sequence 40, Appl	806	553	100.0	323	5	US-10-994-116-67	Sequence 67, Appl
734	553	100.0	239	4	US-10-292-088-56	Sequence 56, Appl	807	553	100.0	323	5	US-10-994-151-67	Sequence 67, Appl
735	553	100.0	239	4	US-10-292-088-102	Sequence 102, App	808	553	100.0	323	5	US-10-994-151-67	Sequence 108, App
736	553	100.0	239	4	US-10-428-408A-28	Sequence 28, Appl	809	553	100.0	352	3	US-09-746-359A-21	Sequence 21, Appl
737	553	100.0	239	4	US-10-108-260A-4028	Sequence 4028, Ap	810	553	100.0	352	3	US-09-951-268-22	Sequence 22, Appl
738	553	100.0	239	4	US-10-428-894-28	Sequence 28, Appl	811	553	100.0	352	3	US-09-745-792A-21	Sequence 21, Appl
739	553	100.0	239	4	US-10-699-874-28	Sequence 28, Appl	812	553	100.0	352	4	US-10-424-658-21	Sequence 21, Appl
740	553	100.0	239	5	US-10-723-003-14	Sequence 14, Appl	813	553	100.0	352	4	US-10-471-151-28	Sequence 28, Appl
741	553	100.0	239	5	US-10-816-276-2	Sequence 2, Appl	814	553	100.0	352	5	US-10-994-116-66	Sequence 66, Appl
742	553	100.0	239	5	US-10-816-276-6	Sequence 6, Appl	815	553	100.0	352	5	US-10-994-116-66	Sequence 66, Appl
743	553	100.0	239	5	US-10-816-276-8	Sequence 8, Appl	816	553	100.0	366	6	US-11-075-351-38	Sequence 38, Appl
744	553	100.0	239	5	US-10-816-276-35	Sequence 35, Appl	817	553	100.0	367	6	US-10-291-265-899	Sequence 899, App
745	553	100.0	239	5	US-10-816-276-37	Sequence 37, Appl	818	553	100.0	367	6	US-11-000-463-899	Sequence 899, App
746	553	100.0	239	5	US-10-816-276-39	Sequence 39, Appl	819	553	100.0	374	6	US-11-075-351-42	Sequence 42, Appl
747	553	100.0	239	5	US-10-816-276-41	Sequence 41, Appl	820	553	100.0	384	4	US-10-291-265-804	Sequence 804, App
748	553	100.0	239	5	US-10-816-276-43	Sequence 43, Appl	821	553	100.0	384	4	US-10-291-265-805	Sequence 805, App
749	553	100.0	239	5	US-10-816-276-45	Sequence 45, Appl	822	553	100.0	384	4	US-10-291-265-806	Sequence 806, App
750	553	100.0	239	5	US-10-838-854-8	Sequence 8, Appl	823	553	100.0	384	4	US-10-291-265-807	Sequence 807, App
751	553	100.0	239	5	US-10-476-265-19	Sequence 19, Appl	824	553	100.0	384	6	US-11-000-463-804	Sequence 804, App
752	553	100.0	239	5	US-10-644-256-4	Sequence 4, Appl	825	553	100.0	384	6	US-11-000-463-805	Sequence 805, App
753	553	100.0	239	5	US-10-981-738-14	Sequence 14, Appl	826	553	100.0	384	6	US-11-000-463-806	Sequence 806, App
754	553	100.0	239	5	US-10-986-780-6	Sequence 6, Appl	827	553	100.0	384	6	US-11-000-463-807	Sequence 807, App
755	553	100.0	239	6	US-11-131-648-21	Sequence 21, Appl	828	553	100.0	392	4	US-10-272-899A-110	Sequence 110, App
756	553	100.0	239	6	US-11-131-648-51	Sequence 51, Appl	829	553	100.0	411	6	US-11-075-351-47	Sequence 47, Appl
757	553	100.0	239	6	US-11-031-485-32	Sequence 32, Appl	830	553	100.0	488	6	US-11-084-080-18	Sequence 18, Appl

831	553	100.0	491	4	US-10-011-125-2	Sequence 2, Appli	904	550	99.5	263	3	US-09-979-948C-1	Sequence 1, Appli
832	553	100.0	498	5	US-10-491-653-146	Sequence 146, App	905	550	99.5	363	4	US-10-291-265-335	Sequence 335, App
833	553	100.0	512	4	US-10-679-620-70	Sequence 70, Appl	906	550	99.5	363	6	US-11-000-463-335	Sequence 335, App
834	553	100.0	513	6	US-11-132-143-70	Sequence 70, Appl	907	549	99.3	215	3	US-09-791-153A-45	Sequence 45, Appl
835	553	100.0	514	4	US-10-182-975-2	Sequence 2, Appli	908	549	99.3	234	4	US-10-045-674-587	Sequence 587, App
836	553	100.0	517	4	US-10-679-620-68	Sequence 68, Appl	909	549	99.3	239	4	US-10-292-088-64	Sequence 64, Appl
837	553	100.0	517	6	US-11-132-143-68	Sequence 68, Appl	910	548	99.1	106	3	US-09-925-664-49	Sequence 49, Appl
838	553	100.0	519	6	US-10-679-620-66	Sequence 66, Appl	911	548	99.1	106	3	US-09-995-898A-17	Sequence 17, Appl
839	553	100.0	519	6	US-11-132-143-66	Sequence 66, Appl	912	548	99.1	106	3	US-09-892-949-40	Sequence 40, Appl
840	553	100.0	663	4	US-10-412-406-32	Sequence 32, Appl	913	548	99.1	106	3	US-09-925-192-49	Sequence 49, Appl
841	553	100.0	666	5	US-10-981-356A-25	Sequence 25, Appl	914	548	99.1	106	4	US-10-066-895-12	Sequence 12, Appl
842	553	100.0	666	5	US-10-981-356A-27	Sequence 27, Appl	915	548	99.1	106	4	US-10-408-901-4	Sequence 4, Appli
843	553	100.0	666	5	US-10-981-356A-28	Sequence 28, Appl	916	548	99.1	106	4	US-10-420-034A-17	Sequence 17, Appl
844	553	100.0	666	5	US-10-981-356A-29	Sequence 29, Appl	917	548	99.1	106	4	US-10-038-591-26	Sequence 26, Appl
845	553	100.0	666	5	US-10-981-356A-30	Sequence 30, Appl	918	548	99.1	106	4	US-10-772-531-40	Sequence 40, Appl
846	553	100.0	666	6	US-11-096-046-27	Sequence 27, Appl	919	548	99.1	106	4	US-10-775-444A-26	Sequence 26, Appl
847	553	100.0	667	5	US-10-764-428-7	Sequence 7, Appli	920	548	99.1	106	5	US-10-733-969A-63	Sequence 63, Appl
848	553	100.0	667	5	US-10-764-428-13	Sequence 13, Appl	921	548	99.1	106	5	US-10-887-954-12	Sequence 12, Appl
849	553	100.0	667	5	US-10-764-428-25	Sequence 25, Appl	922	548	99.1	106	5	US-10-706-689-4	Sequence 4, Appli
850	553	100.0	667	5	US-10-764-428-25	Sequence 25, Appl	923	548	99.1	106	5	US-10-988-360-4	Sequence 4, Appli
851	553	100.0	667	6	US-11-096-046-25	Sequence 28, Appl	924	548	99.1	106	5	US-10-901-736-58	Sequence 58, Appl
852	553	100.0	667	6	US-11-096-046-29	Sequence 29, Appl	925	548	99.1	106	5	US-10-982-555-40	Sequence 40, Appl
853	553	100.0	667	6	US-11-096-046-29	Sequence 30, Appl	926	548	99.1	106	6	US-11-013-537-3	Sequence 3, Appli
854	553	100.0	669	3	US-09-807-721-2	Sequence 2, Appli	927	548	99.1	106	6	US-11-013-537-25	Sequence 25, Appl
855	553	100.0	669	5	US-10-764-428-21	Sequence 21, Appl	928	548	99.1	106	6	US-11-090-846-46	Sequence 46, Appl
856	553	100.0	669	5	US-10-764-428-23	Sequence 23, Appl	929	548	99.1	106	6	US-11-090-846-46	Sequence 46, Appl
857	553	100.0	669	5	US-10-900-928-3	Sequence 3, Appli	930	548	99.1	106	6	US-11-090-847-46	Sequence 46, Appl
858	553	100.0	670	5	US-10-764-428-5	Sequence 5, Appli	931	548	99.1	106	6	US-11-144-248-26	Sequence 26, Appl
859	553	100.0	670	5	US-10-764-428-9	Sequence 9, Appli	932	548	99.1	106	6	US-11-024-251-29	Sequence 29, Appl
860	553	100.0	670	5	US-10-764-428-11	Sequence 11, Appl	933	548	99.1	106	6	US-11-163-141-17	Sequence 17, Appl
861	553	100.0	670	5	US-10-764-428-27	Sequence 27, Appl	934	548	99.1	106	6	US-11-144-222-26	Sequence 26, Appl
862	553	100.0	692	5	US-10-981-356A-26	Sequence 26, Appl	935	548	99.1	106	6	US-11-005-726-165	Sequence 165, App
863	553	100.0	695	6	US-11-096-046-26	Sequence 26, Appl	936	548	99.1	106	6	US-11-182-343-26	Sequence 26, Appl
864	553	100.0	713	4	US-10-679-620-64	Sequence 64, Appl	937	548	99.1	108	3	US-09-313-942-13	Sequence 13, Appl
865	553	100.0	713	6	US-11-132-143-64	Sequence 64, Appl	938	548	99.1	108	3	US-09-935-868-13	Sequence 13, Appl
866	553	100.0	715	4	US-10-679-620-62	Sequence 62, Appl	939	548	99.1	108	4	US-10-287-035-13	Sequence 13, Appl
867	553	100.0	715	6	US-11-132-143-62	Sequence 62, Appl	940	548	99.1	108	4	US-10-282-162-13	Sequence 13, Appl
868	553	100.0	738	4	US-10-418-836-19	Sequence 19, Appl	941	548	99.1	108	4	US-10-741-481-58	Sequence 58, Appl
869	553	100.0	738	6	US-11-007-886-19	Sequence 19, Appl	942	548	99.1	108	6	US-11-134-114-13	Sequence 13, Appl
870	553	100.0	739	4	US-10-418-836-26	Sequence 26, Appl	943	548	99.1	138	3	US-09-837-306-355	Sequence 355, App
871	553	100.0	739	4	US-10-418-836-27	Sequence 27, Appl	944	548	99.1	138	4	US-10-045-674-54	Sequence 524, App
872	553	100.0	739	6	US-11-007-886-26	Sequence 26, Appl	945	548	99.1	214	3	US-09-754-998-1	Sequence 1, Appli
873	553	100.0	740	6	US-11-007-886-27	Sequence 27, Appl	946	548	99.1	214	6	US-11-173-564-1	Sequence 1, Appli
874	553	100.0	740	4	US-10-418-836-28	Sequence 28, Appl	947	548	99.1	220	3	US-09-822-698A-24	Sequence 24, Appl
875	553	100.0	740	4	US-10-418-836-34	Sequence 34, Appl	948	548	99.1	235	4	US-10-016-986-153	Sequence 153, App
876	553	100.0	740	6	US-11-007-886-28	Sequence 28, Appl	949	548	99.1	235	4	US-10-410-907A-2	Sequence 2, Appli
877	553	100.0	740	6	US-11-007-886-34	Sequence 34, Appl	950	548	99.1	236	4	US-10-235-175-79	Sequence 79, Appl
878	553	100.0	741	4	US-10-418-836-30	Sequence 30, Appl	951	548	99.1	237	3	US-09-726-238-25	Sequence 25, Appl
879	553	100.0	741	6	US-11-007-886-30	Sequence 30, Appl	952	548	99.1	237	6	US-11-259-232-25	Sequence 25, Appl
880	553	100.0	742	4	US-10-418-836-29	Sequence 29, Appl	953	548	99.1	238	4	US-10-027-075-30	Sequence 30, Appl
881	553	100.0	742	6	US-11-007-886-29	Sequence 29, Appl	954	548	99.1	238	4	US-10-027-075-32	Sequence 32, Appl
882	553	100.0	743	4	US-10-418-836-9	Sequence 9, Appli	955	548	99.1	238	4	US-10-792-637-30	Sequence 30, Appl
883	553	100.0	743	4	US-10-418-836-31	Sequence 31, Appl	956	548	99.1	238	4	US-10-792-637-32	Sequence 32, Appl
884	553	100.0	743	4	US-10-418-836-35	Sequence 35, Appl	957	548	99.1	238	5	US-10-985-832-30	Sequence 30, Appl
885	553	100.0	743	6	US-11-007-886-31	Sequence 31, Appli	958	548	99.1	238	5	US-10-985-832-32	Sequence 32, Appl
886	553	100.0	743	6	US-11-007-886-35	Sequence 35, Appl	959	548	99.1	307	3	US-09-746-359A-58	Sequence 58, Appl
887	553	100.0	743	6	US-11-007-886-35	Sequence 35, Appl	960	548	99.1	307	3	US-09-746-359A-58	Sequence 58, Appl
888	553	100.0	750	6	US-11-084-080-16	Sequence 16, Appl	961	548	99.1	307	3	US-09-951-268-42	Sequence 42, Appl
889	553	100.0	750	6	US-11-084-080-20	Sequence 20, Appl	962	548	99.1	307	4	US-09-745-792A-58	Sequence 58, Appl
890	553	100.0	750	6	US-11-084-080-22	Sequence 22, Appl	963	548	99.1	307	4	US-10-424-658-58	Sequence 58, Appl
891	553	100.0	750	6	US-11-084-080-22	Sequence 22, Appl	964	548	99.1	310	2	US-10-471-151-35	Sequence 35, Appli
892	553	100.0	751	6	US-11-084-080-26	Sequence 26, Appl	965	548	99.1	310	2	US-08-485-163-7	Sequence 7, Appli
893	553	100.0	759	6	US-11-084-080-28	Sequence 28, Appl	966	548	99.1	310	3	US-09-766-995-6	Sequence 6, Appli
894	553	100.0	4852	4	US-10-412-406-33	Sequence 33, Appl	967	548	99.1	336	3	US-09-746-359A-57	Sequence 57, Appl
895	550	99.5	135	4	US-10-408-765A-153	Sequence 153, App	968	548	99.1	336	3	US-09-951-268-34	Sequence 34, Appl
896	550	99.5	214	5	US-10-484-790A-19	Sequence 19, Appl	969	548	99.1	336	3	US-09-745-792A-57	Sequence 57, Appl
897	550	99.5	215	3	US-09-791-153A-49	Sequence 49, Appl	970	548	99.1	336	4	US-10-424-658-57	Sequence 57, Appl
898	550	99.5	223	3	US-09-837-306-305	Sequence 305, App	971	548	99.1	360	3	US-10-471-151-34	Sequence 34, Appl
899	550	99.5	223	4	US-10-045-674-482	Sequence 482, App	972	548	99.1	360	5	US-09-825-561A-18	Sequence 18, Appl
900	550	99.5	228	3	US-09-909-567B-50	Sequence 50, Appl	973	547	98.9	107	4	US-10-872-087-18	Sequence 18, Appl
901	550	99.5	232	6	US-11-013-537-23	Sequence 23, Appl	974	547	98.9	107	4	US-10-350-555-30	Sequence 30, Appl
902	550	99.5	239	4	US-10-292-088-80	Sequence 80, Appl	975	547	98.9	107	5	US-10-625-047-30	Sequence 30, Appl
903	550	99.5	241	4	US-10-221-945-1	Sequence 1, Appli	976	547	98.9	143	4	US-10-631-258-30	Sequence 30, Appl
												US-10-106-698-6554	Sequence 6554, Ap

```
977 547 98.9 206 4 US-10-264-049-4325 Sequence 4325, Ap
978 547 98.9 212 4 US-10-006-593-118 Sequence 118, App
979 547 98.9 212 4 US-10-307-724-118 Sequence 118, App
980 547 98.9 212 5 US-10-737-290-118 Sequence 118, App
981 547 98.9 214 5 US-10-745-775-117 Sequence 17, Appl
982 547 98.9 215 4 US-10-307-724-122 Sequence 122, App
983 547 98.9 215 4 US-10-698-041-6 Sequence 6, Appl
984 547 98.9 215 5 US-10-737-290-122 Sequence 122, App
985 547 98.9 217 4 US-10-251-215-39 Sequence 39, Appl
986 547 98.9 218 4 US-10-350-555-27 Sequence 27, Appl
987 547 98.9 218 4 US-10-350-555-28 Sequence 28, Appl
988 547 98.9 218 4 US-10-625-047-27 Sequence 27, Appl
989 547 98.9 218 4 US-10-625-047-28 Sequence 28, Appl
990 547 98.9 218 5 US-10-631-258-27 Sequence 27, Appl
991 547 98.9 218 5 US-10-631-258-28 Sequence 28, Appl
992 547 98.9 219 4 US-10-698-041-4 Sequence 4, Appl
993 547 98.9 239 5 US-10-737-280-142 Sequence 142, App
994 546 98.7 237 5 US-10-828-782A-16 Sequence 16, Appl
995 545 98.6 106 5 US-10-977-369-140 Sequence 140, App
996 545 98.6 216 5 US-10-916-758-22 Sequence 22, Appl
997 545 98.6 256 5 US-10-901-011-6 Sequence 6, Appl
998 544 98.4 211 3 US-09-974-449-36 Sequence 36, Appl
999 544 98.4 212 4 US-10-281-479A-72 Sequence 72, Appl
1000 544 98.4 212 4 US-10-275-180A-72 Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-09-301-593-20
; Sequence 20, Application US/09301593A
; Publication No. US20020052480A1
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-20

Query Match 100.0%; Score 553; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYKHKYKACVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYKHKYKACVTHQGLSSPVTKSFNRGEC 107

RESULT 2
US-09-811-384-5
; Sequence 5, Application US/09811384
; Patent No. US20020081294A1

Query Match 100.0%; Score 553; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYKHKYKACVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYKHKYKACVTHQGLSSPVTKSFNRGEC 107

RESULT 3
US-09-990-586-97
; Sequence 97, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
```



```
; SEQ ID NO 97
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-97

Query Match      100.0%; Score 553; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 4
US-09-990-586-99
; Sequence 99, Application US/0990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-99

Query Match      100.0%; Score 553; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 5
US-10-121-464-18
; Sequence 18, Application US/10121464
; Publication No. US20030103968A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim International GmbH
; APPLICANT: Boehringer Ingelheim Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer treatment by using FAP-alpha specific antibodies
; FILE REFERENCE: 1-1203ff
; CURRENT APPLICATION NUMBER: US/10/121,464
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/283,868
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Antibody
; OTHER INFORMATION: sequence
US-10-121-464-18

Query Match      100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 6
US-10-269-805-67
; Sequence 67, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-67

Query Match      100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 7
US-10-159-006-20
; Sequence 20, Application US/10159006
; Publication No. US20030143229A1
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652-1890002
; CURRENT APPLICATION NUMBER: US/10/159,006
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 09/301,593
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: EP 98107925.4
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 60/086,049
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
```

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-159-006-20

Query Match          100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
    |||||
Db 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
    |||||

Qy 61 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
    |||||
Db 61 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
    |||||

RESULT 8
US-10-310-113-166
; Sequence 166, Application US/10310113
; Publication No. US20030176664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: NIEVES, ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 166
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-166

Query Match          100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
    |||||
Db 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
    |||||

Qy 61 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
    |||||
Db 61 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
    |||||

RESULT 9
US-10-310-113-168
; Sequence 168, Application US/10310113
; Publication No. US20030176664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: NIEVES, ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
```

```
; TITLE OF INVENTION: THROMBOSES
; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 168
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-168

Query Match          100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
    |||||
Db 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
    |||||

Qy 61 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
    |||||
Db 61 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
    |||||

RESULT 10
US-10-230-880-97
; Sequence 97, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-97

Query Match          100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
    |||||
Db 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
    |||||

Qy 61 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
    |||||
Db 61 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
    |||||

RESULT 11
```

US-10-230-880-99
; Sequence 99, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-99

Query Match 100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 12
US-10-366-709-54
; Sequence 54, Application US/10366709
; Publication No. US20030219433A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, HANS
; APPLICANT: QU, ZHENGXING
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: ANTI-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
; METHODS OF USE
; FILE REFERENCE: 18733/115
; CURRENT APPLICATION NUMBER: US/10/366,709
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/356,132
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/416,232
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-709-54

Query Match 100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107

US-10-404-286-5
; Sequence 5, Application US/10404286
; Publication No. US20040057951A1
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/404,286
; FILING DATE: 31-Mar-2006
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/811384
; FILING DATE: 20-DEC-2000
; APPLICATION NUMBER: 09/251652
; FILING DATE: 17-FEB-2000
; APPLICATION NUMBER: 08/788800
; FILING DATE: 22-JAN-1997
; APPLICATION NUMBER: 60/093038
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, David W.
; REGISTRATION NUMBER: NONE
; REFERENCE/DOCKET NUMBER: P1729C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1739
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-404-286-5

Query Match 100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 14
US-10-656-769-4
; Sequence 4, Application US/10656769
; Publication No. US20040097712A1
; GENERAL INFORMATION:
; APPLICANT: Varnum, Brian
; APPLICANT: Witte, Alison

```
; APPLICANT: Vezina, Chris
; APPLICANT: Wong, Lu Min
; APPLICANT: Qian, Xueming
; TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
; FILE REFERENCE: 01.1554
; CURRENT APPLICATION NUMBER: US/10/656,769
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-656-769-4

Query Match      100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIIPPDSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPDSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 15
US-10-679-620-60
; Sequence 60, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reisl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: huscFabmla6 , see Example 15
US-10-679-620-60

Query Match      100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIIPPDSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPDSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 16
US-10-733-563-112
; Sequence 112, Application US/10733563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Ponath, Paul
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
```

```
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 112
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human C Kappa protein
US-10-733-563-112

Query Match      100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIIPPDSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPDSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 17
US-10-815-449-10
; Sequence 10, Application US/10815449
; Publication No. US20040228859A1
; GENERAL INFORMATION:
; APPLICANT: GRAUS, Ivo
; APPLICANT: KOPETZKI, Erhard
; APPLICANT: KUENKELE, Klaus-Peter
; APPLICANT: MUNDIGL, Olaf
; APPLICANT: PARREN, Paul
; APPLICANT: REERS, Frank
; APPLICANT: SCHUMACHER, Ralf
; APPLICANT: Van de WINKEL, Jan
; APPLICANT: Vugt, Martine
; TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and uses
; FILE REFERENCE: 21655 US2
; CURRENT APPLICATION NUMBER: US/10/815,449
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: US 60/459,837
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US 60/463,003
; PRIOR FILING DATE: 2003-04-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-815-449-10

Query Match      100.0%; Score 553; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIIPPDSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPDSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
```

Db 61 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
|||||

RESULT 18
US-10-684-957-4
; Sequence 4, Application US/10684957
; Publication No. US20050004953A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
; TITLE OF INVENTION: Pathway Inhibitors
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-957-4

Query Match 100.0%; Score 553; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 19
US-10-886-838-8
; Sequence 8, Application US/10886838
; Publication No. US20050008642A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and uses
; TITLE OF INVENTION: thereof
; FILE REFERENCE: 21695
; CURRENT APPLICATION NUMBER: US/10/886,838
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: EP 03015526
; PRIOR FILING DATE: 2003-07-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-886-838-8

Query Match 100.0%; Score 553; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 20
US-10-822-300-9
; Sequence 9, Application US/10822300
; Publication No. US20050014934A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTERATION OF FC γ n BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.CPUS01
; CURRENT APPLICATION NUMBER: US/10/822,300
; CURRENT FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 107
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody
US-10-822-300-9

Query Match 100.0%; Score 553; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 21
US-10-687-118-9
; Sequence 9, Application US/10687118
; Publication No. US20050032114A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTERATION OF FC γ n BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.NFUS04
; CURRENT APPLICATION NUMBER: US/10/687,118
; CURRENT FILING DATE: 2003-10-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 107
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody
US-10-687-118-9

Query Match 100.0%; Score 553; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107

```
RESULT 22
US-10-872-932A-41
; Sequence 41, Application US/10872932A
; Publication No. US20050033029A1
; GENERAL INFORMATION:
; APPLICANT: Jin Lu
; TITLE OF INVENTION: ENGINEERED ANTI-TARGET IMMUNOGLOBULIN DERIVED PROTEINS
; FILE REFERENCE: CEN5031NP
; CURRENT APPLICATION NUMBER: US/10/872,932A
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/483,654
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 41
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-932A-41

Query Match      100.0%; Score 553; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 60
        |||||||
Db      1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 60
        |||||||

Qy      61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
        |||||||
Db      61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
        |||||||

RESULT 23
US-10-891-658-8
; Sequence 8, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,431
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-891-658-8

Query Match      100.0%; Score 553; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 60
        |||||||
Db      1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 60
        |||||||

Qy      61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
        |||||||
Db      61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
        |||||||

RESULT 24
US-10-891-658-8
; Sequence 8, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,431
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-891-658-8

Query Match      100.0%; Score 553; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 60
        |||||||
Db      1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 60
        |||||||

Qy      61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
        |||||||
Db      61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
        |||||||

RESULT 25
US-10-893-576-44
; Sequence 44, Application US/10893576
; Publication No. US20050118643A1
; GENERAL INFORMATION:
; APPLICANT: BURGESS, TERESA L.
; APPLICANT: COXON, ANGELA
; APPLICANT: GREEN, LARRY L.
; APPLICANT: ZHANG, KE
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR
; FILE REFERENCE: 06843.0051-00000
; CURRENT APPLICATION NUMBER: US/10/893,576
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/488,681
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 44
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Human Kappa
; OTHER INFORMATION: Constant Region
US-10-893-576-44

Query Match      100.0%; Score 553; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 60
        |||||||
Db      1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 60
        |||||||

Qy      61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
        |||||||
Db      61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
        |||||||
```

```
US-10-937-596-29
; Sequence 29, Application US/10937596
; Publication No. US20050118169A1
; GENERAL INFORMATION:
; APPLICANT: BARTKE, ILSE
; APPLICANT: CARR, FRANCIS
; APPLICANT: CHIZZONITE, RICHARD ANTHONY
; APPLICANT: EUGUI, ELSIE M.
; APPLICANT: FERTIG, GEORG
; APPLICANT: HAMILTON, ANITA
; APPLICANT: LANZENDOERFER, MARTIN
; APPLICANT: RUEGER, PETRA
; APPLICANT: SCHUMACHER, RALF
; APPLICANT: TRUITT, THERESA PATRICIA
; TITLE OF INVENTION: ANTIBODIES AGAINST INTERLEUKIN-1 RECEPTOR AND USSES THEREOF
; FILE REFERENCE: CD21842-US1
; CURRENT APPLICATION NUMBER: US/10/937,596
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: 60/501,681
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: EP 03029659.4
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-937-596-29

Query Match      100.0%; Score 553; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 60
        |||||||
Db      1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 60
        |||||||

Qy      61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
        |||||||
Db      61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
        |||||||
```

Qy	1	RTVAAPSVEIFPPSDQOLSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD	60
Db	1	RTVAAPSVEIFPPSDQOLSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD	60
Qy	61	SKDSTVSLSGSTLTLSKADYERHKYACEVTHOGLSSPVTKGFNRGEC	107
Db	61	SKDSTVSLSGSTLTLSKADYERHKYACEVTHOGLSSPVTKGFNRGEC	107

```

RESULT 26
US-10-810-881A-40
; Sequence 40, Application US/10810881A
; Publication No. US20050129695A1
; GENERAL INFORMATION:
; APPLICANT: Mercken, Marc; Benson, Jacqueline M.
; TITLE OF INVENTION: ANTI-AMYLOID ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5021 NP
; CURRENT APPLICATION NUMBER: US/10/810.881A
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/458,474
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,469
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,509
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,510
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 40
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(107)
; OTHER INFORMATION: Light chain kappa constant region (Igkc)
US-10-810-881A-40

```

Query Match	100.0%;	Score 553;	DB 5;	Length 107;
Best Local Similarity	100.0%;	Pred. No. 1.9e-51;		
Matches 107;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD	60	
Db	1	RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD	60	
QY	61	SKDSTVLSLTLLSKADYEKHKYACEVTHOGLSSPVTKSFNRGEC	107	
Db	61	SKDSTVLSLTLLSKADYEKHKYACEVTHOGLSSPVTKSFNRGEC	107	

```

RESULT 27
US-10-981-936-40
; Sequence 40, Application US/10981936
; Publication No. US20050232923A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yan; Nakada, Marian T.; Das, Anuk
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING MCP-1 RELATED PATHOLOGIES
; FILE REFERENCE: CEN5041 NP
; CURRENT APPLICATION NUMBER: US/10/981,936
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,370
; PRIOR FILING DATE: 2003/11/05
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver 3.3
; SEQ ID NO 40
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC.FEATURE
; LOCATION: (1)-(107)

```

```
; FEATURE:
; OTHER INFORMATION: mab TGN1412 constant region light chain
US-10-988-207-21

Query Match          100.0%; Score 553; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||

QY 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
   |||||
Db 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
   |||||

RESULT 30
US-10-982-440-67
; Sequence 67, Application US/10982440
; Publication No. US20060018909A1
; GENERAL INFORMATION:
; APPLICANT: Oliner, John
; APPLICANT: Graham, Kevin
; TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
; FILE REFERENCE: 04-881-A
; CURRENT APPLICATION NUMBER: US/10/982,440
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/620,161
; PRIOR FILING DATE: 2004-10-19
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 67
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-440-67

Query Match          100.0%; Score 553; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||

QY 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
   |||||
Db 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
   |||||

RESULT 31
US-10-935-005B-71
; Sequence 71, Application US/10935005B
; Publication No. US20060051844A1
; GENERAL INFORMATION:
; APPLICANT: NESSFOR, George A.; KNIGHT, David; GHAYEB, John; SCALLON, Bernard;
; APPLICANT: HEAVNER, Thomas; HUANG, Chichang
; TITLE OF INVENTION: HUMAN EPO MIMETIC HINGE CORE MIMETIBODIES,
; FILE REFERENCE: CEN5039NP
; CURRENT APPLICATION NUMBER: US/10/935,005B
; CURRENT FILING DATE: 2004-09-03
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 71
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(107)
; OTHER INFORMATION: Light chain kappa constant region (IgKc)
US-10-935-005B-71
```

```
Query Match          100.0%; Score 553; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||

QY 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
   |||||
Db 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
   |||||

RESULT 32
US-11-001-980-4
; Sequence 4, Application US/11001980
; Publication No. US20050136055A1
; GENERAL INFORMATION:
; APPLICANT: Gladue et al., Ronald P.
; TITLE OF INVENTION: CD40 ANTIBODY FORMULATION AND METHODS
; FILE REFERENCE: PC32065A
; CURRENT APPLICATION NUMBER: US/11/001,980
; CURRENT FILING DATE: 2004-12-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: 3.1.1: Human
US-11-001-980-4

Query Match          100.0%; Score 553; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||

QY 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
   |||||
Db 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
   |||||

RESULT 33
US-11-001-980-8
; Sequence 8, Application US/11001980
; Publication No. US20050136055A1
; GENERAL INFORMATION:
; APPLICANT: Gladue et al., Ronald P.
; TITLE OF INVENTION: CD40 ANTIBODY FORMULATION AND METHODS
; FILE REFERENCE: PC32065A
; CURRENT APPLICATION NUMBER: US/11/001,980
; CURRENT FILING DATE: 2004-12-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: 21.4.1: Human
US-11-001-980-8

Query Match          100.0%; Score 553; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||

QY 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
   |||||
Db 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
   |||||
```


Db 61 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 34
US-11-132-143-60
; Sequence 60, Application US/11132143
; Publication No. US20050207977A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/11/132,143
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US/10/679,620
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: huscFabmiA6 , see Example 15
US-11-132-143-60

Query Match 100.0%; Score 553; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Qy 61 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 35
US-11-102-403-23
; Sequence 23, Application US/11102403
; Publication No. US20050226876A1
; GENERAL INFORMATION:
; APPLICANT: GRAUS, YVO
; APPLICANT: HIMBER, JACQUES
; APPLICANT: JANSSEN-MOLENAAR, MIRANDA
; APPLICANT: KLING, DOROTHEE
; APPLICANT: KOPETZKI, ERHARD
; APPLICANT: PAREN, PAUL
; APPLICANT: REBERS, FRANK
; APPLICANT: STEINER, BEAT
; APPLICANT: STERN, ANNE
; APPLICANT: STUBENRAUCH, KAY-GUNNAR
; APPLICANT: VAN DE WINKEL, JAN
; APPLICANT: VAN VUGT, MARTINE
; TITLE OF INVENTION: ANTI-P SELECTIN ANTIBODIES
; FILE REFERENCE: 22354
; CURRENT APPLICATION NUMBER: US/11/102,403
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: EP 04008722.3
; PRIOR FILING DATE: 2004-04-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 23
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-403-23

Query Match 100.0%; Score 553; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Qy 61 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 36
US-11-025-712-5
; Sequence 5, Application US/11025712
; Publication No. US20050255108A1
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/025,712
; FILING DATE: 28-Dec-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/404,286
; FILING DATE: 31-Mar-2003
; APPLICATION NUMBER: 09/811384
; FILING DATE: 20-DEC-2000
; APPLICATION NUMBER: 09/251652
; FILING DATE: 17-FEB-2000
; APPLICATION NUMBER: 08/788800
; FILING DATE: 22-JAN-1997
; APPLICATION NUMBER: 60/093038
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, David W.
; REGISTRATION NUMBER: NONE
; REFERENCE/DOCKET NUMBER: P1729C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1739
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-11-025-712-5

Query Match 100.0%; Score 553; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSTLTLSKADYEHKVVACEVTHQGLSSPVTKSFNRGEC 107
|||||
Db 61 SKDSTYSLSTLTLSKADYEHKVVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 37
US-11-075-351-61
; Sequence 61, Application US/11075351
; Publication No. US20050260716A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Margaret D.
; APPLICANT: Fox, Brian A.
; TITLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS
; TITLE OF INVENTION: METHODS FOR PRODUCING THEM
; FILE REFERENCE: 02-16
; CURRENT APPLICATION NUMBER: US/11/075,351
; CURRENT FILING DATE: 2005-03-08
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-075-351-61

Query Match 100.0%; Score 553; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQMKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQMKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSTLTLSKADYEHKVVACEVTHQGLSSPVTKSFNRGEC 107
|||||
Db 61 SKDSTYSLSTLTLSKADYEHKVVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 38
US-11-061-821-40
; Sequence 40, Application US/11061821
; Publication No. US20050266005A1
; GENERAL INFORMATION:
; APPLICANT: Heavner, George; Li, Li; Oneil, Karyn
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING IL-13 RELATED PATHOLOGIES
; FILE REFERENCE: CEN5048 NP
; CURRENT APPLICATION NUMBER: US/11/061,821
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 60/548,648
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver 3.3
; SEQ ID NO 40
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(107)
; OTHER INFORMATION: Light chain kappa constant region (IgKc)
US-11-061-821-40

Query Match 100.0%; Score 553; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQMKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQMKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSTLTLSKADYEHKVVACEVTHQGLSSPVTKSFNRGEC 107
|||||

Db 61 SKDSTYSLSTLTLSKADYEHKVVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 39
US-11-102-621-9
; Sequence 9, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FORN BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 107
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody
US-11-102-621-9

Query Match 100.0%; Score 553; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQMKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQMKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSTLTLSKADYEHKVVACEVTHQGLSSPVTKSFNRGEC 107
|||||
Db 61 SKDSTYSLSTLTLSKADYEHKVVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 40
US-11-122-622-97
; Sequence 97, Application US/11122622
; Publication No. US20060039901A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/11/122,622
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: US/09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-122-622-97

Query Match 100.0%; Score 553; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQMKVDNALQSGNSQESVTEQD 60
|||||

```
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYLSSTLTLSKADYKHKYKACVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYKHKYKACVTHQGLSSPVTKSFNRGEC 107

RESULT 41
US-11-122-622-99
; Sequence 99, Application US/11122622
; Publication No. US20060039901A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/11/122,622
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: US/09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 99
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-122-622-99

Query Match 100.0%; Score 553; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYKHKYKACVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYKHKYKACVTHQGLSSPVTKSFNRGEC 107

RESULT 42
US-11-218-813-134
; Sequence 134, Application US/11218813
; Publication No. US20060062793A1
; GENERAL INFORMATION:
; APPLICANT: Webb, Iain J.
; APPLICANT: Horvath, Christopher J.
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 10448-163005
; CURRENT APPLICATION NUMBER: US/11/218,813
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US2004/006543
; PRIOR FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain variable and constant region of deJ591.
US-11-218-813-134

Query Match 100.0%; Score 553; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
```

```
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYLSSTLTLSKADYKHKYKACVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYKHKYKACVTHQGLSSPVTKSFNRGEC 107

RESULT 43
US-11-149-309-18
; Sequence 18, Application US/11149309
; Publication No. US20060063228A1
; GENERAL INFORMATION:
; APPLICANT: Kasaian, Marion T.
; APPLICANT: Tchistiakova, Lioudmila
; APPLICANT: Veldman, Geertuida M.
; APPLICANT: Marquette, Kimberly Ann
; APPLICANT: Tan, Xiang-Yang
; APPLICANT: Donaldson, Debra D.
; APPLICANT: Shane, Tania
; APPLICANT: Tam, Amy Szepui
; APPLICANT: Peyfant, Eric
; APPLICANT: Wood, Nancy L.
; APPLICANT: Fitz, Lori J.
; APPLICANT: Widom, Angela M.
; APPLICANT: Parris, Kevin D.
; APPLICANT: Goldman, Samuel J.
; TITLE OF INVENTION: Antibodies against Human Interleukin-13 and Uses Therefor
; FILE REFERENCE: 16158-048001 / AM101493
; CURRENT APPLICATION NUMBER: US/11/149,309
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/578,473
; PRIOR FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: US 60/581,375
; PRIOR FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: US 60/578,736
; PRIOR FILING DATE: 2004-06-09
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: The "r" in position #1 represents amino acid residue #112 when
; OTHER INFORMATION: the sequence follows residue #111 of, e.g., SEQ ID NOS:11 or 12.
US-11-149-309-18

Query Match 100.0%; Score 553; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYKHKYKACVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYKHKYKACVTHQGLSSPVTKSFNRGEC 107

RESULT 44
US-10-272-899A-12
; Sequence 12, Application US/10272899A
; Publication No. US2004003561A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa L.
; APPLICANT: Healy, Judith Jacques
; APPLICANT: Newman, Walter
; APPLICANT: Ponath, Paul
; APPLICANT: Bruce Keyt
```

```
; TITLE OF INVENTION: IMMUNOGLOBULIN DNA CASSETTE MOLECULES.
; TITLE OF INVENTION: MONOBODY CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS OF
; TITLE OF INVENTION: USE THEREFOR
; FILE REFERENCE: MPI01-244P2RM
; CURRENT APPLICATION NUMBER: US/10/272,899A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/350,166
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/392,364
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human C Kappa protein
US-10-733-563-116

Query Match          100.0%; Score 553; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||
Db 3 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 62
   |||||

QY 61 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107
   |||||
Db 63 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 109
   |||||

RESULT 45
US-10-733-563-116
; Sequence 116, Application US/10733563
; Publication No. US20040151721a1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 116
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human C Kappa protein
US-10-733-563-116

Query Match          100.0%; Score 553; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||
Db 3 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 62
   |||||

QY 61 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107
   |||||
Db 63 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 109
   |||||
```

```
RESULT 46
US-11-024-251-27
; Sequence 27, Application US/11024251
; Publication No. US20050266425a1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Paris, Mark
; TITLE OF INVENTION: Methods for Producing and Identifying Multispecific Antibodies
; FILE REFERENCE: 1843.0230001
; CURRENT APPLICATION NUMBER: US/11/024,251
; CURRENT FILING DATE: 2004-12-29
; PRIOR APPLICATION NUMBER: 60/533,241
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: cLambda Constant Domain
US-11-024-251-27

Query Match          100.0%; Score 553; DB 6; Length 110;
Best Local Similarity 100.0%; Pred. No. 2e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||
Db 4 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 63
   |||||

QY 61 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107
   |||||
Db 64 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 110
   |||||

RESULT 47
US-10-272-899A-66
; Sequence 66, Application US/10272899A
; Publication No. US20040033561a1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa L.
; APPLICANT: Healy, Judith Jacques
; APPLICANT: Newman, Walter
; APPLICANT: Ponath, Paul
; APPLICANT: Bruce Keyt
; TITLE OF INVENTION: IMMUNOGLOBULIN DNA CASSETTE MOLECULES,
; TITLE OF INVENTION: MONOBODY CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS OF
; TITLE OF INVENTION: USE THEREFOR
; FILE REFERENCE: MPI01-244P2RM
; CURRENT APPLICATION NUMBER: US/10/272,899A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/350,166
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/392,364
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin cassette protein sequence
; OTHER INFORMATION: Leader-HuKc_57
US-10-272-899A-66

Query Match          100.0%; Score 553; DB 4; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
```

Db 28 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 87
Qy 61 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
Db 88 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 134

RESULT 48
US-10-011-125-5
; Sequence 5, Application US/10011125
; Publication No. US20020142388A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 5
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.

US-10-011-125-5
Query Match 100.0%; Score 553; DB 4; Length 212;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 106 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165

Qy 61 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
Db 166 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 212

RESULT 49
US-10-320-231A-77
; Sequence 77, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; TITLE OF INVENTION: Treatment Of Asthma
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 77
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic sequence

US-10-320-231A-77
Query Match 100.0%; Score 553; DB 4; Length 212;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Db 106 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165
Qy 61 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
Db 166 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 212

RESULT 50
US-10-867-506-77
; Sequence 77, Application US/10867506
; Publication No. US20050112698A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; APPLICANT: Delaria, Kathy
; APPLICANT: Yan, Kelly
; APPLICANT: Wong, Teresa
; APPLICANT: Longphre, Malinda
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; TITLE OF INVENTION: Treatment Of Asthma
; FILE REFERENCE: 11334*10
; CURRENT APPLICATION NUMBER: US/10/867,506
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 10/320,231
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 77
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic sequence

US-10-867-506-77
Query Match 100.0%; Score 553; DB 5; Length 212;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 106 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165

Qy 61 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
Db 166 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 212

RESULT 51
US-09-796-848A-38
; Sequence 38, Application US/09796848A
; Patent No. US20020098189A1
; GENERAL INFORMATION:
; APPLICANT: Young, James F.
; APPLICANT: Johnson, Leslie S.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
; TITLE OF INVENTION: Producing Them
; FILE REFERENCE: 469201-526
; CURRENT APPLICATION NUMBER: US/09/796,848A
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: U.S. 60/186,252
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 213
; TYPE: PRT

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Light chain of
; OTHER INFORMATION: high potency antibody.
US-09-796-848A-38

Query Match          100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 52
US-09-796-848A-40
; Sequence 40, Application US/09796848A
; Patent No. US20020098189A1
; GENERAL INFORMATION:
; APPLICANT: Young, James F.
; APPLICANT: Johnson, Leslie S.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffry D.
; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
; FILE REFERENCE: 469201-526
; CURRENT APPLICATION NUMBER: US/09/796,848A
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: U.S. 60/186,252
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Light chain of
; OTHER INFORMATION: high potency antibody.
US-09-796-848A-40

Query Match          100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 53
US-09-796-848A-42
; Sequence 42, Application US/09796848A
; Patent No. US20020098189A1
; GENERAL INFORMATION:
; APPLICANT: Young, James F.
; APPLICANT: Johnson, Leslie S.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffry D.
; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
; FILE REFERENCE: 469201-526
; CURRENT APPLICATION NUMBER: US/09796848A
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: U.S. 60/186,252
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Light chain of
; OTHER INFORMATION: high potency antibody.
US-09-796-848A-42

Query Match          100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 54
US-09-796-848A-44
; Sequence 44, Application US/09796848A
; Patent No. US20020098189A1
; GENERAL INFORMATION:
; APPLICANT: Young, James F.
; APPLICANT: Johnson, Leslie S.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffry D.
; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
; FILE REFERENCE: 469201-526
; CURRENT APPLICATION NUMBER: US/09/796,848A
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: U.S. 60/186,252
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Light chain of
; OTHER INFORMATION: high potency antibody.
US-09-796-848A-44

Query Match          100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 55
US-09-796-848A-46
; Sequence 46, Application US/09796848A
; Patent No. US20020098189A1
```

```
; CURRENT APPLICATION NUMBER: US/09/796,848A
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: U.S. 60/186,252
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Light chain of
; OTHER INFORMATION: high potency antibody.
US-09-796-848A-42

Query Match          100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 54
US-09-796-848A-44
; Sequence 44, Application US/09796848A
; Patent No. US20020098189A1
; GENERAL INFORMATION:
; APPLICANT: Young, James F.
; APPLICANT: Johnson, Leslie S.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffry D.
; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
; FILE REFERENCE: 469201-526
; CURRENT APPLICATION NUMBER: US/09/796,848A
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: U.S. 60/186,252
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Light chain of
; OTHER INFORMATION: high potency antibody.
US-09-796-848A-44

Query Match          100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 55
US-09-796-848A-46
; Sequence 46, Application US/09796848A
; Patent No. US20020098189A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Young, James F.
; APPLICANT: Johnson, Leslie S.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
; FILE REFERENCE: 469201-526
; CURRENT APPLICATION NUMBER: US/09/796,848A
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: U.S. 60/186,252
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Light chain of
; OTHER INFORMATION: high potency antibody.
US-09-796-848A-46

Query Match      100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db      107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy      61 SKDSTYLSSTLTLSKADYEHKHKYVACEVTHQGLSSPVTKSPNRGEC 107
Db      167 SKDSTYLSSTLTLSKADYEHKHKYVACEVTHQGLSSPVTKSPNRGEC 213

Query Match      100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db      107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy      61 SKDSTYLSSTLTLSKADYEHKHKYVACEVTHQGLSSPVTKSPNRGEC 107
Db      167 SKDSTYLSSTLTLSKADYEHKHKYVACEVTHQGLSSPVTKSPNRGEC 213

RESULT 56
US-09-796-848A-48
; Sequence 48, Application US/09796848A
; Patent No. US20020098189A1
; GENERAL INFORMATION:
; APPLICANT: Young, James F.
; APPLICANT: Johnson, Leslie S.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
; FILE REFERENCE: 469201-526
; CURRENT APPLICATION NUMBER: US/09/796,848A
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: U.S. 60/186,252
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Light chain of
; OTHER INFORMATION: high potency antibody.
US-09-796-848A-48

Query Match      100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db      107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
```

```

Qy      61 SKDSTYLSSTLTLSKADYEHKHKYVACEVTHQGLSSPVTKSPNRGEC 107
Db      167 SKDSTYLSSTLTLSKADYEHKHKYVACEVTHQGLSSPVTKSPNRGEC 213

RESULT 57
US-09-796-848A-50
; Sequence 50, Application US/09796848A
; Patent No. US20020098189A1
; GENERAL INFORMATION:
; APPLICANT: Young, James F.
; APPLICANT: Johnson, Leslie S.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
; FILE REFERENCE: 469201-526
; CURRENT APPLICATION NUMBER: US/09/796,848A
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: U.S. 60/186,252
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Light chain of
; OTHER INFORMATION: high potency antibody.
US-09-796-848A-50

Query Match      100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db      107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy      61 SKDSTYLSSTLTLSKADYEHKHKYVACEVTHQGLSSPVTKSPNRGEC 107
Db      167 SKDSTYLSSTLTLSKADYEHKHKYVACEVTHQGLSSPVTKSPNRGEC 213

RESULT 58
US-09-796-848A-52
; Sequence 52, Application US/09796848A
; Patent No. US20020098189A1
; GENERAL INFORMATION:
; APPLICANT: Young, James F.
; APPLICANT: Johnson, Leslie S.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
; FILE REFERENCE: 469201-526
; CURRENT APPLICATION NUMBER: US/09/796,848A
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: U.S. 60/186,252
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Light chain of
; OTHER INFORMATION: high potency antibody.
US-09-796-848A-52
```


Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Db 107 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSSITLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 |||
Db 167 SKDSTYSLSSITLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213

```

RESULT 63
US-09-996-288-215
; Sequence 215, Application US/09996288
; Patent NO. US2002017126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996, 288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 215
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-215

```

RESULT 64
 US-09-996-288-217
 ; Sequence 217, Application US/09996288
 ; Patent No. US20020177126A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, James
 ; APPLICANT: Scott, Koenig
 ; APPLICANT: Leslie, Johnson
 ; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
 ; TITLE OF INVENTION: and Treatment
 ; FILE REFERENCE: 10271-047-999
 ; CURRENT APPLICATION NUMBER: US/09/996,288
 ; CURRENT FILING DATE: 2001-11-28
 ; NUMBER OF SEQ ID NOS: 259
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 217
 ; LENGTH: 213
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-996-288-217

Qy	61	SKDSTYSLSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC	107
Db	167	SKDSTYSLSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC	213

```

RESULT 65
US-09-996-288-219
; Sequence 219, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koening
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Admin
; TITLE OF INVENTION: Methods and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/99
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 219
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-219

```

```

RESULT 66
US-09-996-288-221
; Sequence 221, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-959
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 221
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-221

```

Qy	1	RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD	60
Db	107	RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD	166
Qy	61	SKDSTVLSLTLLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC	107
Db	167	SKDSTVLSLTLLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC	213

```
RESULT 67
US-09-996-288-223
; Sequence 223, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 223
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-223

Query Match      100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 68
US-09-996-288-225
; Sequence 225, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 225
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-225

Query Match      100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 69
US-09-996-288-227
; Sequence 227, Application US/09996288
; Patent No. US20020177126A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 227
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-227

Query Match      100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 70
US-09-996-288-229
; Sequence 229, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 229
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-229

Query Match      100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 71
US-09-996-288-231
; Sequence 231, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
```

```

; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 231
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-231

Query Match 100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 72
US-09-996-288-233
; Sequence 233, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 233
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-233

Query Match 100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 73
US-09-996-288-235
; Sequence 235, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
```

```

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 235
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-235

Query Match 100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 74
US-09-996-288-237
; Sequence 237, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 237
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-237

Query Match 100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 75
US-09-996-288-239
; Sequence 239, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 239
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
```


Qy	61	SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC	107
Db	167	SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC	213

RESULT 80
 US-09-996-288-251
 ; Sequence 251, Application US/09996288
 ; Patent No. US20020177126A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, James
 ; APPLICANT: Scott, Koenig
 ; APPLICANT: Leslie, Johnson
 ; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
 ; TITLE OF INVENTION: and Treatment
 ; FILE REFERENCE: 10271-047-999
 ; CURRENT APPLICATION NUMBER: US/09/996,288
 ; CURRENT FILING DATE: 2001-11-28
 ; NUMBER OF SEQ ID NOS: 259
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 251
 ; LENGTH: 213
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-996-288-251

```

RESULT 81
US-09-996-288-253
; Sequence 253, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 253
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-253

```

```

RESULT 82
US-09-996-288-255
; Sequence 255, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing for
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 255
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-255

```

```

RESULT 83
US-09-996-288-257
; Sequence 257, Application US/09996288
; Patent NO. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 257
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-257

```

RESULT 84
US-09-996-265-209
; Sequence 209, Application US/09995265
; Publication No. US20030091584A1
; GENERAL INFORMATION:


```

; SEQ ID NO 217
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-217

Query Match      100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 107 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 167 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 89
US-09-996-265-219
; Sequence 219, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 219
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-219

Query Match      100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 107 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 167 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 90
US-09-996-265-221
; Sequence 221, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 221
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-221
```

```

Query Match      100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 107 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 167 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 91
US-09-996-265-223
; Sequence 223, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 223
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-223

Query Match      100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 107 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 167 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 92
US-09-996-265-225
; Sequence 225, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 225
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-225

Query Match      100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVIVCLNNFYPRKVKVQVKNALQSGNSQESVTEQD 60
pb 107 RTVAAPSVFIFPPSDEQLKSGTASVIVCLNNFYPRKVKVQVKNALQSGNSQESVTEQD 166

[illegible]

```

RESULT 93
US-09-996-265-227
; Sequence 227, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 227
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-996-265-227

```

QY 61 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107
 |||||
 Db 167 SKDSTYSLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 213
 |||||

```

RESULT 94
US-09-996-265-229
; Sequence 229, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 229
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-996-265-229

```

61 SKDSTYSLSSLTLTLTKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 107 Qv

db 167 SKDSTYSLSTLTLISKADYEKKHVAACEVTHOGLSSPVTXSNRGEC 213

```

RESULT 95
US-09-996-265-231
; Sequence 231, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Adminsteri
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 231
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-231

```

Qy 61 SKDSTYSLSTLTLSKADYEHKVACEVTHQGLSSPVTKSFNRGEC 107
| | | | |
pB 167 SKDSTYSLSTLTLSKADYEHKVACEVTHQGLSSPVTKSFNRGEC 213
| | | | |

```

RESULT 96
US-09-996-265-233
; Sequence 233, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Adminsterin
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 233
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-233

```

Qy 61 SKDSTYLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
|||
167 SKDSTYLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 213
pb

RESULT 97


```
US-09-996-265-235
; Sequence 235, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 235
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-235

Query Match 100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 98
US-09-996-265-237
; Sequence 237, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 237
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-237

Query Match 100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 99
US-09-996-265-239
; Sequence 239, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
```

```
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 239
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-239

Query Match 100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 100
US-09-996-285-241
; Sequence 241, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-285-241

Query Match 100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

Search completed: June 12, 2006, 17:30:48
Job time : 111.654 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 12:32:32 ; Search time 3.6952 Seconds
(without alignments)
366.103 Million cell updates/sec

Title: US-10-733-563-112
Perfect score: 553
Sequence: 1 RTVAAPSVFIPPPSDEQLK.....EVTHQGLSSPVTKSFNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 64916 seqs, 12643201 residues

Total number of hits satisfying chosen parameters: 64916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_New.*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	107	6	US-10-983-104-7
2	553	100.0	107	7	US-11-091-234A-40
3	553	100.0	107	7	US-11-219-563-134
4	553	100.0	107	7	US-11-291-140-43
5	553	100.0	213	7	US-11-254-182-63
6	553	100.0	213	7	US-11-254-182-64
7	553	100.0	213	7	US-11-106-762-3
8	553	100.0	213	7	US-11-106-762-24
9	553	100.0	213	7	US-11-106-762-33
10	553	100.0	213	7	US-11-106-762-35
11	553	100.0	213	7	US-11-106-762-38
12	553	100.0	213	7	US-11-238-281-13
13	553	100.0	213	7	US-11-238-281-28
14	553	100.0	213	7	US-11-238-281-30
15	553	100.0	213	7	US-11-263-230-209
16	553	100.0	213	7	US-11-263-230-211
17	553	100.0	213	7	US-11-263-230-213
18	553	100.0	213	7	US-11-263-230-215
19	553	100.0	213	7	US-11-263-230-217
20	553	100.0	213	7	US-11-263-230-219
21	553	100.0	213	7	US-11-263-230-221
22	553	100.0	213	7	US-11-263-230-223
23	553	100.0	213	7	US-11-263-230-225
24	553	100.0	213	7	US-11-263-230-227
25	553	100.0	213	7	US-11-263-230-229

26	553	100.0	213	7	US-11-263-230-231	Sequence 231, App
27	553	100.0	213	7	US-11-263-230-233	Sequence 233, App
28	553	100.0	213	7	US-11-263-230-235	Sequence 235, App
29	553	100.0	213	7	US-11-263-230-237	Sequence 237, App
30	553	100.0	213	7	US-11-263-230-239	Sequence 239, App
31	553	100.0	213	7	US-11-263-230-241	Sequence 241, App
32	553	100.0	213	7	US-11-263-230-243	Sequence 243, App
33	553	100.0	213	7	US-11-263-230-245	Sequence 245, App
34	553	100.0	213	7	US-11-263-230-247	Sequence 247, App
35	553	100.0	213	7	US-11-263-230-249	Sequence 249, App
36	553	100.0	213	7	US-11-263-230-251	Sequence 251, App
37	553	100.0	213	7	US-11-263-230-253	Sequence 253, App
38	553	100.0	213	7	US-11-263-230-255	Sequence 255, App
39	553	100.0	213	7	US-11-263-230-257	Sequence 257, App
40	553	100.0	213	7	US-11-263-230-306	Sequence 306, App
41	553	100.0	213	7	US-11-263-230-312	Sequence 312, App
42	553	100.0	213	7	US-11-263-230-318	Sequence 318, App
43	553	100.0	213	7	US-11-263-230-324	Sequence 324, App
44	553	100.0	213	7	US-11-263-230-330	Sequence 330, App
45	553	100.0	213	7	US-11-263-230-333	Sequence 333, App

ALIGNMENTS

RESULT 1

US-10-983-104-7
; Sequence 7, Application US/10983104
; Publication No. US20060099203A1
; GENERAL INFORMATION:
; APPLICANT: Pease, Larry
; APPLICANT: Van Keulen, Virginia
; APPLICANT: Ciric, Bogoljub
; TITLE OF INVENTION: B7-DC Binding Antibody
; FILE REFERENCE: 07039-558001
; CURRENT APPLICATION NUMBER: US/10/983,104
; CURRENT FILING DATE: 2004-11-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-983-104-7

Query Match 100.0%; Score 553; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.3e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQMKVDNALQSGNSQESVTEQD	60
Db	1	RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQMKVDNALQSGNSQESVTEQD	60
Qy	61	SKDSTYLSSTLTLSKADYEHKHYACVTHQGLSSPVTKSFNRGEC	107
Db	61	SKDSTYLSSTLTLSKADYEHKHYACVTHQGLSSPVTKSFNRGEC	107

RESULT 2

US-11-091-234A-40
; Sequence 40, Application US/11091234A
; Publication No. US2006008845A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Jin
; TITLE OF INVENTION: METHOD AND APPARATUS FOR ANALYZING AND GENERATING
; TITLE OF INVENTION: HUMAN ANTIBODY AMINO ACID AND NUCLEIC ACID SEQUENCES
; FILE REFERENCE: CEN5052NP
; CURRENT APPLICATION NUMBER: US/11/091,234A
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/558,090
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in version 3.3

US-11-254-182-63

Query Match 100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 7.8e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
|||||
DB 107 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
|||||

QY 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
|||||

DB 167 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 213
|||||

RESULT 6

US-11-254-182-64
; Sequence 64, Application US/11254182
; Publication No. US2006008823A1
; GENERAL INFORMATION:
; APPLICANT: ANDYA, JAMES
; APPLICANT: GWEE, SHIANG C.
; APPLICANT: LIU, JUN
; APPLICANT: SHEN, YE
; TITLE OF INVENTION: ANTIBODY FORMULATIONS
; FILE REFERENCE: P2104R1
; CURRENT APPLICATION NUMBER: US/11/254,182
; CURRENT FILING DATE: 2005-10-19
; PRIOR APPLICATION NUMBER: US 60/620,413
; PRIOR FILING DATE: 2004-10-20
; NUMBER OF SEQ ID NOS: 74
; SEQ ID NO 64
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.

US-11-254-182-64

Query Match 100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 7.8e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
|||||

DB 107 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
|||||

QY 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
|||||

DB 167 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 213
|||||

RESULT 7

US-11-106-762-3
; Sequence 3, Application US/11106762
; Publication No. US20060099662A1
; GENERAL INFORMATION:
; APPLICANT: CHUNTHARAPAI, ANAN ET AL.
; TITLE OF INVENTION: ASSAY FOR ANTIBODIES
; FILE REFERENCE: P2075R1
; CURRENT APPLICATION NUMBER: US/11/106,762
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,193
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 3
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized

US-11-106-762-3

Query Match 100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 7.8e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
|||||

DB 107 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
|||||

QY 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
|||||

DB 167 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 213
|||||

RESULT 8

US-11-106-762-24
; Sequence 24, Application US/11106762
; Publication No. US20060099662A1
; GENERAL INFORMATION:
; APPLICANT: CHUNTHARAPAI, ANAN ET AL.
; TITLE OF INVENTION: ASSAY FOR ANTIBODIES
; FILE REFERENCE: P2075R1
; CURRENT APPLICATION NUMBER: US/11/106,762
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,193
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 24
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized

US-11-106-762-24

Query Match 100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 7.8e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
|||||

DB 107 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
|||||

QY 61 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 107
|||||

DB 167 SKDSTYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 213
|||||

RESULT 9

US-11-106-762-33
; Sequence 33, Application US/11106762
; Publication No. US20060099662A1
; GENERAL INFORMATION:
; APPLICANT: CHUNTHARAPAI, ANAN ET AL.
; TITLE OF INVENTION: ASSAY FOR ANTIBODIES
; FILE REFERENCE: P2075R1
; CURRENT APPLICATION NUMBER: US/11/106,762
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,193
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 33
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized

US-11-106-762-33

Query Match 100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 7.8e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
|||||

```
|||||
Db 107 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107
|||||
Db 167 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 10
US-11-106-762-35
; Sequence 35, Application US/11106762
; Publication No. US20060099662A1
; GENERAL INFORMATION:
; APPLICANT: CHUNTHARAPAI, ANAN ET AL.
; TITLE OF INVENTION: ASSAY FOR ANTIBODIES
; FILE REFERENCE: P2075R1
; CURRENT APPLICATION NUMBER: US/11/106,762
; PRIOR FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,193
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 35
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-106-762-35

Query Match 100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 7.8e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
|||||
Db 107 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107
|||||
Db 167 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 11
US-11-106-762-38
; Sequence 38, Application US/11106762
; Publication No. US20060099662A1
; GENERAL INFORMATION:
; APPLICANT: CHUNTHARAPAI, ANAN ET AL.
; TITLE OF INVENTION: ASSAY FOR ANTIBODIES
; FILE REFERENCE: P2075R1
; CURRENT APPLICATION NUMBER: US/11/106,762
; PRIOR FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,193
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 38
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-106-762-38

Query Match 100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 7.8e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
|||||
Db 107 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107
|||||
```

```
Db 167 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 12
US-11-238-281-13
; Sequence 13, Application US/11238281
; Publication No. US20060110387A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; TITLE OF INVENTION: METHOD FOR TREATING VASCULITIS
; FILE REFERENCE: P2177R1
; CURRENT APPLICATION NUMBER: US/11/238,281
; CURRENT FILING DATE: 2005-09-28
; PRIOR APPLICATION NUMBER: US 60/616,104
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NO 13
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-238-281-13

Query Match 100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 7.8e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
|||||
Db 107 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107
|||||
Db 167 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 13
US-11-238-281-28
; Sequence 28, Application US/11238281
; Publication No. US20060110387A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; TITLE OF INVENTION: METHOD FOR TREATING VASCULITIS
; FILE REFERENCE: P2177R1
; CURRENT APPLICATION NUMBER: US/11/238,281
; CURRENT FILING DATE: 2005-09-28
; PRIOR APPLICATION NUMBER: US 60/616,104
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NO 28
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-238-281-28

Query Match 100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 7.8e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
|||||
Db 107 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107
|||||
Db 167 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 14
US-11-238-281-30
```

```

Qy 1 RVAPAPSVFI PPPDDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQD 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 107 RVAPAPSVFI PPPDDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQD 166
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 SKDSTYSLSSTLTLSKADYEKKHYACVETHQGLSSPVTKSFNRGEC 107
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 167 SKDSTYSLSSTLTLSKADYEKKHYACVETHQGLSSPVTKSFNRGEC 213
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Search completed: June 10, 2006, 12:39:09
Job time : 4.6952 secs

```

Search completed: June 10, 2006, 12:39:09
Job time : 4.6952 secs

THIS PAGE BLANK (USPTO)